



## SEQUENCE LISTING

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TECH CENTER 1600/2900

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<120> Essential Genes and Gene Products for Identifying, Developing and Optimizing Immunological and Pharmacological Active Ingredients for the Treatment of Microbial Infections

<130> 2923-514

<140> 09/980,116

<141> 2001-11-30

<160> 263

<170> PatentIn version 3.2

<210> 1

<211> 873

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(873)

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acg	att	gtt	att	gtg	ctg	ttg	gtt	atc	ttt	ttt	atc	gcg	caa	gcc	ttt	96
Thr	Ile	Val	Ile	Val	Leu	Leu	Val	Ile	Phe	Phe	Ile	Ala	Gln	Ala	Phe	
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atc	att	ccc	tct	cgc	tct	atg	gtt	ggc	acg	ctc	tat	gag	ggc	gac	atg	144
Ile	Ile	Pro	Ser	Arg	Ser	Met	Val	Gly	Thr	Leu	Tyr	Glu	Gly	Asp	Met	
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ctc	ttt	gtc	aaa	aag	ttt	tct	tac	ggc	ata	ccc	att	cct	aaa	atc	cca	192
Leu	Phe	Val	Lys	Lys	Phe	Ser	Tyr	Gly	Ile	Pro	Ile	Pro	Lys	Ile	Pro	
	50					55					60					

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Trp	Ile	Glu	Leu	Pro	Val	Met	Pro	Asp	Phe	Lys	Asn	Asn	Gly	His	Leu	
65					70					75				80		

ata	gag	ggg	gat	cgc	cct	aag	cgt	ggc	gaa	gtg	gtg	gtg	ttt	atc	cct	288
Ile	Glu	Gly	Asp	Arg	Pro	Lys	Arg	Gly	Glu	Val	Val	Val	Phe	Ile	Pro	
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ccc cat gaa aaa aag tct tac tat gtt aaa agg aat ttt gcc att gga	336
Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe Ala Ile Gly	
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ggc gat gag gtg ttg ttc act aat gag ggt ttt tat ttg cac cct ttt	384
Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr Leu His Pro Phe	
115 120 125	
gag agc gac acg gac aaa aat tac atc gct aaa cat tac cct aac gcc	432
Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His Tyr Pro Asn Ala	
130 135 140	
atg aca aaa gaa ttt atg ggt aaa att ttt gtt tta aac cct tat aaa	480
Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu Asn Pro Tyr Lys	
145 150 155 160	
aat gag cat ccg ggt atc cat tac caa aaa gac aat gaa acc ttc cac	528
Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn Glu Thr Phe His	
165 170 175	
tta atg gag caa tta gcc act caa ggc gca gaa gct aat atc agc atg	576
Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala Asn Ile Ser Met	
180 185 190	
caa ctc att caa atg gag ggc gaa aag gtg ttt tat aag aaa atc aat	624
Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr Lys Lys Ile Asn	
195 200 205	
gac gat gaa ttt ttc atg atc ggc gac aac aga gac aat tct agc gac	672
Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp Asn Ser Ser Asp	
210 215 220	
tcg cgc ttt tgg ggg agt gtg gct tat aaa aac atc gtg ggt tcg cca	720
Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile Val Gly Ser Pro	
225 230 235 240	
tgg ttt gtt tat ttc agt ttg agt tta aaa aat agc cta gaa atg gat	768
Trp Phe Val Tyr Phe Ser Leu Ser Leu Lys Asn Ser Leu Glu Met Asp	
245 250 255	
gca gaa aat aac cct aaa aaa cgc tat ctg gtg cgt tgg gaa cgc atg	816
Ala Glu Asn Asn Pro Lys Lys Arg Tyr Leu Val Arg Trp Glu Arg Met	
260 265 270	
ttt aaa agc gtt gga ggc tta gaa aaa atc att aaa aaa gaa aac gca	864
Phe Lys Ser Val Gly Gly Leu Glu Lys Ile Ile Lys Lys Glu Asn Ala	
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Thr His	
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Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr Glu Gly Asp Met  
 35 40 45

Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile Pro Lys Ile Pro  
 50 55 60

Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn Gly His Leu  
 65 70 75 80

Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val Val Phe Ile Pro  
 85 90 95

Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe Ala Ile Gly  
 100 105 110

Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr Leu His Pro Phe  
 115 120 125

Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His Tyr Pro Asn Ala  
 130 135 140

Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu Asn Pro Tyr Lys  
 145 150 155 160

Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn Glu Thr Phe His  
 165 170 175

Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala Asn Ile Ser Met  
 180 185 190

Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr Lys Lys Ile Asn

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Trp	Phe	Val	Tyr	Phe	Ser	Leu	Ser	Leu	Lys	Asn	Ser	Leu	Glu	Met	Asp
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Ala	Glu	Asn	Asn	Pro	Lys	Lys	Arg	Tyr	Leu	Val	Arg	Trp	Glu	Arg	Met
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Phe	Lys	Ser	Val	Gly	Gly	Leu	Glu	Lys	Ile	Ile	Lys	Lys	Glu	Asn	Ala
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Thr	His														
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ttg atg att tct tta ccg gta tta tta gcg ggc tta gtg gtg ggg cta	96
Leu Met Ile Ser Leu Pro Val Leu Leu Ala Gly Leu Val Val Gly Leu	
20 25 30	
tta gtc agt att ttt caa gcg acc act caa atc aat gaa atg acc ttg	144
Leu Val Ser Ile Phe Gln Ala Thr Thr Gln Ile Asn Glu Met Thr Leu	
35 40 45	
tct ttt gtg cct aag att tta gcc gtg att ggg gtg ctg att tta acc	192
Ser Phe Val Pro Lys Ile Leu Ala Val Ile Gly Val Leu Ile Leu Thr	
50 55 60	
atg ccg tgg atg act aac atg ctt tta gat tac acc aaa acc tta atc	240



Met Pro Trp Met Thr Asn Met Leu Leu Asp Tyr Thr Lys Thr Leu Ile  
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267

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20 25 30

Leu Val Ser Ile Phe Gln Ala Thr Thr Gln Ile Asn Glu Met Thr Leu  
35 40 45

Ser Phe Val Pro Lys Ile Leu Ala Val Ile Gly Val Leu Ile Leu Thr  
50 55 60

Met Pro Trp Met Thr Asn Met Leu Leu Asp Tyr Thr Lys Thr Leu Ile  
65 70 75 80

Lys Leu Ile Pro Lys Ile Ile Gly  
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<210> 5  
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48

agt att ttt tta ggc atg atg agt att ttt tac gct tcc agt tac caa

96

Ser	Ile	Phe	Leu	Gly	Met	Met	Ser	Ile	Phe	Tyr	Ala	Ser	Ser	Tyr	Gln	
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Phe	Val	Met	Ala	Cys	Trp	Leu	Val	Val	Ala	Ser	Leu	Ile	Leu	Asp	Gly	
		35					40					45				
ctt	gat	ggg	cgt	gtc	gca	agg	ctt	acc	aac	acc	acc	agc	aag	ttt	ggg	192
Leu	Asp	Gly	Arg	Val	Ala	Arg	Leu	Thr	Asn	Thr	Thr	Ser	Lys	Phe	Gly	
	50					55					60					
ata	gaa	ttt	gac	tca	ctg	gct	gat	gta	atc	gct	ttt	ggg	gta	gcc	cca	240
Ile	Glu	Phe	Asp	Ser	Leu	Ala	Asp	Val	Ile	Ala	Phe	Gly	Val	Ala	Pro	
65					70				75						80	
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Ser	Leu	Ile	Thr	Tyr	Phe	Tyr	Val	Gly	Tyr	Asn	Phe	Gly	Arg	Ile	Gly	
			85						90					95		
atg	gcg	gtg	agc	gcg	ttg	ttt	gtg	att	ttt	gga	gcg	ata	cga	ttg	gca	336
Met	Ala	Val	Ser	Ala	Leu	Phe	Val	Ile	Phe	Gly	Ala	Ile	Arg	Leu	Ala	
			100					105					110			
cga	ttc	aat	atc	agc	acc	aac	aca	agc	gac	ccc	tat	tct	ttt	atc	ggg	384
Arg	Phe	Asn	Ile	Ser	Thr	Asn	Thr	Ser	Asp	Pro	Tyr	Ser	Phe	Ile	Gly	
		115					120					125				
atc	ccc	att	cct	gcg	gcg	gcg	gta	ttg	gtg	gtg	ctt	tgt	gtg	tta	ttg	432
Ile	Pro	Ile	Pro	Ala	Ala	Ala	Val	Leu	Val	Val	Leu	Cys	Val	Leu	Leu	
	130					135					140					
gat	aac	aaa	tac	cat	ttt	tta	gaa	gga	aat	acc	gaa	aag	tta	ttt	tta	480
Asp	Asn	Lys	Tyr	His	Phe	Leu	Glu	Gly	Asn	Thr	Glu	Lys	Leu	Phe	Leu	
145					150				155						160	
agc	ttt	att	gtt	tta	ttg	ggg	gtg	ctt	atg	gtg	agc	aat	atc	cgc	tac	528
Ser	Phe	Ile	Val	Leu	Leu	Gly	Val	Leu	Met	Val	Ser	Asn	Ile	Arg	Tyr	
			165					170						175		
cct	aat	ttt	aaa	aaa	gtc	aaa	tgg	aat	ctc	aag	ctt	ttt	atc	tta	gtg	576
Pro	Asn	Phe	Lys	Lys	Val	Lys	Trp	Asn	Leu	Lys	Leu	Phe	Ile	Leu	Val	
			180					185					190			
ttg	att	ttt	tta	tcg	tta	gtg	ttt	gtg	cgc	cct	tta	gag	gct	tta	agc	624
Leu	Ile	Phe	Leu	Ser	Leu	Val	Phe	Val	Arg	Pro	Leu	Glu	Ala	Leu	Ser	
		195					200					205				
gtg	ttt	atg	ggg	ttg	tat	ttg	att	tat	ggc	atc	att	cgg	tgg	ctt	ttt	672
Val	Phe	Met	Gly	Leu	Tyr	Leu	Ile	Tyr	Gly	Ile	Ile	Arg	Trp	Leu	Phe	
	210					215					220					
tta	atg	gta	aaa	att	att	ttt	aat	aaa	aat	aaa	agt	gca	tga			714
Leu	Met	Val	Lys	Ile	Ile	Phe	Asn	Lys	Asn	Lys	Ser	Ala				
225					230					235						

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Ser Ile Phe Leu Gly Met Met Ser Ile Phe Tyr Ala Ser Ser Tyr Gln  
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Phe Val Met Ala Cys Trp Leu Val Val Ala Ser Leu Ile Leu Asp Gly  
 35 40 45

Leu Asp Gly Arg Val Ala Arg Leu Thr Asn Thr Thr Ser Lys Phe Gly  
 50 55 60

Ile Glu Phe Asp Ser Leu Ala Asp Val Ile Ala Phe Gly Val Ala Pro  
 65 70 75 80

Ser Leu Ile Thr Tyr Phe Tyr Val Gly Tyr Asn Phe Gly Arg Ile Gly  
 85 90 95

Met Ala Val Ser Ala Leu Phe Val Ile Phe Gly Ala Ile Arg Leu Ala  
 100 105 110

Arg Phe Asn Ile Ser Thr Asn Thr Ser Asp Pro Tyr Ser Phe Ile Gly  
 115 120 125

Ile Pro Ile Pro Ala Ala Ala Val Leu Val Val Leu Cys Val Leu Leu  
 130 135 140

Asp Asn Lys Tyr His Phe Leu Glu Gly Asn Thr Glu Lys Leu Phe Leu  
 145 150 155 160

Ser Phe Ile Val Leu Leu Gly Val Leu Met Val Ser Asn Ile Arg Tyr  
 165 170 175

Pro Asn Phe Lys Lys Val Lys Trp Asn Leu Lys Leu Phe Ile Leu Val  
 180 185 190

Leu Ile Phe Leu Ser Leu Val Phe Val Arg Pro Leu Glu Ala Leu Ser  
195 200 205

Val Phe Met Gly Leu Tyr Leu Ile Tyr Gly Ile Ile Arg Trp Leu Phe  
210 215 220

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225 230 235

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<212> DNA  
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aaa gcc ctt tta ttt gtc att att gga agc gtg tta gtg atg ctt ttg 96  
Lys Ala Leu Leu Phe Val Ile Ile Gly Ser Val Leu Val Met Leu Leu  
20 25 30  
ttg gtg ggg gtg att atc atg ctg ctt atg ggg aat aag gaa gaa tcc 144  
Leu Val Gly Val Ile Ile Met Leu Leu Met Gly Asn Lys Glu Glu Ser  
35 40 45  
aaa gaa aac gct tct aaa aac acc caa gaa gtc caa gct aat cct atg 192  
Lys Glu Asn Ala Ser Lys Asn Thr Gln Glu Val Gln Ala Asn Pro Met  
50 55 60  
gcg aac aaa aat caa gaa gcc aaa gaa ggc tct aat atc cag caa tat 240  
Ala Asn Lys Asn Gln Glu Ala Lys Glu Gly Ser Asn Ile Gln Gln Tyr  
65 70 75 80  
ctg gtg ctt ggg cct ttg tat gcg att gat gcg cct ttt gcg gtg aat 288  
Leu Val Leu Gly Pro Leu Tyr Ala Ile Asp Ala Pro Phe Ala Val Asn  
85 90 95  
ttg gtt tct caa aat ggc aga cgc tac ctt aag gct tcc att tcg tta 336  
Leu Val Ser Gln Asn Gly Arg Arg Tyr Leu Lys Ala Ser Ile Ser Leu  
100 105 110  
gaa ttg agc aat gaa aag ctt tta aat gaa gtc aag gtt aaa gac aca 384  
Glu Leu Ser Asn Glu Lys Leu Leu Asn Glu Val Lys Val Lys Asp Thr  
115 120 125

gcg att aag gac acg att ata gag att cta tcg tct aaa agc gtg gaa	432
Ala Ile Lys Asp Thr Ile Ile Glu Ile Leu Ser Ser Lys Ser Val Glu	
130 135 140	
gaa gtg gtt act aac aaa ggt aaa aac aag ctt aaa gat gaa att aag	480
Glu Val Val Thr Asn Lys Gly Lys Asn Lys Leu Lys Asp Glu Ile Lys	
145 150 155 160	
agc cat ttg aat tcg ttt ttg att gat ggc ttt att aaa aat gtc ttt	528
Ser His Leu Asn Ser Phe Leu Ile Asp Gly Phe Ile Lys Asn Val Phe	
165 170 175	
ttc act gat ttc att att caa taa	552
Phe Thr Asp Phe Ile Ile Gln	
180	

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 <212> PRT  
 <213> Helicobacter pylori

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Leu Val Gly Val Ile Ile Met Leu Leu Met Gly Asn Lys Glu Glu Ser	
35 40 45	
Lys Glu Asn Ala Ser Lys Asn Thr Gln Glu Val Gln Ala Asn Pro Met	
50 55 60	
Ala Asn Lys Asn Gln Glu Ala Lys Glu Gly Ser Asn Ile Gln Gln Tyr	
65 70 75 80	
Leu Val Leu Gly Pro Leu Tyr Ala Ile Asp Ala Pro Phe Ala Val Asn	
85 90 95	
Leu Val Ser Gln Asn Gly Arg Arg Tyr Leu Lys Ala Ser Ile Ser Leu	
100 105 110	
Glu Leu Ser Asn Glu Lys Leu Leu Asn Glu Val Lys Val Lys Asp Thr	
115 120 125	

Ala Ile Lys Asp Thr Ile Ile Glu Ile Leu Ser Ser Lys Ser Val Glu  
 130 135 140

Glu Val Val Thr Asn Lys Gly Lys Asn Lys Leu Lys Asp Glu Ile Lys  
 145 150 155 160

Ser His Leu Asn Ser Phe Leu Ile Asp Gly Phe Ile Lys Asn Val Phe  
 165 170 175

Phe Thr Asp Phe Ile Ile Gln  
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 1 5 10 15  
 att tat tat ggg gtt gag cct tat gcg cat tcg gtg atg cac cct aaa 96  
 Ile Tyr Tyr Gly Val Glu Pro Tyr Ala His Ser Val Met His Pro Lys  
 20 25 30  
 gtc gct ccg gca gat ttt gct ttc aag gat tta gag ccg atg gat tta 144  
 Val Ala Pro Ala Asp Phe Ala Phe Lys Asp Leu Glu Pro Met Asp Leu  
 35 40 45  
 aaa aat ggc gat gct aat aag ggc aaa cag ctt gta gct gaa aat tgc 192  
 Lys Asn Gly Asp Ala Asn Lys Gly Lys Gln Leu Val Ala Glu Asn Cys  
 50 55 60  
 acc gct tgc cat ggc att aaa tcc caa aac att cca gcc cct atg gac 240  
 Thr Ala Cys His Gly Ile Lys Ser Gln Asn Ile Pro Ala Pro Met Asp  
 65 70 75 80  
 agc ctt agc gcg agc aac tct ttt ggg gtc gtg cca ccg gat tta agc 288  
 Ser Leu Ser Ala Ser Asn Ser Phe Gly Val Val Pro Pro Asp Leu Ser  
 85 90 95  
 cat gtg gcg ggg gtt ttg aac gcg aat ttc tta gcc cac ttc atc aaa 336  
 His Val Ala Gly Val Leu Asn Ala Asn Phe Leu Ala His Phe Ile Lys

100										105					110					
gac	cct	gta	aaa	acg	gcg	aaa	ttg	agc	cat	aag	ttc	aac	gat	gaa	agg	384				
Asp	Pro	Val	Lys	Thr	Ala	Lys	Leu	Ser	His	Lys	Phe	Asn	Asp	Glu	Arg					
		115					120					125								
ccc	tat	cct	atg	ccg	gcg	ttt	tct	caa	ttt	agc	gat	aaa	gac	ttg	agc	432				
Pro	Tyr	Pro	Met	Pro	Ala	Phe	Ser	Gln	Phe	Ser	Asp	Lys	Asp	Leu	Ser					
	130					135					140									
gat	att	gtg	gcg	tat	ctc	act	tct	att	ttg	cct	aaa	aat	ttg	agc	gat	480				
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145					150					155					160					
aag	gaa	gtg	ttc	gcg	caa	agc	tgt	caa	agg	tgc	cat	agc	ttg	gat	tat	528				
Lys	Glu	Val	Phe	Ala	Gln	Ser	Cys	Gln	Arg	Cys	His	Ser	Leu	Asp	Tyr					
				165					170					175						
gcg	aaa	gat	aag	gcc	ttt	agc	gat	cct	aaa	gat	cta	gcc	aat	tat	tta	576				
Ala	Lys	Asp	Lys	Ala	Phe	Ser	Asp	Pro	Lys	Asp	Leu	Ala	Asn	Tyr	Leu					
			180					185					190							
ggc	tct	cat	gca	cct	gat	ttg	tcc	atg	atg	att	aga	gct	aaa	ggc	gaa	624				
Gly	Ser	His	Ala	Pro	Asp	Leu	Ser	Met	Met	Ile	Arg	Ala	Lys	Gly	Glu					
		195					200					205								
cat	ggt	ttg	aat	att	ttc	atc	aac	gat	ccg	caa	aag	ctt	ttg	cct	ggc	672				
His	Gly	Leu	Asn	Ile	Phe	Ile	Asn	Asp	Pro	Gln	Lys	Leu	Leu	Pro	Gly					
	210					215					220									
acg	gct	atg	ccc	aga	gtg	gga	ttg	agt	gaa	caa	gct	caa	aaa	caa	gtc	720				
Thr	Ala	Met	Pro	Arg	Val	Gly	Leu	Ser	Glu	Gln	Ala	Gln	Lys	Gln	Val					
225					230					235					240					
atc	gca	tat	ttg	gaa	aaa	gca	ggc	gat	agg	aaa	aaa	cat	gaa	agg	aat	768				
Ile	Ala	Tyr	Leu	Glu	Lys	Ala	Gly	Asp	Arg	Lys	Lys	His	Glu	Arg	Asn					
				245				250						255						
acc	tta	ggg	ata	aaa	atc	atg	att	ttc	ttt	gcg	gtg	ctg	tcg	ttc	ttg	816				
Thr	Leu	Gly	Ile	Lys	Ile	Met	Ile	Phe	Phe	Ala	Val	Leu	Ser	Phe	Leu					
			260					265					270							
gct	tat	gcg	tgg	aaa	aga	aaa	gtt	tgg	agc	gaa	gtg	cat	tga			858				
Ala	Tyr	Ala	Trp	Lys	Arg	Lys	Val	Trp	Ser	Glu	Val	His								
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 <212> PRT  
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<400> 10

Met Lys Glu Phe Lys Ile Leu Ile Ile Leu Ile Val Val Val Gly Val

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			20					25					30				
Val	Ala	Pro	Ala	Asp	Phe	Ala	Phe	Lys	Asp	Leu	Glu	Pro	Met	Asp	Leu		
		35					40					45					
Lys	Asn	Gly	Asp	Ala	Asn	Lys	Gly	Lys	Gln	Leu	Val	Ala	Glu	Asn	Cys		
	50					55					60						
Thr	Ala	Cys	His	Gly	Ile	Lys	Ser	Gln	Asn	Ile	Pro	Ala	Pro	Met	Asp		
65					70					75					80		
Ser	Leu	Ser	Ala	Ser	Asn	Ser	Phe	Gly	Val	Val	Pro	Pro	Asp	Leu	Ser		
				85					90					95			
His	Val	Ala	Gly	Val	Leu	Asn	Ala	Asn	Phe	Leu	Ala	His	Phe	Ile	Lys		
			100					105					110				
Asp	Pro	Val	Lys	Thr	Ala	Lys	Leu	Ser	His	Lys	Phe	Asn	Asp	Glu	Arg		
		115					120					125					
Pro	Tyr	Pro	Met	Pro	Ala	Phe	Ser	Gln	Phe	Ser	Asp	Lys	Asp	Leu	Ser		
	130					135					140						
Asp	Ile	Val	Ala	Tyr	Leu	Thr	Ser	Ile	Leu	Pro	Lys	Asn	Leu	Ser	Asp		
145					150					155					160		
Lys	Glu	Val	Phe	Ala	Gln	Ser	Cys	Gln	Arg	Cys	His	Ser	Leu	Asp	Tyr		
				165					170					175			
Ala	Lys	Asp	Lys	Ala	Phe	Ser	Asp	Pro	Lys	Asp	Leu	Ala	Asn	Tyr	Leu		
			180					185					190				
Gly	Ser	His	Ala	Pro	Asp	Leu	Ser	Met	Met	Ile	Arg	Ala	Lys	Gly	Glu		
		195					200					205					
His	Gly	Leu	Asn	Ile	Phe	Ile	Asn	Asp	Pro	Gln	Lys	Leu	Leu	Pro	Gly		
	210					215					220						



Thr Ala Met Pro Arg Val Gly Leu Ser Glu Gln Ala Gln Lys Gln Val  
 225 230 235 240

Ile Ala Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys His Glu Arg Asn  
 245 250 255

Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val Leu Ser Phe Leu  
 260 265 270

Ala Tyr Ala Trp Lys Arg Lys Val Trp Ser Glu Val His  
 275 280 285

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 <211> 192  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 <222> (1)..(192)

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 1 5 10 15  
 gga ttg gta ggc tta ata gcg ttt ttg tgg ggg gtt aaa agc ggt cag 96  
 Gly Leu Val Gly Leu Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln  
 20 25 30  
 ttt gac gat gaa aaa cgc atg ctt gaa agc gtg ttg tat gac agc gtg 144  
 Phe Asp Asp Glu Lys Arg Met Leu Glu Ser Val Leu Tyr Asp Ser Val  
 35 40 45  
 agc gat ttg aac gaa gcg att tta caa gaa aaa cgc caa aag aat taa 192  
 Ser Asp Leu Asn Glu Ala Ile Leu Gln Glu Lys Arg Gln Lys Asn  
 50 55 60

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 <211> 63  
 <212> PRT  
 <213> Helicobacter pylori

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 1 5 10 15

Gly Leu Val Gly Leu Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln  
 20 25 30

Phe Asp Asp Glu Lys Arg Met Leu Glu Ser Val Leu Tyr Asp Ser Val  
 35 40 45

Ser Asp Leu Asn Glu Ala Ile Leu Gln Glu Lys Arg Gln Lys Asn  
 50 55 60

<210> 13  
 <211> 957  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(957)

<400> 13  
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 Met Pro Asp Ser Ala Asn Met Ile Ile Leu Phe Phe Thr Tyr Asp Ile  
 1 5 10 15  
 tta ttc gct ctc aat tac acc ttg ccc att tcc ttg ctt ttg gcg atg 96  
 Leu Phe Ala Leu Asn Tyr Thr Leu Pro Ile Ser Leu Leu Leu Ala Met  
 20 25 30  
 gtt tta ttt tat atc gca ttc att aaa tcc aac caa tac acc gcc ctg 144  
 Val Leu Phe Tyr Ile Ala Phe Ile Lys Ser Asn Gln Tyr Thr Ala Leu  
 35 40 45  
 ctc tcc att ggc ttt tcc aaa tgc cag att tta agc cct att ttt ttg 192  
 Leu Ser Ile Gly Phe Ser Lys Cys Gln Ile Leu Ser Pro Ile Phe Leu  
 50 55 60  
 att agt ctg ttt ttc acg gct att tat gtg ggg ttg aac gcg act cct 240  
 Ile Ser Leu Phe Phe Thr Ala Ile Tyr Val Gly Leu Asn Ala Thr Pro  
 65 70 75 80  
 ttt gtg tat atg gaa gaa aaa acg caa aat tta atc tat aaa gac aat 288  
 Phe Val Tyr Met Glu Glu Lys Thr Gln Asn Leu Ile Tyr Lys Asp Asn  
 85 90 95  
 tct ttg agc gtc tca gag cat ttg tta gtg aaa tat aac gat gat tac 336  
 Ser Leu Ser Val Ser Glu His Leu Leu Val Lys Tyr Asn Asp Asp Tyr  
 100 105 110  
 gtg tat ttt gat aag att aat ccc cta ttg caa aaa gcc caa aac atc 384  
 Val Tyr Phe Asp Lys Ile Asn Pro Leu Leu Gln Lys Ala Gln Asn Ile  
 115 120 125

aag gtt ttt cgc cta aaa gat aag act tta gaa tct tac gct gaa gct	432
Lys Val Phe Arg Leu Lys Asp Lys Thr Leu Glu Ser Tyr Ala Glu Ala	
130 135 140	
aaa gaa gct ttt ttt gaa gac aag tat tgg att ttg cat gac act act	480
Lys Glu Ala Phe Phe Glu Asp Lys Tyr Trp Ile Leu His Asp Thr Thr	
145 150 155 160	
atc tat gag atg ccc ttg agt ttt gaa ctg ggt gca aac gct tta agc	528
Ile Tyr Glu Met Pro Leu Ser Phe Glu Leu Gly Ala Asn Ala Leu Ser	
165 170 175	
acc acg cgt tta aaa acc ttt aaa acg ctc aaa aat ttc cgc cct aaa	576
Thr Thr Arg Leu Lys Thr Phe Lys Thr Leu Lys Asn Phe Arg Pro Lys	
180 185 190	
gtt tta gac acc att tat caa aac aag ccc gcg gtt tct atc aca gac	624
Val Leu Asp Thr Ile Tyr Gln Asn Lys Pro Ala Val Ser Ile Thr Asp	
195 200 205	
gct ctt tta tct ttg cat gct tta gtg cgc caa aac gca gac acg aaa	672
Ala Leu Leu Ser Leu His Ala Leu Val Arg Gln Asn Ala Asp Thr Lys	
210 215 220	
aaa gtg cga tcg ttt ttg tat gtg ttt gcg att ttg ccc ttt ttt gtg	720
Lys Val Arg Ser Phe Leu Tyr Val Phe Ala Ile Leu Pro Phe Phe Val	
225 230 235 240	
ccg ttt tta agc gtt tta atc gct tat ttt tcg ccc agt ctc gcc cgc	768
Pro Phe Leu Ser Val Leu Ile Ala Tyr Phe Ser Pro Ser Leu Ala Arg	
245 250 255	
tat gaa aac ctg gct ctt tta ggg cta aag ttt atc att atc acg ctc	816
Tyr Glu Asn Leu Ala Leu Leu Gly Leu Lys Phe Ile Ile Ile Thr Leu	
260 265 270	
gtt gtt tgg ggg cta ttc ttt gct tta ggg aag ttc agc att tca ggg	864
Val Val Trp Gly Leu Phe Phe Ala Leu Gly Lys Phe Ser Ile Ser Gly	
275 280 285	
ata ctc att cct gaa ata ggc gtg cta tcg ccc ttt ttt ata ttc tta	912
Ile Leu Ile Pro Glu Ile Gly Val Leu Ser Pro Phe Phe Ile Phe Leu	
290 295 300	
gct ctt agt ctt tgg tat ttt aaa aag ctt aat aag agg ttg tag	957
Ala Leu Ser Leu Trp Tyr Phe Lys Lys Leu Asn Lys Arg Leu	
305 310 315	

<210> 14  
 <211> 318  
 <212> PRT  
 <213> Helicobacter pylori

<400> 14

Met Pro Asp Ser Ala Asn Met Ile Ile Leu Phe Phe Thr Tyr Asp Ile  
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Leu Phe Ala Leu Asn Tyr Thr Leu Pro Ile Ser Leu Leu Leu Ala Met  
20 25 30

Val Leu Phe Tyr Ile Ala Phe Ile Lys Ser Asn Gln Tyr Thr Ala Leu  
35 40 45

Leu Ser Ile Gly Phe Ser Lys Cys Gln Ile Leu Ser Pro Ile Phe Leu  
50 55 60

Ile Ser Leu Phe Phe Thr Ala Ile Tyr Val Gly Leu Asn Ala Thr Pro  
65 70 75 80

Phe Val Tyr Met Glu Glu Lys Thr Gln Asn Leu Ile Tyr Lys Asp Asn  
85 90 95

Ser Leu Ser Val Ser Glu His Leu Leu Val Lys Tyr Asn Asp Asp Tyr  
100 105 110

Val Tyr Phe Asp Lys Ile Asn Pro Leu Leu Gln Lys Ala Gln Asn Ile  
115 120 125

Lys Val Phe Arg Leu Lys Asp Lys Thr Leu Glu Ser Tyr Ala Glu Ala  
130 135 140

Lys Glu Ala Phe Phe Glu Asp Lys Tyr Trp Ile Leu His Asp Thr Thr  
145 150 155 160

Ile Tyr Glu Met Pro Leu Ser Phe Glu Leu Gly Ala Asn Ala Leu Ser  
165 170 175

Thr Thr Arg Leu Lys Thr Phe Lys Thr Leu Lys Asn Phe Arg Pro Lys  
180 185 190

Val Leu Asp Thr Ile Tyr Gln Asn Lys Pro Ala Val Ser Ile Thr Asp  
195 200 205

Ala Leu Leu Ser Leu His Ala Leu Val Arg Gln Asn Ala Asp Thr Lys

210		215		220
Lys Val Arg Ser Phe Leu Tyr Val Phe Ala Ile Leu Pro Phe Phe Val				
225		230	235	240
Pro Phe Leu Ser Val Leu Ile Ala Tyr Phe Ser Pro Ser Leu Ala Arg				
	245		250	255
Tyr Glu Asn Leu Ala Leu Leu Gly Leu Lys Phe Ile Ile Ile Thr Leu				
	260		265	270
Val Val Trp Gly Leu Phe Phe Ala Leu Gly Lys Phe Ser Ile Ser Gly				
	275		280	285
Ile Leu Ile Pro Glu Ile Gly Val Leu Ser Pro Phe Phe Ile Phe Leu				
	290		295	300
Ala Leu Ser Leu Trp Tyr Phe Lys Lys Leu Asn Lys Arg Leu				
305		310	315	

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 <211> 1629  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
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 <222> (1)..(1629)

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1 5 10 15	
ggc tgt aac atg aga aaa tat ttc aaa ccc gct aaa cac caa att aaa	96
Gly Cys Asn Met Arg Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys	
20 25 30	
ggc gaa gcg tat ttc cct aac cat ttg caa gaa agt atc gtt tcg tct	144
Gly Glu Ala Tyr Phe Pro Asn His Leu Gln Glu Ser Ile Val Ser Ser	
35 40 45	
aat cgt tat gga gcc att ttg aaa aat gga gcg gtt ata ggc gat aaa	192
Asn Arg Tyr Gly Ala Ile Leu Lys Asn Gly Ala Val Ile Gly Asp Lys	
50 55 60	
ggt tta acg cag cta aga atc ggt aag aac ttc aat tac gaa agc agt	240

Gly 65	Leu	Thr	Gln	Leu	Arg 70	Ile	Gly	Lys	Asn	Phe 75	Asn	Tyr	Glu	Ser	Ser 80	
ttt	tta	aat	gag	agt	caa	ggg	ttt	ttt	att	ctt	gcg	caa	gat	tgt	ttg	288
Phe	Leu	Asn	Glu	Ser 85	Gln	Gly	Phe	Phe	Ile 90	Leu	Ala	Gln	Asp	Cys 95	Leu	
aac	aag	att	gat	aaa	aaa	aca	aac	aaa	agc	aag	gtg	gct	aag	act	gaa	336
Asn	Lys	Ile	Asp 100	Lys	Lys	Thr	Asn	Lys 105	Ser	Lys	Val	Ala	Lys 110	Thr	Glu	
gaa	acg	gaa	ttg	aaa	tta	aag	ggc	gtt	gaa	gcg	gaa	gtc	caa	gat	aaa	384
Glu	Thr	Glu 115	Leu	Lys	Leu	Lys	Gly 120	Val	Glu	Ala	Glu	Val 125	Gln	Asp	Lys	
gtc	tgt	cat	caa	gtg	gaa	ttg	att	agc	aat	aac	cct	aac	gcc	agc	caa	432
Val	Cys 130	His	Gln	Val	Glu	Leu 135	Ile	Ser	Asn	Asn	Pro 140	Asn	Ala	Ser	Gln	
caa	tct	atc	gtt	att	cct	ttg	gag	act	ttt	gcc	ttg	agc	gca	agc	gtt	480
Gln	Ser	Ile	Val	Ile	Pro 150	Leu	Glu	Thr	Phe	Ala 155	Leu	Ser	Ala	Ser	Val 160	
aaa	ggg	aat	ctt	tta	gcg	gtg	gtg	tta	gcg	gac	aat	tca	gcg	aac	tta	528
Lys	Gly	Asn	Leu 165	Leu	Ala	Val	Val	Leu	Ala 170	Asp	Asn	Ser	Ala	Asn 175	Leu	
tac	gac	atc	act	tct	caa	aaa	ttg	ctt	ttt	agt	gag	aaa	ggc	tcc	cca	576
Tyr	Asp	Ile	Thr 180	Ser	Gln	Lys	Leu	Leu 185	Phe	Ser	Glu	Lys	Gly 190	Ser	Pro	
agc	acc	acg	atc	aat	tct	tta	atg	gcg	atg	cct	att	ttt	atg	gat	acg	624
Ser	Thr	Thr 195	Ile	Asn	Ser	Leu	Met 200	Ala	Met	Pro	Ile	Phe 205	Met	Asp	Thr	
gtc	gtg	gtg	ttc	ccc	atg	cta	gat	ggg	cgc	ttg	ttg	gtc	gtg	gat	tat	672
Val	Val	Val	Phe	Pro	Met	Leu 215	Asp	Gly	Arg	Leu 220	Leu	Val	Val	Asp	Tyr	
gtg	cac	gga	aac	cct	acg	cct	att	aga	aac	att	gtt	atc	agc	agc	gat	720
Val	His	Gly	Asn	Pro 225	Thr	Pro	Ile	Arg	Asn 235	Ile	Val	Ile	Ser	Ser	Asp 240	
aag	ttt	ttt	aac	aat	atc	acc	tac	ctt	atc	gta	gat	ggc	aat	aac	atg	768
Lys	Phe	Phe	Asn 245	Asn	Ile	Thr	Tyr	Leu	Ile 250	Val	Asp	Gly	Asn	Asn 255	Met	
atc	gct	tct	aca	ggg	aaa	agg	ata	ctc	tca	gta	gtg	agc	ggc	caa	gag	816
Ile	Ala	Ser	Thr 260	Gly	Lys	Arg	Ile	Leu 265	Ser	Val	Val	Ser	Gly 270	Gln	Glu	
ttc	aac	tat	gat	ggg	gat	att	gtg	gat	ttg	ctt	tat	gat	aag	ggg	act	864
Phe	Asn	Tyr 275	Asp	Gly	Asp	Ile	Val 280	Asp	Leu	Leu	Tyr	Asp 285	Lys	Gly	Thr	

tta	tat	gtg	ctc	acg	cta	gac	ggg	cag	att	ttg	caa	atg	gat	aag	agt	912
Leu	Tyr	Val	Leu	Thr	Leu	Asp	Gly	Gln	Ile	Leu	Gln	Met	Asp	Lys	Ser	
	290					295					300					
ttg	agg	gaa	tta	aac	agc	gtg	aaa	ctg	cct	tcg	tcg	ctc	aac	acg	att	960
Leu	Arg	Glu	Leu	Asn	Ser	Val	Lys	Leu	Pro	Ser	Ser	Leu	Asn	Thr	Ile	
	305				310					315					320	
gta	tta	aac	cat	aat	aaa	ttg	tat	tct	tta	gaa	aaa	cga	ggg	tat	gtg	1008
Val	Leu	Asn	His	Asn	Lys	Leu	Tyr	Ser	Leu	Glu	Lys	Arg	Gly	Tyr	Val	
				325					330					335		
ata	gag	gtg	gat	tta	aat	gat	ttt	gat	tcg	tat	aat	gtc	tat	aaa	acg	1056
Ile	Glu	Val	Asp	Leu	Asn	Asp	Phe	Asp	Ser	Tyr	Asn	Val	Tyr	Lys	Thr	
			340					345					350			
cca	act	ata	ggc	agt	ttt	aag	ttt	ttt	tca	tct	aat	cgt	ttg	gat	aaa	1104
Pro	Thr	Ile	Gly	Ser	Phe	Lys	Phe	Phe	Ser	Ser	Asn	Arg	Leu	Asp	Lys	
		355					360					365				
ggg	gtg	ttt	tat	gat	aaa	aat	cgg	gtg	tat	tac	gat	cgc	tac	tat	tta	1152
Gly	Val	Phe	Tyr	Asp	Lys	Asn	Arg	Val	Tyr	Tyr	Asp	Arg	Tyr	Tyr	Leu	
	370					375					380					
gat	tat	aac	gat	ttt	aaa	cca	aaa	ctt	tat	ccc	gtt	gtg	gaa	aaa	tcg	1200
Asp	Tyr	Asn	Asp	Phe	Lys	Pro	Lys	Leu	Tyr	Pro	Val	Val	Glu	Lys	Ser	
					390					395					400	
gca	tct	aaa	aaa	tct	caa	aaa	ggc	gaa	aaa	ggg	aac	gct	cct	att	tat	1248
Ala	Ser	Lys	Lys	Ser	Gln	Lys	Gly	Glu	Lys	Gly	Asn	Ala	Pro	Ile	Tyr	
				405				410						415		
ttg	caa	gaa	agg	cat	aaa	gct	aaa	gaa	aat	aaa	cag	cct	tta	gaa	gaa	1296
Leu	Gln	Glu	Arg	His	Lys	Ala	Lys	Glu	Asn	Lys	Gln	Pro	Leu	Glu	Glu	
			420					425					430			
aac	aaa	gtt	aaa	cca	aga	aat	agc	ggg	ttt	gaa	gaa	gaa	gag	gtt	aaa	1344
Asn	Lys	Val	Lys	Pro	Arg	Asn	Ser	Gly	Phe	Glu	Glu	Glu	Glu	Val	Lys	
		435					440					445				
acc	aga	agg	cct	gag	cct	att	agg	gat	caa	aat	aac	gcc	acc	caa	caa	1392
Thr	Arg	Arg	Pro	Glu	Pro	Ile	Arg	Asp	Gln	Asn	Asn	Ala	Thr	Gln	Gln	
			450			455					460					
ggc	gaa	aca	aaa	aac	aat	gaa	agt	aaa	aac	gct	cct	gtc	tta	aaa	gaa	1440
Gly	Glu	Thr	Lys	Asn	Asn	Glu	Ser	Lys	Asn	Ala	Pro	Val	Leu	Lys	Glu	
	465				470					475					480	
aac	gcc	gct	aaa	aaa	gaa	gtg	cca	aaa	cca	aat	tct	aaa	gaa	gaa	aaa	1488
Asn	Ala	Ala	Lys	Lys	Glu	Val	Pro	Lys	Pro	Asn	Ser	Lys	Glu	Glu	Lys	
				485					490					495		
cgc	cgc	ttg	aaa	gaa	gaa	aag	aaa	aaa	gcc	aaa	gcc	gaa	caa	aga	gcg	1536
Arg	Arg	Leu	Lys	Glu	Glu	Lys	Lys	Lys	Ala	Lys	Ala	Glu	Gln	Arg	Ala	
			500					505					510			

aga gaa ttt gaa caa aga gcg aga gag cat caa gaa aga gat gaa aaa	1584
Arg Glu Phe Glu Gln Arg Ala Arg Glu His Gln Glu Arg Asp Glu Lys	
515 520 525	

gag ctt gaa gaa aga aga aaa gct tta gaa atg aat aag aag tag	1629
Glu Leu Glu Glu Arg Arg Lys Ala Leu Glu Met Asn Lys Lys	
530 535 540	

<210> 16  
 <211> 542  
 <212> PRT  
 <213> Helicobacter pylori

<400> 16

Met Asn Lys Pro Phe Leu Ile Leu Leu Ile Ala Leu Ile Val Phe Ser
1 5 10 15

Gly Cys Asn Met Arg Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys
20 25 30

Gly Glu Ala Tyr Phe Pro Asn His Leu Gln Glu Ser Ile Val Ser Ser
35 40 45

Asn Arg Tyr Gly Ala Ile Leu Lys Asn Gly Ala Val Ile Gly Asp Lys
50 55 60

Gly Leu Thr Gln Leu Arg Ile Gly Lys Asn Phe Asn Tyr Glu Ser Ser
65 70 75 80

Phe Leu Asn Glu Ser Gln Gly Phe Phe Ile Leu Ala Gln Asp Cys Leu
85 90 95

Asn Lys Ile Asp Lys Lys Thr Asn Lys Ser Lys Val Ala Lys Thr Glu
100 105 110

Glu Thr Glu Leu Lys Leu Lys Gly Val Glu Ala Glu Val Gln Asp Lys
115 120 125

Val Cys His Gln Val Glu Leu Ile Ser Asn Asn Pro Asn Ala Ser Gln
130 135 140

Gln Ser Ile Val Ile Pro Leu Glu Thr Phe Ala Leu Ser Ala Ser Val
145 150 155 160



Lys Gly Asn Leu Leu Ala Val Val Leu Ala Asp Asn Ser Ala Asn Leu  
165 170 175

Tyr Asp Ile Thr Ser Gln Lys Leu Leu Phe Ser Glu Lys Gly Ser Pro  
180 185 190

Ser Thr Thr Ile Asn Ser Leu Met Ala Met Pro Ile Phe Met Asp Thr  
195 200 205

Val Val Val Phe Pro Met Leu Asp Gly Arg Leu Leu Val Val Asp Tyr  
210 215 220

Val His Gly Asn Pro Thr Pro Ile Arg Asn Ile Val Ile Ser Ser Asp  
225 230 235 240

Lys Phe Phe Asn Asn Ile Thr Tyr Leu Ile Val Asp Gly Asn Asn Met  
245 250 255

Ile Ala Ser Thr Gly Lys Arg Ile Leu Ser Val Val Ser Gly Gln Glu  
260 265 270

Phe Asn Tyr Asp Gly Asp Ile Val Asp Leu Leu Tyr Asp Lys Gly Thr  
275 280 285

Leu Tyr Val Leu Thr Leu Asp Gly Gln Ile Leu Gln Met Asp Lys Ser  
290 295 300

Leu Arg Glu Leu Asn Ser Val Lys Leu Pro Ser Ser Leu Asn Thr Ile  
305 310 315 320

Val Leu Asn His Asn Lys Leu Tyr Ser Leu Glu Lys Arg Gly Tyr Val  
325 330 335

Ile Glu Val Asp Leu Asn Asp Phe Asp Ser Tyr Asn Val Tyr Lys Thr  
340 345 350

Pro Thr Ile Gly Ser Phe Lys Phe Phe Ser Ser Asn Arg Leu Asp Lys  
355 360 365

Gly Val Phe Tyr Asp Lys Asn Arg Val Tyr Tyr Asp Arg Tyr Tyr Leu  
 370 375 380

Asp Tyr Asn Asp Phe Lys Pro Lys Leu Tyr Pro Val Val Glu Lys Ser  
 385 390 395 400

Ala Ser Lys Lys Ser Gln Lys Gly Glu Lys Gly Asn Ala Pro Ile Tyr  
 405 410 415

Leu Gln Glu Arg His Lys Ala Lys Glu Asn Lys Gln Pro Leu Glu Glu  
 420 425 430

Asn Lys Val Lys Pro Arg Asn Ser Gly Phe Glu Glu Glu Glu Val Lys  
 435 440 445

Thr Arg Arg Pro Glu Pro Ile Arg Asp Gln Asn Asn Ala Thr Gln Gln  
 450 455 460

Gly Glu Thr Lys Asn Asn Glu Ser Lys Asn Ala Pro Val Leu Lys Glu  
 465 470 475 480

Asn Ala Ala Lys Lys Glu Val Pro Lys Pro Asn Ser Lys Glu Glu Lys  
 485 490 495

Arg Arg Leu Lys Glu Glu Lys Lys Lys Ala Lys Ala Glu Gln Arg Ala  
 500 505 510

Arg Glu Phe Glu Gln Arg Ala Arg Glu His Gln Glu Arg Asp Glu Lys  
 515 520 525

Glu Leu Glu Glu Arg Arg Lys Ala Leu Glu Met Asn Lys Lys  
 530 535 540

<210> 17  
 <211> 1377  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1377)

<400> 17

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1				5					10					15		
tat	ata	ggg	ttt	tta	ttg	att	tct	tta	gcg	tta	tta	atc	acg	ccc	ttt	96
Tyr	Ile	Gly	Phe	Leu	Leu	Ile	Ser	Leu	Ala	Leu	Leu	Ile	Thr	Pro	Phe	
			20					25					30			
gtt	cgc	att	gat	ggg	gcg	cat	ttg	ttt	ttg	atc	tct	ttt	gag	cat	aag	144
Val	Arg	Ile	Asp	Gly	Ala	His	Leu	Phe	Leu	Ile	Ser	Phe	Glu	His	Lys	
		35					40					45				
caa	ctg	cat	ttt	tta	ggc	aag	atc	ttt	agc	gct	gaa	gaa	ttg	caa	gtc	192
Gln	Leu	His	Phe	Leu	Gly	Lys	Ile	Phe	Ser	Ala	Glu	Glu	Leu	Gln	Val	
	50					55					60					
atg	cct	ttt	atg	gtt	att	ttg	ctt	ttt	ata	ggg	att	ttt	ttc	atc	acc	240
Met	Pro	Phe	Met	Val	Ile	Leu	Leu	Phe	Ile	Gly	Ile	Phe	Phe	Ile	Thr	
65				70						75				80		
act	agc	ctt	ggg	cgt	gtg	tgg	tgc	ggg	tgg	gct	tgc	ccg	caa	acc	ttt	288
Thr	Ser	Leu	Gly	Arg	Val	Trp	Cys	Gly	Trp	Ala	Cys	Pro	Gln	Thr	Phe	
			85					90						95		
tta	agg	gtg	ctt	tat	aga	gat	gtg	att	gaa	acc	aag	att	ttc	aaa	ctc	336
Leu	Arg	Val	Leu	Tyr	Arg	Asp	Val	Ile	Glu	Thr	Lys	Ile	Phe	Lys	Leu	
			100					105					110			
cat	aaa	aag	atc	agc	aac	aag	caa	gaa	agc	cct	aaa	aac	acc	cca	agc	384
His	Lys	Lys	Ile	Ser	Asn	Lys	Gln	Glu	Ser	Pro	Lys	Asn	Thr	Pro	Ser	
		115					120					125				
tac	aag	atc	cgt	aaa	gta	ttg	agc	gtt	tta	ttg	ttc	gct	cct	gtt	gtg	432
Tyr	Lys	Ile	Arg	Lys	Val	Leu	Ser	Val	Leu	Leu	Phe	Ala	Pro	Val	Val	
	130					135					140					
gcg	ggg	cta	atg	atg	ttg	ttt	ttc	ttt	tat	ttc	atc	gcc	cca	gaa	gat	480
Ala	Gly	Leu	Met	Met	Leu	Phe	Phe	Phe	Tyr	Phe	Ile	Ala	Pro	Glu	Asp	
145					150					155				160		
ttt	ttt	atg	tat	ctt	aaa	aac	cct	agc	gat	cac	cct	att	gct	atg	ggg	528
Phe	Phe	Met	Tyr	Leu	Lys	Asn	Pro	Ser	Asp	His	Pro	Ile	Ala	Met	Gly	
				165					170					175		
ttt	tgg	ctt	ttt	agc	acg	gct	gtg	gtg	cta	ttt	gat	ata	gtg	gtg	gtt	576
Phe	Trp	Leu	Phe	Ser	Thr	Ala	Val	Val	Leu	Phe	Asp	Ile	Val	Val	Val	
			180					185					190			
gcg	gag	cgt	ttt	tgc	att	tat	tta	tgc	cct	tac	gct	agg	gtg	caa	tcg	624
Ala	Glu	Arg	Phe	Cys	Ile	Tyr	Leu	Cys	Pro	Tyr	Ala	Arg	Val	Gln	Ser	
		195					200					205				
gtg	ttg	tat	gac	aat	gac	acc	tta	aac	cct	att	tat	gat	gaa	aag	cgc	672
Val	Leu	Tyr	Asp	Asn	Asp	Thr	Leu	Asn	Pro	Ile	Tyr	Asp	Glu	Lys	Arg	
	210					215					220					

ggc gga gcg ctt tat aat aat cag ggc cat ctc ttc ccc tta cct ccc	720
Gly Gly Ala Leu Tyr Asn Asn Gln Gly His Leu Phe Pro Leu Pro Pro	
225 230 235 240	
aaa aaa cgc agc cca gaa aac gaa tgc gtg aat tgt ttg cat tgc gtg	768
Lys Lys Arg Ser Pro Glu Asn Glu Cys Val Asn Cys Leu His Cys Val	
245 250 255	
cag gtt tgc ccc acg cat att gac atc agg aag ggc ttg caa tta gaa	816
Gln Val Cys Pro Thr His Ile Asp Ile Arg Lys Gly Leu Gln Leu Glu	
260 265 270	
tgc atc aat tgt tta gaa tgc gtg gat gca tgc acg att acc atg gct	864
Cys Ile Asn Cys Leu Glu Cys Val Asp Ala Cys Thr Ile Thr Met Ala	
275 280 285	
aaa ttt aac cgc cct tca ctc atc caa tgg tct tca act aac gct att	912
Lys Phe Asn Arg Pro Ser Leu Ile Gln Trp Ser Ser Thr Asn Ala Ile	
290 295 300	
aat acg cgc caa aaa gtg cac ctg gtg cgt tta aaa acg atc gct tac	960
Asn Thr Arg Gln Lys Val His Leu Val Arg Leu Lys Thr Ile Ala Tyr	
305 310 315 320	
atg ggg gtt atc gct att gtg atc gct ctt tta gcc atc act tcg ttt	1008
Met Gly Val Ile Ala Ile Val Ile Ala Leu Leu Ala Ile Thr Ser Phe	
325 330 335	
aaa aaa gaa cgc atg ctc tta gac att aac cgc aac agc gat ctg tat	1056
Lys Lys Glu Arg Met Leu Leu Asp Ile Asn Arg Asn Ser Asp Leu Tyr	
340 345 350	
gaa ttg cgc tct agc ggg tat gtg gat aac gat tac gtg ttt tta ttc	1104
Glu Leu Arg Ser Ser Gly Tyr Val Asp Asn Asp Tyr Val Phe Leu Phe	
355 360 365	
cac aac acg gac aat aaa gac cat gag ttt tat ttc aaa gtt tta ggg	1152
His Asn Thr Asp Asn Lys Asp His Glu Phe Tyr Phe Lys Val Leu Gly	
370 375 380	
caa aaa gac att cag atc aaa aag cct tta aat cct atc gcc att aaa	1200
Gln Lys Asp Ile Gln Ile Lys Lys Pro Leu Asn Pro Ile Ala Ile Lys	
385 390 395 400	
gcc ggg caa aag att aaa gcg gta gtg att tta aga aaa ccc cta aag	1248
Ala Gly Gln Lys Ile Lys Ala Val Val Ile Leu Arg Lys Pro Leu Lys	
405 410 415	
agt aac gcc aca gaa tac aag aac gct aaa gac gct cta atc ccc att	1296
Ser Asn Ala Thr Glu Tyr Lys Asn Ala Lys Asp Ala Leu Ile Pro Ile	
420 425 430	
acc ata caa gct tat agc gcg gac gat aag aat att acg ata gaa agg	1344
Thr Ile Gln Ala Tyr Ser Ala Asp Asp Lys Asn Ile Thr Ile Glu Arg	

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450	455		1377

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		20						25					30		

Val	Arg	Ile	Asp	Gly	Ala	His	Leu	Phe	Leu	Ile	Ser	Phe	Glu	His	Lys
		35					40					45			

Gln	Leu	His	Phe	Leu	Gly	Lys	Ile	Phe	Ser	Ala	Glu	Glu	Leu	Gln	Val
	50					55					60				

Met	Pro	Phe	Met	Val	Ile	Leu	Leu	Phe	Ile	Gly	Ile	Phe	Phe	Ile	Thr
65					70					75					80

Thr	Ser	Leu	Gly	Arg	Val	Trp	Cys	Gly	Trp	Ala	Cys	Pro	Gln	Thr	Phe
				85					90					95	

Leu	Arg	Val	Leu	Tyr	Arg	Asp	Val	Ile	Glu	Thr	Lys	Ile	Phe	Lys	Leu
		100						105					110		

His	Lys	Lys	Ile	Ser	Asn	Lys	Gln	Glu	Ser	Pro	Lys	Asn	Thr	Pro	Ser
		115					120					125			

Tyr	Lys	Ile	Arg	Lys	Val	Leu	Ser	Val	Leu	Leu	Phe	Ala	Pro	Val	Val
	130					135					140				

Ala	Gly	Leu	Met	Met	Leu	Phe	Phe	Phe	Tyr	Phe	Ile	Ala	Pro	Glu	Asp
145					150					155					160

Phe Phe Met Tyr Leu Lys Asn Pro Ser Asp His Pro Ile Ala Met Gly

165								170				175			
Phe	Trp	Leu	Phe	Ser	Thr	Ala	Val	Val	Leu	Phe	Asp	Ile	Val	Val	Val
			180						185				190		
Ala	Glu	Arg	Phe	Cys	Ile	Tyr	Leu	Cys	Pro	Tyr	Ala	Arg	Val	Gln	Ser
		195					200					205			
Val	Leu	Tyr	Asp	Asn	Asp	Thr	Leu	Asn	Pro	Ile	Tyr	Asp	Glu	Lys	Arg
	210					215					220				
Gly	Gly	Ala	Leu	Tyr	Asn	Asn	Gln	Gly	His	Leu	Phe	Pro	Leu	Pro	Pro
225					230					235					240
Lys	Lys	Arg	Ser	Pro	Glu	Asn	Glu	Cys	Val	Asn	Cys	Leu	His	Cys	Val
				245					250					255	
Gln	Val	Cys	Pro	Thr	His	Ile	Asp	Ile	Arg	Lys	Gly	Leu	Gln	Leu	Glu
			260					265					270		
Cys	Ile	Asn	Cys	Leu	Glu	Cys	Val	Asp	Ala	Cys	Thr	Ile	Thr	Met	Ala
		275					280					285			
Lys	Phe	Asn	Arg	Pro	Ser	Leu	Ile	Gln	Trp	Ser	Ser	Thr	Asn	Ala	Ile
	290					295					300				
Asn	Thr	Arg	Gln	Lys	Val	His	Leu	Val	Arg	Leu	Lys	Thr	Ile	Ala	Tyr
305					310					315					320
Met	Gly	Val	Ile	Ala	Ile	Val	Ile	Ala	Leu	Leu	Ala	Ile	Thr	Ser	Phe
				325				330						335	
Lys	Lys	Glu	Arg	Met	Leu	Leu	Asp	Ile	Asn	Arg	Asn	Ser	Asp	Leu	Tyr
			340					345					350		
Glu	Leu	Arg	Ser	Ser	Gly	Tyr	Val	Asp	Asn	Asp	Tyr	Val	Phe	Leu	Phe
		355					360					365			
His	Asn	Thr	Asp	Asn	Lys	Asp	His	Glu	Phe	Tyr	Phe	Lys	Val	Leu	Gly
	370					375					380				

Gln Lys Asp Ile Gln Ile Lys Lys Pro Leu Asn Pro Ile Ala Ile Lys  
385 390 395 400

Ala Gly Gln Lys Ile Lys Ala Val Val Ile Leu Arg Lys Pro Leu Lys  
405 410 415

Ser Asn Ala Thr Glu Tyr Lys Asn Ala Lys Asp Ala Leu Ile Pro Ile  
420 425 430

Thr Ile Gln Ala Tyr Ser Ala Asp Asp Lys Asn Ile Thr Ile Glu Arg  
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Glu Ser Val Phe Ile Ala Pro Ser Glu Asp  
450 455

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1 5 10 15  
tta aat gct gtt gat ggg att tct aaa acc gat ctt tct tct ttg aat 96  
Leu Asn Ala Val Asp Gly Ile Ser Lys Thr Asp Leu Ser Ser Leu Asn  
20 25 30  
ttg gct gaa gac agc gcg cct ttg aac cat cct aac gct caa aaa ctc 144  
Leu Ala Glu Asp Ser Ala Pro Leu Asn His Pro Asn Ala Gln Lys Leu  
35 40 45  
tcc tta aaa aac gca tgg act agg gta ttg tct aac cat gaa ggc ttg 192  
Ser Leu Lys Asn Ala Trp Thr Arg Val Leu Ser Asn His Glu Gly Leu  
50 55 60  
cat gcg caa gaa tac gcc att aag cga gcg agt aaa atg aaa tta gcg 240  
His Ala Gln Glu Tyr Ala Ile Lys Arg Ala Ser Lys Met Lys Leu Ala  
65 70 75 80  
gct aaa ctt tct ttt ttg cct caa att gat ttg agc gct ttt tat gtg 288  
Ala Lys Leu Ser Phe Leu Pro Gln Ile Asp Leu Ser Ala Phe Tyr Val

85								90				95				
tat	ctc	tct	aac	ccc	att	aaa	atg	gat	ttt	gcc	agc	caa	aaa	caa	ccg	336
Tyr	Leu	Ser	Asn	Pro	Ile	Lys	Met	Asp	Phe	Ala	Ser	Gln	Lys	Gln	Pro	
			100					105					110			
ggc	gtg	caa	aaa	gcc	acc	aac	cag	atc	cat	caa	ggc	ata	caa	aac	atc	384
Gly	Val	Gln	Lys	Ala	Thr	Asn	Gln	Ile	His	Gln	Gly	Ile	Gln	Asn	Ile	
		115					120					125				
cag	caa	aat	atc	cct	tct	caa	gta	tta	acc	cct	caa	atc	caa	gcg	ggc	432
Gln	Gln	Asn	Ile	Pro	Ser	Gln	Val	Leu	Thr	Pro	Gln	Ile	Gln	Ala	Gly	
		130				135					140					
atg	caa	ggg	gtg	atg	caa	ggg	ttt	ggg	gct	ttg	agc	agc	act	tta	gaa	480
Met	Gln	Gly	Val	Met	Gln	Gly	Phe	Gly	Ala	Leu	Ser	Ser	Thr	Leu	Glu	
145					150					155					160	
gcc	ccc	tta	ttg	ttt	tct	aag	caa	aat	gtg	gtg	att	ggg	gct	ttg	agc	528
Ala	Pro	Leu	Leu	Phe	Ser	Lys	Gln	Asn	Val	Val	Ile	Gly	Ala	Leu	Ser	
				165					170					175		
att	att	tat	ccc	ctt	tat	atg	ggt	ggg	gca	aga	ttc	acg	atg	gtg	cgc	576
Ile	Ile	Tyr	Pro	Leu	Tyr	Met	Gly	Gly	Ala	Arg	Phe	Thr	Met	Val	Arg	
			180					185					190			
att	gcg	gat	ttg	atg	caa	aaa	gat	gct	aat	gaa	gtg	tat	cgt	ttg	aaa	624
Ile	Ala	Asp	Leu	Met	Gln	Lys	Asp	Ala	Asn	Glu	Val	Tyr	Arg	Leu	Lys	
		195					200					205				
aag	ctt	tcc	act	ttt	caa	gag	ctt	gtg	agc	gtg	tat	tac	ggc	atg	gtg	672
Lys	Leu	Ser	Thr	Phe	Gln	Glu	Leu	Val	Ser	Val	Tyr	Tyr	Gly	Met	Val	
	210					215					220					
tta	aac	gca	gaa	gtg	gct	gaa	act	tta	gaa	gag	gtg	gaa	aaa	ggc	cat	720
Leu	Asn	Ala	Glu	Val	Ala	Glu	Thr	Leu	Glu	Glu	Val	Glu	Lys	Gly	His	
225					230				235						240	
tat	aag	cat	ttc	caa	aac	gct	ttg	aaa	atg	caa	aaa	gtg	ggg	caa	atc	768
Tyr	Lys	His	Phe	Gln	Asn	Ala	Leu	Lys	Met	Gln	Lys	Val	Gly	Gln	Ile	
			245					250						255		
gct	agg	gta	gaa	acc	tta	ggc	gct	caa	gtg	gct	tat	gat	aag	gcc	cat	816
Ala	Arg	Val	Glu	Thr	Leu	Gly	Ala	Gln	Val	Ala	Tyr	Asp	Lys	Ala	His	
		260					265						270			
atc	gct	agc	gtt	aag	gct	aaa	gac	gtg	tta	gaa	gtt	tcg	cag	ctc	tcg	864
Ile	Ala	Ser	Val	Lys	Ala	Lys	Asp	Val	Leu	Glu	Val	Ser	Gln	Leu	Ser	
		275					280					285				
ttc	aat	tcc	att	tta	tct	agc	aag	gac	gat	tta	gtg	cct	tca	agc	aaa	912
Phe	Asn	Ser	Ile	Leu	Ser	Ser	Lys	Asp	Asp	Leu	Val	Pro	Ser	Ser	Lys	
		290				295					300					
tta	gag	atc	cgc	acg	gag	aaa	aat	ctg	ccc	gat	ctg	agc	ttt	ttt	gtt	960



Leu	Glu	Ile	Arg	Thr	Glu	Lys	Asn	Leu	Pro	Asp	Leu	Ser	Phe	Phe	Val	
305					310					315					320	
tct	tcc	acg	ctc	aat	tcc	tac	ccg	gtt	tta	aag	act	tta	gaa	aat	cag	1008
Ser	Ser	Thr	Leu	Asn	Ser	Tyr	Pro	Val	Leu	Lys	Thr	Leu	Glu	Asn	Gln	
				325					330					335		
att	caa	atc	tct	aaa	gaa	aac	acg	aaa	tta	cag	atc	gct	aaa	ttc	ttg	1056
Ile	Gln	Ile	Ser	Lys	Glu	Asn	Thr	Lys	Leu	Gln	Ile	Ala	Lys	Phe	Leu	
			340					345					350			
ccc	caa	gtg	agt	ttt	ttt	ggc	tct	tat	att	atg	aag	caa	aac	aat	tcg	1104
Pro	Gln	Val	Ser	Phe	Phe	Gly	Ser	Tyr	Ile	Met	Lys	Gln	Asn	Asn	Ser	
		355					360					365				
gtg	ttt	gaa	gac	atg	atc	cct	agt	tgg	ttt	gtg	ggc	gtg	gcc	ggg	cgc	1152
Val	Phe	Glu	Asp	Met	Ile	Pro	Ser	Trp	Phe	Val	Gly	Val	Ala	Gly	Arg	
	370					375					380					
atg	cct	att	ctt	tct	ccc	aca	ggg	cgc	att	caa	aaa	tac	caa	gcg	agc	1200
Met	Pro	Ile	Leu	Ser	Pro	Thr	Gly	Arg	Ile	Gln	Lys	Tyr	Gln	Ala	Ser	
385					390					395					400	
aaa	tta	gcg	gag	ttg	caa	gtg	agt	agc	gaa	caa	atc	cag	gct	aaa	aaa	1248
Lys	Leu	Ala	Glu	Leu	Gln	Val	Ser	Ser	Glu	Gln	Ile	Gln	Ala	Lys	Lys	
				405					410					415		
aac	atg	gaa	tta	tta	gtg	aat	aag	act	tat	aaa	gag	acg	ctt	tct	tat	1296
Asn	Met	Glu	Leu	Leu	Val	Asn	Lys	Thr	Tyr	Lys	Glu	Thr	Leu	Ser	Tyr	
			420					425					430			
ttg	aaa	gaa	tac	aaa	agc	ttg	ctt	tct	agc	gtg	gaa	tta	gcc	aag	gaa	1344
Leu	Lys	Glu	Tyr	Lys	Ser	Leu	Leu	Ser	Ser	Val	Glu	Leu	Ala	Lys	Glu	
		435					440					445				
aac	tta	aaa	ctc	caa	gag	cag	gct	ttt	tta	caa	ggc	tta	agc	acg	aac	1392
Asn	Leu	Lys	Leu	Gln	Glu	Gln	Ala	Phe	Leu	Gln	Gly	Leu	Ser	Thr	Asn	
	450					455					460					
gct	caa	gtc	att	gat	gcg	agg	aac	acg	ctt	tct	tct	atc	gtc	gtg	gag	1440
Ala	Gln	Val	Ile	Asp	Ala	Arg	Asn	Thr	Leu	Ser	Ser	Ile	Val	Val	Glu	
465					470					475					480	
caa	aaa	agc	gtg	gct	tat	aaa	tac	atc	gtt	tca	tta	gcg	aat	tta	atg	1488
Gln	Lys	Ser	Val	Ala	Tyr	Lys	Tyr	Ile	Val	Ser	Leu	Ala	Asn	Leu	Met	
				485					490					495		
gcg	tta	agc	gat	cat	att	gat	tta	ttt	tat	gaa	ttt	gtt	tat	taa		1533
Ala	Leu	Ser	Asp	His	Ile	Asp	Leu	Phe	Tyr	Glu	Phe	Val	Tyr			
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<213> Helicobacter pylori

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Leu Ala Glu Asp Ser Ala Pro Leu Asn His Pro Asn Ala Gln Lys Leu  
35 40 45

Ser Leu Lys Asn Ala Trp Thr Arg Val Leu Ser Asn His Glu Gly Leu  
50 55 60

His Ala Gln Glu Tyr Ala Ile Lys Arg Ala Ser Lys Met Lys Leu Ala  
65 70 75 80

Ala Lys Leu Ser Phe Leu Pro Gln Ile Asp Leu Ser Ala Phe Tyr Val  
85 90 95

Tyr Leu Ser Asn Pro Ile Lys Met Asp Phe Ala Ser Gln Lys Gln Pro  
100 105 110

Gly Val Gln Lys Ala Thr Asn Gln Ile His Gln Gly Ile Gln Asn Ile  
115 120 125

Gln Gln Asn Ile Pro Ser Gln Val Leu Thr Pro Gln Ile Gln Ala Gly  
130 135 140

Met Gln Gly Val Met Gln Gly Phe Gly Ala Leu Ser Ser Thr Leu Glu  
145 150 155 160

Ala Pro Leu Leu Phe Ser Lys Gln Asn Val Val Ile Gly Ala Leu Ser  
165 170 175

Ile Ile Tyr Pro Leu Tyr Met Gly Gly Ala Arg Phe Thr Met Val Arg  
180 185 190

Ile Ala Asp Leu Met Gln Lys Asp Ala Asn Glu Val Tyr Arg Leu Lys  
195 200 205

Lys Leu Ser Thr Phe Gln Glu Leu Val Ser Val Tyr Tyr Gly Met Val  
 210 215 220

Leu Asn Ala Glu Val Ala Glu Thr Leu Glu Glu Val Glu Lys Gly His  
 225 230 235 240

Tyr Lys His Phe Gln Asn Ala Leu Lys Met Gln Lys Val Gly Gln Ile  
 245 250 255

Ala Arg Val Glu Thr Leu Gly Ala Gln Val Ala Tyr Asp Lys Ala His  
 260 265 270

Ile Ala Ser Val Lys Ala Lys Asp Val Leu Glu Val Ser Gln Leu Ser  
 275 280 285

Phe Asn Ser Ile Leu Ser Ser Lys Asp Asp Leu Val Pro Ser Ser Lys  
 290 295 300

Leu Glu Ile Arg Thr Glu Lys Asn Leu Pro Asp Leu Ser Phe Phe Val  
 305 310 315 320

Ser Ser Thr Leu Asn Ser Tyr Pro Val Leu Lys Thr Leu Glu Asn Gln  
 325 330 335

Ile Gln Ile Ser Lys Glu Asn Thr Lys Leu Gln Ile Ala Lys Phe Leu  
 340 345 350

Pro Gln Val Ser Phe Phe Gly Ser Tyr Ile Met Lys Gln Asn Asn Ser  
 355 360 365

Val Phe Glu Asp Met Ile Pro Ser Trp Phe Val Gly Val Ala Gly Arg  
 370 375 380

Met Pro Ile Leu Ser Pro Thr Gly Arg Ile Gln Lys Tyr Gln Ala Ser  
 385 390 395 400

Lys Leu Ala Glu Leu Gln Val Ser Ser Glu Gln Ile Gln Ala Lys Lys  
 405 410 415

Asn Met Glu Leu Leu Val Asn Lys Thr Tyr Lys Glu Thr Leu Ser Tyr

420	425	430
Leu Lys Glu Tyr Lys Ser Leu Leu Ser Ser Val Glu Leu Ala Lys Glu		
435	440	445
Asn Leu Lys Leu Gln Glu Gln Ala Phe Leu Gln Gly Leu Ser Thr Asn		
450	455	460
Ala Gln Val Ile Asp Ala Arg Asn Thr Leu Ser Ser Ile Val Val Glu		
465	470	475
Gln Lys Ser Val Ala Tyr Lys Tyr Ile Val Ser Leu Ala Asn Leu Met		
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Ala Leu Ser Asp His Ile Asp Leu Phe Tyr Glu Phe Val Tyr		
500	505	510

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tac gct tat ctt acc tat ttg ttt tcg cac aat atc cgc aac cac ctc	96
Tyr Ala Tyr Leu Thr Tyr Leu Phe Ser His Asn Ile Arg Asn His Leu	
20 25 30	
cct gaa atc act ttg gat tat tta aac aaa cag atc aga aaa atg cac	144
Pro Glu Ile Thr Leu Asp Tyr Leu Asn Lys Gln Ile Arg Lys Met His	
35 40 45	
gct gaa atc aaa atg gca aaa aat ttt ttt gtg tta gac gct aag ggc	192
Ala Glu Ile Lys Met Ala Lys Asn Phe Phe Val Leu Asp Ala Lys Gly	
50 55 60	
atg cta att ctt aag cca agc cag ctt aaa gag cag ggg cat aag gaa	240
Met Leu Ile Leu Lys Pro Ser Gln Leu Lys Glu Gln Gly His Lys Glu	
65 70 75 80	
ggg ata tta gag cat gat tta aca gaa ggg att gaa cta gaa tcg cat	288

Gly	Ile	Leu	Glu	His	Asp	Leu	Thr	Glu	Gly	Ile	Glu	Leu	Glu	Ser	His	
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gcc	agt	ttt	agc	gat	aag	tat	tat	ttt	tat	caa	gcc	gtg	agc	gaa	aag	336
Ala	Ser	Phe	Ser	Asp	Lys	Tyr	Tyr	Phe	Tyr	Gln	Ala	Val	Ser	Glu	Lys	
			100					105					110			
cgt	tgc	att	tta	acg	gac	ccc	tat	cct	tct	aaa	aaa	gga	aac	cat	tta	384
Arg	Cys	Ile	Leu	Thr	Asp	Pro	Tyr	Pro	Ser	Lys	Lys	Gly	Asn	His	Leu	
		115					120					125				
gta	gtg	agc	gcg	tct	tac	ccg	gtg	tat	gat	caa	aat	aac	gat	cta	gcg	432
Val	Val	Ser	Ala	Ser	Tyr	Pro	Val	Tyr	Asp	Gln	Asn	Asn	Asp	Leu	Ala	
	130					135					140					
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Phe	Val	Val	Cys	Leu	Gln	Ile	Pro	Leu	Arg	Val	Ala	Ile	Glu	Ile	Ser	
145					150					155					160	
tcg	cct	tca	aag	tat	ttc	aga	acc	ttt	agc	gaa	ggg	agc	atg	gtt	atg	528
Ser	Pro	Ser	Lys	Tyr	Phe	Arg	Thr	Phe	Ser	Glu	Gly	Ser	Met	Val	Met	
				165					170					175		
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Tyr	Phe	Met	Ile	Ser	Ile	Met	Leu	Thr	Leu	Val	Ser	Leu	Leu	Leu	Phe	
			180					185					190			
gtg	aaa	tgc	att	tct	agc	ttt	tgg	aca	gcg	att	gtt	aat	ttt	agc	agt	624
Val	Lys	Cys	Ile	Ser	Ser	Phe	Trp	Thr	Ala	Ile	Val	Asn	Phe	Ser	Ser	
	195						200					205				
ttt	gac	att	aaa	gaa	gtg	ttc	cac	ccc	att	gtg	ctt	tta	acc	cta	gcc	672
Phe	Asp	Ile	Lys	Glu	Val	Phe	His	Pro	Ile	Val	Leu	Leu	Thr	Leu	Ala	
	210					215					220					
tta	gcc	acc	ttt	gat	cta	gtc	aag	gcg	att	ttt	gaa	gag	gaa	gtt	ttg	720
Leu	Ala	Thr	Phe	Asp	Leu	Val	Lys	Ala	Ile	Phe	Glu	Glu	Glu	Val	Leu	
225					230					235					240	
ggt	aaa	aat	agc	ggg	gac	aac	cac	cat	gcg	atc	cac	cgc	acg	atg	atc	768
Gly	Lys	Asn	Ser	Gly	Asp	Asn	His	His	Ala	Ile	His	Arg	Thr	Met	Ile	
				245					250					255		
agg	ttt	tta	ggc	tct	atc	att	atc	gca	tta	gcc	att	gaa	gcg	tta	atg	816
Arg	Phe	Leu	Gly	Ser	Ile	Ile	Ile	Ala	Leu	Ala	Ile	Glu	Ala	Leu	Met	
			260					265					270			
tta	gtg	ttt	aaa	ttc	agc	gtg	agc	gaa	ccg	gat	aaa	atc	act	tat	gcg	864
Leu	Val	Phe	Lys	Phe	Ser	Val	Ser	Glu	Pro	Asp	Lys	Ile	Thr	Tyr	Ala	
		275					280					285				
gtg	tat	ttg	gct	gtt	ggc	gtg	gcg	gtg	ctt	ttg	atc	agt	ttg	gcg	att	912
Val	Tyr	Leu	Ala	Val	Gly	Val	Ala	Val	Leu	Leu	Ile	Ser	Leu	Ala	Ile	
	290					295					300					

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Pro Glu Ile Thr Leu Asp Tyr Leu Asn Lys Gln Ile Arg Lys Met His  
 35 40 45

Ala Glu Ile Lys Met Ala Lys Asn Phe Phe Val Leu Asp Ala Lys Gly  
 50 55 60

Met Leu Ile Leu Lys Pro Ser Gln Leu Lys Glu Gln Gly His Lys Glu  
 65 70 75 80

Gly Ile Leu Glu His Asp Leu Thr Glu Gly Ile Glu Leu Glu Ser His  
 85 90 95

Ala Ser Phe Ser Asp Lys Tyr Tyr Phe Tyr Gln Ala Val Ser Glu Lys  
 100 105 110

Arg Cys Ile Leu Thr Asp Pro Tyr Pro Ser Lys Lys Gly Asn His Leu  
 115 120 125

Val Val Ser Ala Ser Tyr Pro Val Tyr Asp Gln Asn Asn Asp Leu Ala  
 130 135 140

Phe Val Val Cys Leu Gln Ile Pro Leu Arg Val Ala Ile Glu Ile Ser  
 145 150 155 160

Ser Pro Ser Lys Tyr Phe Arg Thr Phe Ser Glu Gly Ser Met Val Met  
 165 170 175

Tyr Phe Met Ile Ser Ile Met Leu Thr Leu Val Ser Leu Leu Leu Phe  
180 185 190

Phe Asp Ile Lys Glu Val Phe His Pro Ile Val Leu Leu Thr Leu Ala  
210 215 220

Gly Lys Asn Ser Gly Asp Asn His His Ala Ile His Arg Thr Met Ile  
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Leu Leu Asp Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn	
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cct att tat cac agc gca ttt gtt gcg atg ggt ttt atc atc ttg tat	240
Pro Ile Tyr His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr	
65 70 75 80	
ggc gtt tat gaa atc ttt ttt gtg tgt ttg tgc aag atg agc ttg gct	288
Gly Val Tyr Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala	
85 90 95	
aaa ctg gtt ttt agg att aag att att gat att tat ttg gca gat tgc	336
Lys Leu Val Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys	
100 105 110	
ccc agt agg gct att tta ttg aag cgt tta ggg tta aag atc gtg gtt	384
Pro Ser Arg Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val	
115 120 125	
ttt cta tgc ccc ttt tta tgg ttt gtt gcg ttt aaa aac ccc tat cat	432
Phe Leu Cys Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His	
130 135 140	
agg gcg tgg cat gaa gaa aaa agc aaa agt ctt ttg gta ttg ttt taa	480
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35 40 45	
Leu Leu Asp Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn	
50 55 60	



Pro Ile Tyr His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr  
65 70 75 80

Gly Val Tyr Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala  
85 90 95

Lys Leu Val Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys  
100 105 110

Pro Ser Arg Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val  
115 120 125

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gac gct aaa gaa atc gct atg caa cga ttt gac aaa caa aac cat aag 96  
Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys  
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att ttt gaa atc ctt gcg gat aaa gtg agc gct aaa gac aat gtg ata 144  
Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile  
35 40 45  
acc gca tca ggg aat gcg atc tta ttg aat tat gat gtg tat att cta 192  
Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu  
50 55 60  
gcg gac aag gtg cgt tat gac act aaa acc aaa gaa gcg tta tta gag 240  
Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu

65	70					75					80					
ggg aat atc aag gtt tat agg ggc gag ggt ttg ctc gtt aaa acc gat	85					90					95					288
Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp																
tac gtg aaa ttg agt ttg aat gaa aaa tat gaa atc att ttc ccc ttt	100					105					110					336
Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe																
tat gtc caa gac agc gtg agc ggg att tgg gtg agc gcg gat att gcc	115					120					125					384
Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala																
agc gga aag gat caa aaa tat aag gtt aaa aac atg agc act tca ggg	130					135					140					432
Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr Ser Gly																
tgc agc att gat aac ccc att tgg cat gtc aat gcg act tca ggc tca	145					150					155					480
Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser																
ttc aac atg caa aaa tcg cat ttg tct atg tgg aat cct aag atc tat	165					170					175					528
Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr																
gtc ggt gat att cct gta ttg tat ttg ccc tat att ttc atg tcc acg	180					185					190					576
Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr																
agc aat aaa aga act act ggg ttt tta tac cct gag ttt ggc act tcc	195					200					205					624
Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser																
aac tta gac ggc ttt att tat ttg caa ccc ttt tat tta gcc ccc aaa	210					215					220					672
Asn Leu Asp Gly Phe Ile Tyr Leu Gln Pro Phe Tyr Leu Ala Pro Lys																
aac tca tgg gat atg acc ttt acc cca caa atc cgc tat aaa agg ggt	225					230					235					720
Asn Ser Trp Asp Met Thr Phe Thr Pro Gln Ile Arg Tyr Lys Arg Gly																
ttt ggc ttg aat ttt gaa gcg cgc tac att aac tct aaa aac gac agg	245					250					255					768
Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Ser Lys Asn Asp Arg																
ttt tta ttc aac gcg cgc tat ttt agg aat tac acc caa tat gtc aaa	260					265					270					816
Phe Leu Phe Asn Ala Arg Tyr Phe Arg Asn Tyr Thr Gln Tyr Val Lys																
cgc tac gat ttg agg aat caa aat atc tac ggg ttt gaa ttt tta agc	275					280					285					864
Arg Tyr Asp Leu Arg Asn Gln Asn Ile Tyr Gly Phe Glu Phe Leu Ser																
tct agc agg gac act tta caa aaa tac ttc cac ctt aag tct aat att																912

Ser	Ser	Arg	Asp	Thr	Leu	Gln	Lys	Tyr	Phe	His	Leu	Lys	Ser	Asn	Ile	
290						295					300					
gac	aac	ggg	cat	tac	att	gac	ttt	tta	tac	atg	aac	gat	ttg	gac	tat	960
Asp	Asn	Gly	His	Tyr	Ile	Asp	Phe	Leu	Tyr	Met	Asn	Asp	Leu	Asp	Tyr	
305					310					315					320	
gtg	cgt	ttt	gaa	aag	gtt	aat	aag	cgt	atc	aca	gac	gcc	acg	cac	atg	1008
Val	Arg	Phe	Glu	Lys	Val	Asn	Lys	Arg	Ile	Thr	Asp	Ala	Thr	His	Met	
				325					330					335		
tct	agg	gcg	aat	tac	tat	ttg	caa	aca	gaa	aac	aat	tat	tac	ggc	ttg	1056
Ser	Arg	Ala	Asn	Tyr	Tyr	Leu	Gln	Thr	Glu	Asn	Asn	Tyr	Tyr	Gly	Leu	
			340					345					350			
aat	atc	aag	tat	ttt	tta	aac	ctg	aat	aaa	atc	aac	aat	aac	cgc	act	1104
Asn	Ile	Lys	Tyr	Phe	Leu	Asn	Leu	Asn	Lys	Ile	Asn	Asn	Asn	Arg	Thr	
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ttc	caa	tct	gtc	cct	aat	ttg	caa	tac	cat	aaa	tat	tta	aat	tct	ttg	1152
Phe	Gln	Ser	Val	Pro	Asn	Leu	Gln	Tyr	His	Lys	Tyr	Leu	Asn	Ser	Leu	
	370					375					380					
tat	ttt	aga	aat	ttg	ttg	tat	tcg	gtg	gat	tat	cag	ttt	aga	aac	acc	1200
Tyr	Phe	Arg	Asn	Leu	Leu	Tyr	Ser	Val	Asp	Tyr	Gln	Phe	Arg	Asn	Thr	
385					390					395					400	
gca	aga	gag	att	ggc	tat	ggc	tat	gtg	caa	aac	gct	ttg	aat	gtg	ccg	1248
Ala	Arg	Glu	Ile	Gly	Tyr	Gly	Tyr	Val	Gln	Asn	Ala	Leu	Asn	Val	Pro	
				405					410					415		
gtg	ggc	ttg	caa	ttt	tct	ttg	ttt	aaa	aag	tat	ttg	tct	tta	ggg	ctt	1296
Val	Gly	Leu	Gln	Phe	Ser	Leu	Phe	Lys	Lys	Tyr	Leu	Ser	Leu	Gly	Leu	
			420					425					430			
tgg	aat	gat	ctc	caa	cta	tct	aat	gtg	gct	tta	atg	caa	tct	aaa	aat	1344
Trp	Asn	Asp	Leu	Gln	Leu	Ser	Asn	Val	Ala	Leu	Met	Gln	Ser	Lys	Asn	
		435					440					445				
tcc	ttc	gtg	cct	acg	atc	cct	aat	gaa	tca	agg	gaa	ttt	ggg	aat	ttt	1392
Ser	Phe	Val	Pro	Thr	Ile	Pro	Asn	Glu	Ser	Arg	Glu	Phe	Gly	Asn	Phe	
	450					455					460					
gtg	tct	tca	aat	ttt	tcc	atg	tat	gtc	aat	acg	gat	ttg	gct	aga	gaa	1440
Val	Ser	Ser	Asn	Phe	Ser	Met	Tyr	Val	Asn	Thr	Asp	Leu	Ala	Arg	Glu	
465					470					475					480	
tac	aac	aag	ctt	ttc	cac	acg	atc	caa	cta	gaa	gcg	att	ttc	aac	atc	1488
Tyr	Asn	Lys	Leu	Phe	His	Thr	Ile	Gln	Leu	Glu	Ala	Ile	Phe	Asn	Ile	
				485					490					495		
cct	tat	tac	acc	ttt	aaa	aac	ggc	tta	ttt	tct	caa	aac	atg	tat	gct	1536
Pro	Tyr	Tyr	Thr	Phe	Lys	Asn	Gly	Leu	Phe	Ser	Gln	Asn	Met	Tyr	Ala	
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tta agc gcg caa gcc tta aac agc tac act tcg cct tta ttg aga gat	1584
Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp	
515 520 525	
tat gat tat caa ggg cgt ttg tat gac tcg gtg tgg aat cct agc agt	1632
Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser	
530 535 540	
att tta cct agc aat gcg agc aac aag acg gtg gat tta acc cta acg	1680
Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr Leu Thr	
545 550 555 560	
caa tac ctt tat ggc tta ggg ggg caa gag tta ttg tat ttt aaa ata	1728
Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile	
565 570 575	
tcg caa ctc atc aat ctt gac gat aaa gtt tcg ccc ttt aga atg cca	1776
Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro	
580 585 590	
cta gag agc aag atc ggg ttt tcg ccc tta acg gga ttg aac atc ttt	1824
Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe	
595 600 605	
ggg aat gtc ttt tat tcg ttt tat caa aac cgc tta gaa gaa atc tct	1872
Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser	
610 615 620	
gtg aac gcc aat tac caa cgc aag ttt tta agc ttt aac ctc tct tat	1920
Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr	
625 630 635 640	
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ctg cgg att att taa	1983
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<400> 26

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Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile  
35 40 45

Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu  
50 55 60

Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu  
65 70 75 80

Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp  
85 90 95

Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe  
100 105 110

Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala  
115 120 125

Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr Ser Gly  
130 135 140

Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser  
145 150 155 160

Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr  
165 170 175

Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr  
180 185 190

Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser  
195 200 205

Asn Leu Asp Gly Phe Ile Tyr Leu Gln Pro Phe Tyr Leu Ala Pro Lys  
210 215 220

Asn Ser Trp Asp Met Thr Phe Thr Pro Gln Ile Arg Tyr Lys Arg Gly  
225 230 235 240

Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Ser Lys Asn Asp Arg

245							250							255						
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			260					265					270							
Arg	Tyr	Asp	Leu	Arg	Asn	Gln	Asn	Ile	Tyr	Gly	Phe	Glu	Phe	Leu	Ser					
		275					280					285								
Ser	Ser	Arg	Asp	Thr	Leu	Gln	Lys	Tyr	Phe	His	Leu	Lys	Ser	Asn	Ile					
	290					295					300									
Asp	Asn	Gly	His	Tyr	Ile	Asp	Phe	Leu	Tyr	Met	Asn	Asp	Leu	Asp	Tyr					
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Val	Arg	Phe	Glu	Lys	Val	Asn	Lys	Arg	Ile	Thr	Asp	Ala	Thr	His	Met					
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		355					360					365								
Phe	Gln	Ser	Val	Pro	Asn	Leu	Gln	Tyr	His	Lys	Tyr	Leu	Asn	Ser	Leu					
	370					375					380									
Tyr	Phe	Arg	Asn	Leu	Leu	Tyr	Ser	Val	Asp	Tyr	Gln	Phe	Arg	Asn	Thr					
385					390					395					400					
Ala	Arg	Glu	Ile	Gly	Tyr	Gly	Tyr	Val	Gln	Asn	Ala	Leu	Asn	Val	Pro					
				405					410					415						
Val	Gly	Leu	Gln	Phe	Ser	Leu	Phe	Lys	Lys	Tyr	Leu	Ser	Leu	Gly	Leu					
			420					425					430							
Trp	Asn	Asp	Leu	Gln	Leu	Ser	Asn	Val	Ala	Leu	Met	Gln	Ser	Lys	Asn					
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Ser	Phe	Val	Pro	Thr	Ile	Pro	Asn	Glu	Ser	Arg	Glu	Phe	Gly	Asn	Phe					
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Val Ser Ser Asn Phe Ser Met Tyr Val Asn Thr Asp Leu Ala Arg Glu  
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Tyr Asn Lys Leu Phe His Thr Ile Gln Leu Glu Ala Ile Phe Asn Ile  
485 490 495

Pro Tyr Tyr Thr Phe Lys Asn Gly Leu Phe Ser Gln Asn Met Tyr Ala  
500 505 510

Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp  
515 520 525

Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser  
530 535 540

Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr Leu Thr  
545 550 555 560

Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile  
565 570 575

Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro  
580 585 590

Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe  
595 600 605

Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser  
610 615 620

Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr  
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 aac gct aaa gaa gcg gat ttc atc tct gat ttg gaa tac ggg atg gct 96  
 Asn Ala Lys Glu Ala Asp Phe Ile Ser Asp Leu Glu Tyr Gly Met Ala  
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 Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys Cys His Gly Ile  
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 aaa ggc gaa caa caa gaa atc act ttt tat tat gaa aaa ggc gaa aaa 192  
 Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu Lys Gly Glu Lys  
 50 55 60  
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 Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp Phe Lys Thr Phe  
 65 70 75 80  
 aaa gac gcc ctg agt tta ggc aaa ggc atg atg cct aaa tac aat ctc 288  
 Lys Asp Ala Leu Ser Leu Gly Lys Gly Met Met Pro Lys Tyr Asn Leu  
 85 90 95  
 aat tta gaa gaa atc caa gcg att tac ctt tac atc acc tct tta gag 336  
 Asn Leu Glu Glu Ile Gln Ala Ile Tyr Leu Tyr Ile Thr Ser Leu Glu  
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 cat aaa gac gag cat aag aat cct tcc aag cct taa 372  
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 20 25 30



Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys Cys His Gly Ile  
35 40 45

Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu Lys Gly Glu Lys  
50 55 60

Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp Phe Lys Thr Phe  
65 70 75 80

Lys Asp Ala Leu Ser Leu Gly Lys Gly Met Met Pro Lys Tyr Asn Leu  
85 90 95

Asn Leu Glu Glu Ile Gln Ala Ile Tyr Leu Tyr Ile Thr Ser Leu Glu  
100 105 110

His Lys Asp Glu His Lys Asn Pro Ser Lys Pro  
115 120

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1 5 10 15  
atg gac gct caa aaa aca gac aat aaa ggt ttg aaa aaa gaa aga gaa 96  
Met Asp Ala Gln Lys Thr Asp Asn Lys Gly Leu Lys Lys Glu Arg Glu  
20 25 30  
ctt tta gaa att act ggc aac caa ttt gta gcg aac gac aaa acc aaa 144  
Leu Leu Glu Ile Thr Gly Asn Gln Phe Val Ala Asn Asp Lys Thr Lys  
35 40 45  
acc gcc gtt att caa ggc aat gtg cag atc aaa aaa ggt aaa gac cgg 192  
Thr Ala Val Ile Gln Gly Asn Val Gln Ile Lys Lys Gly Lys Asp Arg  
50 55 60  
ttg ttt gcg gat aag gtg agc gtg ttt tta aac gat aaa cga aag cca 240  
Leu Phe Ala Asp Lys Val Ser Val Phe Leu Asn Asp Lys Arg Lys Pro

65		70		75		80										
gag	cgc	tat	gaa	gcc	aca	ggg	aac	acg	cat	ttt	aac	atc	ttt	aca	gag	288
Glu	Arg	Tyr	Glu	Ala	Thr	Gly	Asn	Thr	His	Phe	Asn	Ile	Phe	Thr	Glu	
			85					90					95			
gac	aat	cgt	gaa	atc	agc	ggg	agc	gct	gac	aag	ctc	att	tat	aac	gca	336
Asp	Asn	Arg	Glu	Ile	Ser	Gly	Ser	Ala	Asp	Lys	Leu	Ile	Tyr	Asn	Ala	
			100					105					110			
ttg	aat	ggg	gaa	tac	aaa	tta	ttg	caa	aat	gcg	gtg	gtt	aga	gaa	gtg	384
Leu	Asn	Gly	Glu	Tyr	Lys	Leu	Leu	Gln	Asn	Ala	Val	Val	Arg	Glu	Val	
		115					120					125				
ggg	aaa	tct	aat	gtc	atc	act	ggc	gat	gaa	atc	att	tta	aac	aaa	act	432
Gly	Lys	Ser	Asn	Val	Ile	Thr	Gly	Asp	Glu	Ile	Ile	Leu	Asn	Lys	Thr	
	130					135					140					
aag	ggt	tat	gct	gat	gtg	tta	ggg	agc	gcg	aaa	cgg	ccc	gct	aaa	ttc	480
Lys	Gly	Tyr	Ala	Asp	Val	Leu	Gly	Ser	Ala	Lys	Arg	Pro	Ala	Lys	Phe	
	145				150					155					160	
gtg	ttt	gat	atg	gaa	gat	att	aat	gaa	gaa	aat	cgt	aag	gct	aaa	ttg	528
Val	Phe	Asp	Met	Glu	Asp	Ile	Asn	Glu	Glu	Asn	Arg	Lys	Ala	Lys	Leu	
				165					170					175		
aag	aag	aaa	ggc	act	aag	gaa	aaa	cca	tga							558
Lys	Lys	Lys	Gly	Thr	Lys	Glu	Lys	Pro								
			180					185								

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 <212> PRT  
 <213> Helicobacter pylori

<400> 30

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Leu	Leu	Glu	Ile	Thr	Gly	Asn	Gln	Phe	Val	Ala	Asn	Asp	Lys	Thr	Lys
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Thr	Ala	Val	Ile	Gln	Gly	Asn	Val	Gln	Ile	Lys	Lys	Gly	Lys	Asp	Arg
	50					55					60				

Leu	Phe	Ala	Asp	Lys	Val	Ser	Val	Phe	Leu	Asn	Asp	Lys	Arg	Lys	Pro
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65		70		75		80									
Glu	Arg	Tyr	Glu	Ala	Thr	Gly	Asn	Thr	His	Phe	Asn	Ile	Phe	Thr	Glu
				85					90					95	
Asp	Asn	Arg	Glu	Ile	Ser	Gly	Ser	Ala	Asp	Lys	Leu	Ile	Tyr	Asn	Ala
			100					105					110		
Leu	Asn	Gly	Glu	Tyr	Lys	Leu	Leu	Gln	Asn	Ala	Val	Val	Arg	Glu	Val
		115					120					125			
Gly	Lys	Ser	Asn	Val	Ile	Thr	Gly	Asp	Glu	Ile	Ile	Leu	Asn	Lys	Thr
	130					135					140				
Lys	Gly	Tyr	Ala	Asp	Val	Leu	Gly	Ser	Ala	Lys	Arg	Pro	Ala	Lys	Phe
145					150					155					160
Val	Phe	Asp	Met	Glu	Asp	Ile	Asn	Glu	Glu	Asn	Arg	Lys	Ala	Lys	Leu
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Lys	Lys	Lys	Gly	Thr	Lys	Glu	Lys	Pro							
			180					185							

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 <212> DNA  
 <213> Helicobacter pylori

<220>  
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1				5				10						15			
cta	tca	ggg	att	ttt	ggc	att	ggt	ggg	ggg	ttg	atc	att	gtc	cct	atc		96
Leu	Ser	Gly	Ile	Phe	Gly	Ile	Gly	Gly	Gly	Leu	Ile	Ile	Val	Pro	Ile		
			20					25					30				
atg	ctc	gca	acc	ggg	cat	tct	ttt	gaa	gaa	tcc	att	ggg	att	tcc	att		144
Met	Leu	Ala	Thr	Gly	His	Ser	Phe	Glu	Glu	Ser	Ile	Gly	Ile	Ser	Ile		
		35					40					45					
ttg	caa	atg	gcg	ctt	tca	tcg	ttc	gtg	ggc	tct	ggt	ttg	aat	ttc	aaa		192

Leu	Gln	Met	Ala	Leu	Ser	Ser	Phe	Val	Gly	Ser	Val	Leu	Asn	Phe	Lys	
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aaa	aaa	tcg	ctt	gat	ttt	tct	tta	ggc	ttg	ttg	ata	ggg	gca	ggg	ggg	240
Lys	Lys	Ser	Leu	Asp	Phe	Ser	Leu	Gly	Leu	Leu	Ile	Gly	Ala	Gly	Gly	
65					70				75						80	
ctg	ata	ggg	gcg	agt	ttt	agc	gga	ttt	gtt	tta	aaa	atc	gtt	tcc	agt	288
Leu	Ile	Gly	Ala	Ser	Phe	Ser	Gly	Phe	Val	Leu	Lys	Ile	Val	Ser	Ser	
				85					90					95		
aaa	att	tta	atg	gtt	att	ttc	gcg	ctt	tta	gtc	gtg	tat	tct	atg	atc	336
Lys	Ile	Leu	Met	Val	Ile	Phe	Ala	Leu	Leu	Val	Val	Tyr	Ser	Met	Ile	
			100					105					110			
caa	ttt	gtt	ttg	aaa	ccc	aaa	aaa	aaa	gat	ttg	ata	gcg	gat	act	aaa	384
Gln	Phe	Val	Leu	Lys	Pro	Lys	Lys	Lys	Asp	Leu	Ile	Ala	Asp	Thr	Lys	
		115					120					125				
cgc	tat	cat	ctg	caa	ggt	ttg	aaa	tta	ttt	tta	att	ggc	acg	ctc	aca	432
Arg	Tyr	His	Leu	Gln	Gly	Leu	Lys	Leu	Phe	Leu	Ile	Gly	Thr	Leu	Thr	
	130					135					140					
ggg	ttt	ttt	gct	atc	act	tta	ggg	att	ggt	ggg	ggg	atg	ctc	atg	gtg	480
Gly	Phe	Phe	Ala	Ile	Thr	Leu	Gly	Ile	Gly	Gly	Gly	Met	Leu	Met	Val	
145					150					155					160	
cct	ttg	atg	cat	tat	ttt	tta	ggg	tat	gat	tct	aaa	aaa	tgc	gtg	gct	528
Pro	Leu	Met	His	Tyr	Phe	Leu	Gly	Tyr	Asp	Ser	Lys	Lys	Cys	Val	Ala	
				165					170					175		
cta	ggg	tta	ttt	ttc	atc	ttg	ttt	tct	tct	att	tca	gga	gct	ttt	tct	576
Leu	Gly	Leu	Phe	Phe	Ile	Leu	Phe	Ser	Ser	Ile	Ser	Gly	Ala	Phe	Ser	
			180					185					190			
tta	atg	tat	cac	cac	atc	atc	aat	aaa	gaa	gtg	ctc	tta	gca	ggg	gcg	624
Leu	Met	Tyr	His	His	Ile	Ile	Asn	Lys	Glu	Val	Leu	Leu	Ala	Gly	Ala	
		195					200					205				
att	gtg	gga	tta	gga	tct	gtt	atg	ggc	gtg	agc	att	ggg	att	aaa	tgg	672
Ile	Val	Gly	Leu	Gly	Ser	Val	Met	Gly	Val	Ser	Ile	Gly	Ile	Lys	Trp	
	210					215					220					
atc	atg	ggg	ctt	ttg	aat	gaa	aaa	atg	cat	aaa	gct	ttg	att	tta	ggg	720
Ile	Met	Gly	Leu	Leu	Asn	Glu	Lys	Met	His	Lys	Ala	Leu	Ile	Leu	Gly	
225					230					235					240	
gtg	tat	ggt	ttg	tcg	cta	ttg	att	gtt	tta	tac	aaa	ctc	ttt	ttt	taa	768
Val	Tyr	Gly	Leu	Ser	Leu	Leu	Ile	Val	Leu	Tyr	Lys	Leu	Phe	Phe		
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<400> 32

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Met Leu Ala Thr Gly His Ser Phe Glu Glu Ser Ile Gly Ile Ser Ile  
 35 40 45

Leu Gln Met Ala Leu Ser Ser Phe Val Gly Ser Val Leu Asn Phe Lys  
 50 55 60

Lys Lys Ser Leu Asp Phe Ser Leu Gly Leu Leu Ile Gly Ala Gly Gly  
 65 70 75 80

Leu Ile Gly Ala Ser Phe Ser Gly Phe Val Leu Lys Ile Val Ser Ser  
 85 90 95

Lys Ile Leu Met Val Ile Phe Ala Leu Leu Val Val Tyr Ser Met Ile  
 100 105 110

Gln Phe Val Leu Lys Pro Lys Lys Lys Asp Leu Ile Ala Asp Thr Lys  
 115 120 125

Arg Tyr His Leu Gln Gly Leu Lys Leu Phe Leu Ile Gly Thr Leu Thr  
 130 135 140

Gly Phe Phe Ala Ile Thr Leu Gly Ile Gly Gly Gly Met Leu Met Val  
 145 150 155 160

Pro Leu Met His Tyr Phe Leu Gly Tyr Asp Ser Lys Lys Cys Val Ala  
 165 170 175

Leu Gly Leu Phe Phe Ile Leu Phe Ser Ser Ile Ser Gly Ala Phe Ser  
 180 185 190

Leu Met Tyr His His Ile Ile Asn Lys Glu Val Leu Leu Ala Gly Ala  
195 200 205

Ile Val Gly Leu Gly Ser Val Met Gly Val Ser Ile Gly Ile Lys Trp  
210 215 220

Ile Met Gly Leu Leu Asn Glu Lys Met His Lys Ala Leu Ile Leu Gly  
225 230 235 240

Val Tyr Gly Leu Ser Leu Leu Ile Val Leu Tyr Lys Leu Phe Phe  
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<210> 33  
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aaa gag gtg atc aat cat aaa gaa ttg cat ttt tgc tgc acg ggg tgc 96  
Lys Glu Val Ile Asn His Lys Glu Leu His Phe Cys Cys Thr Gly Cys  
20 25 30  
gct agg gtg tat gcg tta ttg tta gat ttg aat tta gag agc ttt tat 144  
Ala Arg Val Tyr Ala Leu Leu Leu Asp Leu Asn Leu Glu Ser Phe Tyr  
35 40 45  
gac aaa tta aac gat tcc act tta gcc ccc gta acg ccc caa gat tca 192  
Asp Lys Leu Asn Asp Ser Thr Leu Ala Pro Val Thr Pro Gln Asp Ser  
50 55 60  
atg agc gct ttg gaa tta gaa caa gcc ctt gaa gaa aac aat aag ggc 240  
Met Ser Ala Leu Glu Leu Glu Gln Ala Leu Glu Glu Asn Asn Lys Gly  
65 70 75 80  
gat ttt atc ctt aat ctt ttg tta gaa aaa acg cat tgt aac gct tgc 288  
Asp Phe Ile Leu Asn Leu Leu Leu Glu Lys Thr His Cys Asn Ala Cys  
85 90 95  
ttg tgg ctc aat caa aag gtt tta gaa cgt tta agt ggg gtt aaa aaa 336  
Leu Trp Leu Asn Gln Lys Val Leu Glu Arg Leu Ser Gly Val Lys Lys  
100 105 110

gtg agc gtg aat ttc acc acc cac cac ttg caa atc gtg ttt gag aag	384
Val Ser Val Asn Phe Thr Thr His His Leu Gln Ile Val Phe Glu Lys	
115 120 125	
tcc tta aac cct aaa gag att att caa aaa att gag agt ttg ggc tat	432
Ser Leu Asn Pro Lys Glu Ile Ile Gln Lys Ile Glu Ser Leu Gly Tyr	
130 135 140	
ggg gct aaa att tat aat gcg caa aat tac acc cta aaa gcg caa aaa	480
Gly Ala Lys Ile Tyr Asn Ala Gln Asn Tyr Thr Leu Lys Ala Gln Lys	
145 150 155 160	
gaa cag cgc tcc tac ttg ctc act ttg agc gtg ggg ttt ttt gcc act	528
Glu Gln Arg Ser Tyr Leu Leu Thr Leu Ser Val Gly Phe Phe Ala Thr	
165 170 175	
atg aat ttg atg ttt atc gcc att gcc aaa tac gca agt tat ggt ggc	576
Met Asn Leu Met Phe Ile Ala Ile Ala Lys Tyr Ala Ser Tyr Gly Gly	
180 185 190	
gca agt tat ggc ggt gcg aat tat ggc gct ggc atg gat aag ctt atg	624
Ala Ser Tyr Gly Gly Ala Asn Tyr Gly Ala Gly Met Asp Lys Leu Met	
195 200 205	
caa agg aat ttg gat ctc gta tcg ctc ttt tta agc ttg ttg gtg tta	672
Gln Arg Asn Leu Asp Leu Val Ser Leu Phe Leu Ser Leu Leu Val Leu	
210 215 220	
gtg gtt gtg ggg cgt ttt ttc att aag ggg gcg ttt tat ggg cta aaa	720
Val Val Val Gly Arg Phe Phe Ile Lys Gly Ala Phe Tyr Gly Leu Lys	
225 230 235 240	
aat ggc gtt ttg ggc atg gat ttg agc gtg tct ttt gga gcg tta tcg	768
Asn Gly Val Leu Gly Met Asp Leu Ser Val Ser Phe Gly Ala Leu Ser	
245 250 255	
gcg ttt gtt tat tcc gtt tat gcc atg ttg gtg tcc caa gag act tat	816
Ala Phe Val Tyr Ser Val Tyr Ala Met Leu Val Ser Gln Glu Thr Tyr	
260 265 270	
ttt gaa gcg agc agc acg att cta acg ctt gtt ttt ggc tct aag ttt	864
Phe Glu Ala Ser Ser Thr Ile Leu Thr Leu Val Phe Gly Ser Lys Phe	
275 280 285	
ttg gaa tta aaa gcc agg ctg ttt gcg aat gaa aaa tgt ctg gcc cta	912
Leu Glu Leu Lys Ala Arg Leu Phe Ala Asn Glu Lys Cys Leu Ala Leu	
290 295 300	
gaa tcg cat gaa atc cat agc gtg atc gtt gta gaa aat ggc aag caa	960
Glu Ser His Glu Ile His Ser Val Ile Val Val Glu Asn Gly Lys Gln	
305 310 315 320	

aca gaa aaa cac cct aaa gat gtg gcg ata ggc tct gtt gtt tgg gtg	1008
Thr Glu Lys His Pro Lys Asp Val Ala Ile Gly Ser Val Val Trp Val	
325 330 335	
cca agc ggg gct aaa atc gca cta gat ggc gtg ctt tta aat aat gcg	1056
Pro Ser Gly Ala Lys Ile Ala Leu Asp Gly Val Leu Leu Asn Asn Ala	
340 345 350	
agc gtg gat gcg tct ttg atc agt ggg gag ttt aag cct ttg gaa ttg	1104
Ser Val Asp Ala Ser Leu Ile Ser Gly Glu Phe Lys Pro Leu Glu Leu	
355 360 365	
ggg gtt aat gat cca att tta ggg ggt tat gtg aat gtg ggc gtg cct	1152
Gly Val Asn Asp Pro Ile Leu Gly Gly Tyr Val Asn Val Gly Val Pro	
370 375 380	
ttt agc tat caa gtg agc gct aat ttt caa aac tca cgc ctt tct ggt	1200
Phe Ser Tyr Gln Val Ser Ala Asn Phe Gln Asn Ser Arg Leu Ser Gly	
385 390 395 400	
ttg tta gaa act tta aaa aag agt ttt tta gaa aag ccc tta att gag	1248
Leu Leu Glu Thr Leu Lys Lys Ser Phe Leu Glu Lys Pro Leu Ile Glu	
405 410 415	
agt agc gcg aat caa att gcg gat att ttt tct aaa gcg gtg ttg ttt	1296
Ser Ser Ala Asn Gln Ile Ala Asp Ile Phe Ser Lys Ala Val Leu Phe	
420 425 430	
tta gcc ttt gta agc ttt ttg tta tgg caa ttt ggt ttg ggg ggt aat	1344
Leu Ala Phe Val Ser Phe Leu Leu Trp Gln Phe Gly Leu Gly Gly Asn	
435 440 445	
ttt gaa aaa gcc tta atg gtg tgt att agc gtg cta gtc atc agc tgc	1392
Phe Glu Lys Ala Leu Met Val Cys Ile Ser Val Leu Val Ile Ser Cys	
450 455 460	
cct tgc gcg ttc gct ctg gct acg ccc att gcg tta gtg ata ggg gtg	1440
Pro Cys Ala Phe Ala Leu Ala Thr Pro Ile Ala Leu Val Ile Gly Val	
465 470 475 480	
ttt aaa aac cct ttg atc gtg ttt aaa gaa gcg ttg ttt tta gaa act	1488
Phe Lys Asn Pro Leu Ile Val Phe Lys Glu Ala Leu Phe Leu Glu Thr	
485 490 495	
ctg gct aaa gtg aaa aaa atc ttt ata gac aaa acc ggc acg ctc acg	1536
Leu Ala Lys Val Lys Lys Ile Phe Ile Asp Lys Thr Gly Thr Leu Thr	
500 505 510	
caa aaa gaa gtc ctt tta aaa gaa aaa atc att tat gaa gaa ttt gat	1584
Gln Lys Glu Val Leu Leu Lys Glu Lys Ile Ile Tyr Glu Glu Phe Asp	
515 520 525	
gga agg ctt ttg aag agc ctt tta aaa gtg aga gag cat tta gcc cat	1632



Gly	Arg	Leu	Leu	Lys	Ser	Leu	Leu	Lys	Val	Arg	Glu	His	Leu	Ala	His	
530						535					540					
agc	gcg	att	ctt	aaa	tct	cta	gat	ggc	gat	gag	gtt	agt	tta	gaa	aag	1680
Ser	Ala	Ile	Leu	Lys	Ser	Leu	Asp	Gly	Asp	Glu	Val	Ser	Leu	Glu	Lys	
545					550					555					560	
ata	gag	ttt	ttc	gct	cat	ggc	ctg	aaa	gcg	agc	tat	caa	aac	gaa	acc	1728
Ile	Glu	Phe	Phe	Ala	His	Gly	Leu	Lys	Ala	Ser	Tyr	Gln	Asn	Glu	Thr	
				565					570					575		
ctg	cta	gtg	ggg	agt	ttg	aaa	ttt	ttg	gga	tct	atg	ggg	gtg	gat	ata	1776
Leu	Leu	Val	Gly	Ser	Leu	Lys	Phe	Leu	Gly	Ser	Met	Gly	Val	Asp	Ile	
			580					585					590			
cca	atg	aaa	gag	agc	gct	aat	atc	atg	gta	ggc	ttt	gcg	aaa	aat	gag	1824
Pro	Met	Lys	Glu	Ser	Ala	Asn	Ile	Met	Val	Gly	Phe	Ala	Lys	Asn	Glu	
		595					600					605				
act	tta	tgc	gcg	tta	ttc	att	tta	gaa	gag	cgt	ttg	aaa	gct	aac	gct	1872
Thr	Leu	Cys	Ala	Leu	Phe	Ile	Leu	Glu	Glu	Arg	Leu	Lys	Ala	Asn	Ala	
	610					615					620					
aaa	gaa	gtc	gtt	cag	gct	tta	caa	aat	aaa	ggc	tta	gaa	tta	gag	att	1920
Lys	Glu	Val	Val	Gln	Ala	Leu	Gln	Asn	Lys	Gly	Leu	Glu	Leu	Glu	Ile	
625					630					635					640	
tta	agc	ggg	gat	aat	gaa	agc	tcg	gtt	aag	gag	tgc	gcg	aaa	aaa	tta	1968
Leu	Ser	Gly	Asp	Asn	Glu	Ser	Ser	Val	Lys	Glu	Cys	Ala	Lys	Lys	Leu	
				645					650					655		
ggg	att	tct	aat	tat	cat	gcc	cat	ttg	acc	cct	gaa	gat	aag	gct	caa	2016
Gly	Ile	Ser	Asn	Tyr	His	Ala	His	Leu	Thr	Pro	Glu	Asp	Lys	Ala	Gln	
			660					665					670			
acc	atc	agc	tct	tat	aag	ggc	gtt	tgc	gcg	atg	gta	ggc	gat	ggc	aat	2064
Thr	Ile	Ser	Ser	Tyr	Lys	Gly	Val	Cys	Ala	Met	Val	Gly	Asp	Gly	Asn	
			675				680					685				
aat	gat	gcg	tta	gcc	tta	aaa	caa	gcg	agc	gtt	tct	tta	ggg	ttt	gaa	2112
Asn	Asp	Ala	Leu	Ala	Leu	Lys	Gln	Ala	Ser	Val	Ser	Leu	Gly	Phe	Glu	
	690					695					700					
aaa	agc	gct	ttg	agt	aaa	agc	gca	tgc	gat	att	ttg	ctt	tta	gaa	gag	2160
Lys	Ser	Ala	Leu	Ser	Lys	Ser	Ala	Cys	Asp	Ile	Leu	Leu	Leu	Glu	Glu	
705					710					715					720	
gat	ttg	agt	ttg	cta	aaa	aaa	gcg	ttt	gat	aac	gct	caa	aaa	gtc	tat	2208
Asp	Leu	Ser	Leu	Leu	Lys	Lys	Ala	Phe	Asp	Asn	Ala	Gln	Lys	Val	Tyr	
				725					730					735		
caa	gtg	gtg	ttg	caa	aac	att	gtt	ttg	agc	ttg	att	tat	aac	gct	att	2256
Gln	Val	Val	Leu	Gln	Asn	Ile	Val	Leu	Ser	Leu	Ile	Tyr	Asn	Ala	Ile	
			740					745					750			

tta atc ccg gtc gct atg cta gga tac att aac cct tta ata gcg agt	2304
Leu Ile Pro Val Ala Met Leu Gly Tyr Ile Asn Pro Leu Ile Ala Ser	
755 760 765	

ttg agc atg agc gct agc tca ctc tta gtg gtc tta aat tct ttg agg	2352
Leu Ser Met Ser Ala Ser Ser Leu Leu Val Val Leu Asn Ser Leu Arg	
770 775 780	

ttg aaa cgc tct taa	2367
Leu Lys Arg Ser	
785	

<210> 34  
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 <212> PRT  
 <213> Helicobacter pylori

<400> 34

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20 25 30

Ala Arg Val Tyr Ala Leu Leu Leu Asp Leu Asn Leu Glu Ser Phe Tyr
35 40 45

Asp Lys Leu Asn Asp Ser Thr Leu Ala Pro Val Thr Pro Gln Asp Ser
50 55 60

Met Ser Ala Leu Glu Leu Glu Gln Ala Leu Glu Glu Asn Asn Lys Gly
65 70 75 80

Asp Phe Ile Leu Asn Leu Leu Leu Glu Lys Thr His Cys Asn Ala Cys
85 90 95

Leu Trp Leu Asn Gln Lys Val Leu Glu Arg Leu Ser Gly Val Lys Lys
100 105 110

Val Ser Val Asn Phe Thr Thr His His Leu Gln Ile Val Phe Glu Lys
115 120 125

Ser Leu Asn Pro Lys Glu Ile Ile Gln Lys Ile Glu Ser Leu Gly Tyr
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130		135		140													
Gly	Ala	Lys	Ile	Tyr	Asn	Ala	Gln	Asn	Tyr	Thr	Leu	Lys	Ala	Gln	Lys		
145					150					155					160		
Glu	Gln	Arg	Ser	Tyr	Leu	Leu	Thr	Leu	Ser	Val	Gly	Phe	Phe	Ala	Thr		
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Thr	Glu	Lys	His	Pro	Lys	Asp	Val	Ala	Ile	Gly	Ser	Val	Val	Trp	Val		
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Pro	Ser	Gly	Ala	Lys	Ile	Ala	Leu	Asp	Gly	Val	Leu	Leu	Asn	Asn	Ala		
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Ser Ser Ala Asn Gln Ile Ala Asp Ile Phe Ser Lys Ala Val Leu Phe  
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Leu Ala Phe Val Ser Phe Leu Leu Trp Gln Phe Gly Leu Gly Gly Asn  
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Phe Glu Lys Ala Leu Met Val Cys Ile Ser Val Leu Val Ile Ser Cys  
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Pro Cys Ala Phe Ala Leu Ala Thr Pro Ile Ala Leu Val Ile Gly Val  
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Leu Ala Lys Val Lys Lys Ile Phe Ile Asp Lys Thr Gly Thr Leu Thr  
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Gln Lys Glu Val Leu Leu Lys Glu Lys Ile Ile Tyr Glu Glu Phe Asp  
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Gly Arg Leu Leu Lys Ser Leu Leu Lys Val Arg Glu His Leu Ala His  
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Pro Met Lys Glu Ser Ala Asn Ile Met Val Gly Phe Ala Lys Asn Glu  
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Thr Ile Ser Ser Tyr Lys Gly Val Cys Ala Met Val Gly Asp Gly Asn  
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Lys Ser Ala Leu Ser Lys Ser Ala Cys Asp Ile Leu Leu Leu Glu Glu  
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Asp Leu Ser Leu Leu Lys Lys Ala Phe Asp Asn Ala Gln Lys Val Tyr  
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Gln Val Val Leu Gln Asn Ile Val Leu Ser Leu Ile Tyr Asn Ala Ile  
740 745 750

Leu Ile Pro Val Ala Met Leu Gly Tyr Ile Asn Pro Leu Ile Ala Ser  
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Ser Val Glu Ala Leu Glu Asn Asp Gly Ser Lys Pro Asn Asp Leu Thr  
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Ser Pro Lys Glu Ala Ser Gln Glu Ser Gln Lys Asn Glu Ala Pro Lys  
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Asn Glu Val Gln Arg Asn Glu Ala Gln Lys Glu Thr Pro Gln Ser Asn  
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caa acg cct aaa gaa atg aaa gtc aag tcc att tct tat gtc ggg ctt 240  
Gln Thr Pro Lys Glu Met Lys Val Lys Ser Ile Ser Tyr Val Gly Leu  
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Ser Tyr Met Ser Asp Met Leu Ala Asn Glu Ile Val Lys Ile Arg Val  
85 90 95  
  
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Gly Asp Ile Val Asp Ser Lys Lys Ile Asp Thr Ala Val Leu Ala Leu  
100 105 110  
  
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Phe Asn Gln Gly Tyr Phe Lys Asp Val Tyr Ala Thr Phe Glu Gly Gly  
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Ile Leu Glu Phe His Phe Asp Glu Lys Ala Arg Ile Ala Gly Val Glu  
130 135 140  
  
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Ala Lys Thr Ala Leu Lys Thr Ala Leu Glu Gly Gln Gly Tyr Tyr Gly	
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Ser Val Val Glu Val Arg Thr Glu Lys Val Ser Glu Gly Ala Leu Leu	
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Ser Ala Asn Lys Gln Arg Asp Phe Met Gly Trp Met Trp Gly Leu Asn	
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Asp Gly Lys Leu Arg Leu Asp Gln Leu Glu Tyr Asp Ser Met Arg Ile	
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Gln Asp Val Tyr Met Arg Arg Gly Tyr Leu Asp Ala His Ile Ser Ser	
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Pro Phe Leu Lys Thr Asp Phe Ser Thr His Asp Ala Lys Leu His Tyr	
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Lys Val Lys Glu Gly Ile Gln Tyr Arg Ile Ser Asp Ile Leu Ile Glu	
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Ile Asp Asn Pro Val Val Pro Leu Lys Thr Leu Glu Lys Ala Leu Lys	
325 330 335	
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Gln Ile Leu Lys Thr Glu Ile Ala Asp Lys Gly Tyr Ala Phe Ala Val	
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Val Lys Pro Asp Leu Asp Lys Asp Glu Lys Asn Gly Leu Val Lys Val	

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Val	Ser	Pro	Arg	Gln	Cys	Ser	Thr	Pro	Ala	Ser	Val	Ile	Ile	Asn	Arg	
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Leu	Ser	Gly	Gly	Lys	Thr	Pro	Leu	Gln	Pro	Glu	Ser	Cys	Ser	Ser	Pro	
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Gly	Ala	Ile	Thr	Thr	Ser	Pro	Glu	Ile	Arg	Gly	Ile	Trp	Asp	Arg	Asp	
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Tyr	His	Thr	Pro	Ile	Thr	Ser	Ser	Phe	Thr	Leu	Asp	Val	Ser	Tyr	Asp	
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Ala	Ala	Tyr	His	His	Leu	Gln	Lys	Tyr	Leu	Leu	Ile	Asp	Leu	Ile	Ala	
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Arg	Phe	Lys	Thr	Gln	Gly	Gly	Tyr	Ile	Phe	Arg	Tyr	Asn	Thr	Asp	Asp	
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Tyr	Leu	Pro	Leu	Asn	Ser	Thr	Phe	Tyr	Met	Gly	Gly	Val	Thr	Thr	Val	
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Arg	Gly	Phe	Arg	Asn	Gly	Ser	Val	Thr	Pro	Lys	Asp	Glu	Phe	Gly	Leu	
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Trp	Leu	Gly	Gly	Asp	Gly	Ile	Phe	Thr	Ala	Ser	Thr	Glu	Leu	Ser	Tyr	
	785				790					795					800	
ggg	gtg	cta	aag	gcg	gct	aaa	atg	cgc	tta	gcg	tgg	ttt	ttt	gac	ttt	2448
Gly	Val	Leu	Lys	Ala	Ala	Lys	Met	Arg	Leu	Ala	Trp	Phe	Phe	Asp	Phe	
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Gly Phe Leu Thr Phe Lys Thr Pro Thr Arg Gly Ser Phe Phe Tyr Asn	
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gct cct gtt acg aca gcg aat ttt aaa gat tat ggc gtt ata ggg gct	2544
Ala Pro Val Thr Thr Ala Asn Phe Lys Asp Tyr Gly Val Ile Gly Ala	
835 840 845	
ggg ttt gaa aga gcg act tgg agg gct tcc aca ggc ttg cag att gaa	2592
Gly Phe Glu Arg Ala Thr Trp Arg Ala Ser Thr Gly Leu Gln Ile Glu	
850 855 860	
tgg att tcg ccc atg ggg cct ttg gtg ttg att ttc cct ata gcg ttt	2640
Trp Ile Ser Pro Met Gly Pro Leu Val Leu Ile Phe Pro Ile Ala Phe	
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Phe Asn Gln Trp Gly Asp Gly Asn Gly Lys Lys Cys Lys Gly Leu Cys	
885 890 895	
ttc aac cct aac atg gac gat tac acg caa cac ttt gaa ttt tct atg	2736
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Gln Thr Pro Lys Glu Met Lys Val Lys Ser Ile Ser Tyr Val Gly Leu	
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Val Lys Arg Lys Asp Val Phe Asn Ile Glu His Leu Arg Ala Asp Ala 340 345 350		
Gln Ile Leu Lys Thr Glu Ile Ala Asp Lys Gly Tyr Ala Phe Ala Val 355 360 365		
Val Lys Pro Asp Leu Asp Lys Asp Glu Lys Asn Gly Leu Val Lys Val 370 375 380		
Ile Tyr Arg Ile Glu Val Gly Asp Met Val Tyr Ile Asn Asp Val Ile 385 390 395 400		
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Leu Leu Gly Pro Lys Asp Lys Tyr Asn Leu Thr Lys Leu Arg Asn Ser 420 425 430		
Glu Asn Ser Leu Arg Arg Leu Gly Phe Phe Ser Lys Val Lys Ile Glu 435 440 445		
Glu Lys Arg Val Asn Ser Ser Leu Met Asp Leu Leu Val Ser Val Glu 450 455 460		
Glu Gly Arg Thr Gly Gln Leu Gln Phe Gly Leu Gly Tyr Gly Ser Tyr 465 470 475 480		
Gly Gly Leu Met Leu Asn Gly Ser Val Ser Glu Arg Asn Leu Phe Gly 485 490 495		
Thr Gly Gln Ser Met Ser Leu Tyr Ala Asn Ile Ala Thr Gly Gly Gly 500 505 510		

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Asn	Thr	Asp	Asp	Tyr	Tyr	Phe	Pro	Arg	Asn	Gly	Val	Ile	Phe	Ser	Ser			
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740 745 750

Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr Thr Val  
755 760 765

Arg Gly Phe Arg Asn Gly Ser Val Thr Pro Lys Asp Glu Phe Gly Leu  
770 775 780

Trp Leu Gly Gly Asp Gly Ile Phe Thr Ala Ser Thr Glu Leu Ser Tyr  
785 790 795 800

Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe Asp Phe  
805 810 815

Gly Phe Leu Thr Phe Lys Thr Pro Thr Arg Gly Ser Phe Phe Tyr Asn  
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Ala Pro Val Thr Thr Ala Asn Phe Lys Asp Tyr Gly Val Ile Gly Ala  
835 840 845

Gly Phe Glu Arg Ala Thr Trp Arg Ala Ser Thr Gly Leu Gln Ile Glu  
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Trp Ile Ser Pro Met Gly Pro Leu Val Leu Ile Phe Pro Ile Ala Phe  
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<400> 37

atg	aaa	aga	ttt	ggt	ttg	ttt	tta	ttg	ttc	atg	tgc	ggt	tgc	ggt	caa	48
Met	Lys	Arg	Phe	Val	Leu	Phe	Leu	Leu	Phe	Met	Cys	Val	Cys	Val	Gln	
1				5					10					15		

gct	tac	gcc	gag	caa	gat	tac	ttt	ttt	agg	gat	ttt	aaa	tct	aga	gat	96
Ala	Tyr	Ala	Glu	Gln	Asp	Tyr	Phe	Phe	Arg	Asp	Phe	Lys	Ser	Arg	Asp	
			20					25					30			

ttg	ccc	caa	aaa	ctc	cat	ctt	gat	aaa	aag	ctc	tcc	caa	aca	ata	cag	144
Leu	Pro	Gln	Lys	Leu	His	Leu	Asp	Lys	Lys	Leu	Ser	Gln	Thr	Ile	Gln	
		35					40					45				

cca	tgc	atg	caa	ctt	aac	gca	tca	aaa	cac	tac	act	tct	acc	ggg	ggt	192
Pro	Cys	Met	Gln	Leu	Asn	Ala	Ser	Lys	His	Tyr	Thr	Ser	Thr	Gly	Val	
	50					55					60					

aga	gag	cct	gat	aaa	tgc	aca	aag	agt	ttt	aaa	aaa	tcc	gct	ctc	atg	240
Arg	Glu	Pro	Asp	Lys	Cys	Thr	Lys	Ser	Phe	Lys	Lys	Ser	Ala	Leu	Met	
65					70					75					80	

tcc	tat	gac	tta	gcg	cta	ggt	tat	ttg	gtg	agt	aag	aat	aag	caa	tac	288
Ser	Tyr	Asp	Leu	Ala	Leu	Gly	Tyr	Leu	Val	Ser	Lys	Asn	Lys	Gln	Tyr	
			85						90					95		

ggc	tta	aag	gct	ata	gaa	att	tta	aac	gct	tgg	gct	aaa	gag	ctt	caa	336
Gly	Leu	Lys	Ala	Ile	Glu	Ile	Leu	Asn	Ala	Trp	Ala	Lys	Glu	Leu	Gln	
			100					105					110			

agc	gtg	gat	act	tat	cag	agc	gag	gat	aat	atc	aat	ttt	tac	atg	cct	384
Ser	Val	Asp	Thr	Tyr	Gln	Ser	Glu	Asp	Asn	Ile	Asn	Phe	Tyr	Met	Pro	
		115					120					125				

tat	atg	aac	atg	gct	tat	tgg	ttt	gtc	aaa	aag	gcg	ttt	cct	agc	cca	432
Tyr	Met	Asn	Met	Ala	Tyr	Trp	Phe	Val	Lys	Lys	Ala	Phe	Pro	Ser	Pro	
	130					135					140					

gaa	tat	gaa	gat	ttc	att	aag	cgg	atg	cgc	cag	tat	tct	caa	tca	gct	480
Glu	Tyr	Glu	Asp	Phe	Ile	Lys	Arg	Met	Arg	Gln	Tyr	Ser	Gln	Ser	Ala	
145					150					155					160	

ctt	aac	act	aac	cat	ggg	gcg	tgg	ggc	att	ctt	ttt	gat	gtg	agt	tct	528
Leu	Asn	Thr	Asn	His	Gly	Ala	Trp	Gly	Ile	Leu	Phe	Asp	Val	Ser	Ser	
				165					170					175		

gcg	cta	gcg	tta	gac	gat	aat	gcc	ctt	ttg	cac	aat	agc	gct	aat	cgg	576
Ala	Leu	Ala	Leu	Asp	Asp	Asn	Ala	Leu	Leu	His	Asn	Ser	Ala	Asn	Arg	
			180					185					190			

tgg	cag	gag	tgg	gtg	ttt	aaa	gcc	ata	gat	gag	aat	ggg	ggt	att	gct	624
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Trp	Gln	Glu	Trp	Val	Phe	Lys	Ala	Ile	Asp	Glu	Asn	Gly	Val	Ile	Ala	
		195					200					205				
agc	gcg	atc	act	agg	agc	gat	acg	agc	gat	tat	cat	ggc	ggc	cct	aca	672
Ser	Ala	Ile	Thr	Arg	Ser	Asp	Thr	Ser	Asp	Tyr	His	Gly	Gly	Pro	Thr	
	210					215					220					
aag	ggc	att	aag	ggg	ata	gct	tat	acc	aat	ttc	gcg	ctt	ctt	gcg	cta	720
Lys	Gly	Ile	Lys	Gly	Ile	Ala	Tyr	Thr	Asn	Phe	Ala	Leu	Leu	Ala	Leu	
225					230					235					240	
acc	ata	tca	ggc	gaa	ttg	ctt	ttt	gag	aac	ggg	tat	gat	ttg	tgg	ggt	768
Thr	Ile	Ser	Gly	Glu	Leu	Leu	Phe	Glu	Asn	Gly	Tyr	Asp	Leu	Trp	Gly	
				245					250					255		
agt	gga	gct	ggg	aaa	agg	ctc	tct	gtg	gcg	tat	aac	aaa	gtt	gca	aca	816
Ser	Gly	Ala	Gly	Lys	Arg	Leu	Ser	Val	Ala	Tyr	Asn	Lys	Val	Ala	Thr	
			260					265					270			
tgg	att	tta	aac	cct	gaa	act	ttc	cct	tat	ttc	cag	cct	aac	ctt	atc	864
Trp	Ile	Leu	Asn	Pro	Glu	Thr	Phe	Pro	Tyr	Phe	Gln	Pro	Asn	Leu	Ile	
		275					280					285				
ggg	gtg	cat	aac	aac	gcc	tat	ttc	att	att	tta	gcc	aag	cat	tat	tct	912
Gly	Val	His	Asn	Asn	Ala	Tyr	Phe	Ile	Ile	Leu	Ala	Lys	His	Tyr	Ser	
	290					295					300					
agc	cct	agt	gca	aat	gag	ctt	tta	aag	caa	ggc	gat	tta	cac	gaa	gat	960
Ser	Pro	Ser	Ala	Asn	Glu	Leu	Leu	Lys	Gln	Gly	Asp	Leu	His	Glu	Asp	
305					310					315					320	
ggt	ttc	agg	ctg	aaa	ctc	cga	tcg	cca	tga							990
Gly	Phe	Arg	Leu	Lys	Leu	Arg	Ser	Pro								
				325												

<210> 38  
 <211> 329  
 <212> PRT  
 <213> Helicobacter pylori

<400> 38

Met	Lys	Arg	Phe	Val	Leu	Phe	Leu	Leu	Phe	Met	Cys	Val	Cys	Val	Gln	
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Ala	Tyr	Ala	Glu	Gln	Asp	Tyr	Phe	Phe	Arg	Asp	Phe	Lys	Ser	Arg	Asp	
			20					25					30			
Leu	Pro	Gln	Lys	Leu	His	Leu	Asp	Lys	Lys	Leu	Ser	Gln	Thr	Ile	Gln	
		35					40					45				



Pro	Cys	Met	Gln	Leu	Asn	Ala	Ser	Lys	His	Tyr	Thr	Ser	Thr	Gly	Val	50	55	60
Arg	Glu	Pro	Asp	Lys	Cys	Thr	Lys	Ser	Phe	Lys	Lys	Ser	Ala	Leu	Met	65	70	75
Ser	Tyr	Asp	Leu	Ala	Leu	Gly	Tyr	Leu	Val	Ser	Lys	Asn	Lys	Gln	Tyr	85	90	95
Gly	Leu	Lys	Ala	Ile	Glu	Ile	Leu	Asn	Ala	Trp	Ala	Lys	Glu	Leu	Gln	100	105	110
Ser	Val	Asp	Thr	Tyr	Gln	Ser	Glu	Asp	Asn	Ile	Asn	Phe	Tyr	Met	Pro	115	120	125
Tyr	Met	Asn	Met	Ala	Tyr	Trp	Phe	Val	Lys	Lys	Ala	Phe	Pro	Ser	Pro	130	135	140
Glu	Tyr	Glu	Asp	Phe	Ile	Lys	Arg	Met	Arg	Gln	Tyr	Ser	Gln	Ser	Ala	145	150	155
Leu	Asn	Thr	Asn	His	Gly	Ala	Trp	Gly	Ile	Leu	Phe	Asp	Val	Ser	Ser	165	170	175
Ala	Leu	Ala	Leu	Asp	Asp	Asn	Ala	Leu	Leu	His	Asn	Ser	Ala	Asn	Arg	180	185	190
Trp	Gln	Glu	Trp	Val	Phe	Lys	Ala	Ile	Asp	Glu	Asn	Gly	Val	Ile	Ala	195	200	205
Ser	Ala	Ile	Thr	Arg	Ser	Asp	Thr	Ser	Asp	Tyr	His	Gly	Gly	Pro	Thr	210	215	220
Lys	Gly	Ile	Lys	Gly	Ile	Ala	Tyr	Thr	Asn	Phe	Ala	Leu	Leu	Ala	Leu	225	230	235
Thr	Ile	Ser	Gly	Glu	Leu	Leu	Phe	Glu	Asn	Gly	Tyr	Asp	Leu	Trp	Gly	245	250	255
Ser	Gly	Ala	Gly	Lys	Arg	Leu	Ser	Val	Ala	Tyr	Asn	Lys	Val	Ala	Thr	260	265	270

Trp Ile Leu Asn Pro Glu Thr Phe Pro Tyr Phe Gln Pro Asn Leu Ile  
 275 280 285

Gly Val His Asn Asn Ala Tyr Phe Ile Ile Leu Ala Lys His Tyr Ser  
 290 295 300

Ser Pro Ser Ala Asn Glu Leu Leu Lys Gln Gly Asp Leu His Glu Asp  
 305 310 315 320

Gly Phe Arg Leu Lys Leu Arg Ser Pro  
 325

<210> 39  
 <211> 1482  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1482)

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 Met Gln Ser Leu Ser Trp Leu Asn Leu Ala Phe Arg Trp Leu Phe Ile  
 1 5 10 15  
 aca ggg ctt ggc tat tat ata atg act tta ttg caa tgg tat cat tac 96  
 Thr Gly Leu Gly Tyr Tyr Ile Met Thr Leu Leu Gln Trp Tyr His Tyr  
 20 25 30  
 agc gtg ttt agg atc tta acc aag cac cac aaa atg cgt tgg cat ggg 144  
 Ser Val Phe Arg Ile Leu Thr Lys His His Lys Met Arg Trp His Gly  
 35 40 45  
 att tat ttt tta ttg cct tta ggg gtg ttt att ctg tcg tat gct ttc 192  
 Ile Tyr Phe Leu Leu Pro Leu Gly Val Phe Ile Leu Ser Tyr Ala Phe  
 50 55 60  
 aca atg ccg ttt gtt ttt gat ttc ttt tgc ggc gtt att caa atg ccc 240  
 Thr Met Pro Phe Val Phe Asp Phe Phe Cys Gly Val Ile Gln Met Pro  
 65 70 75 80  
 atg ctc att gtt tgg gcc aaa cgc aac gac aag cct tta gtt ttc acg 288  
 Met Leu Ile Val Trp Ala Lys Arg Asn Asp Lys Pro Leu Val Phe Thr  
 85 90 95  
 cca agg gtg aag cgc ttt ttt atc ttc tta tta tta ttt tta atc ttg 336  
 Pro Arg Val Lys Arg Phe Phe Ile Phe Leu Leu Leu Phe Leu Ile Leu  
 100 105 110

cat	gaa	atc	tta	aat	ata	gaa	tta	gtc	cct	ttg	gat	ggg	att	tcg	ctc	384
His	Glu	Ile	Leu	Asn	Ile	Glu	Leu	Val	Pro	Leu	Asp	Gly	Ile	Ser	Leu	
		115					120					125				
gcg	cta	ggc	tat	ttg	tgt	ttg	ttt	ata	ttc	gtt	tta	agc	gct	tct	tta	432
Ala	Leu	Gly	Tyr	Leu	Cys	Leu	Phe	Ile	Phe	Val	Leu	Ser	Ala	Ser	Leu	
	130					135					140					
atc	tct	gaa	aaa	gcc	tta	tcc	aag	cag	tat	ttg	caa	acc	gct	aaa	gat	480
Ile	Ser	Glu	Lys	Ala	Leu	Ser	Lys	Gln	Tyr	Leu	Gln	Thr	Ala	Lys	Asp	
145					150					155					160	
aaa	atc	acc	tct	tta	aag	aat	tta	aaa	gtc	atc	gcc	att	acc	gga	agc	528
Lys	Ile	Thr	Ser	Leu	Lys	Asn	Leu	Lys	Val	Ile	Ala	Ile	Thr	Gly	Ser	
				165					170					175		
ttt	ggg	aaa	acc	agc	acc	aaa	aat	ttc	ttg	ctt	caa	atc	tta	caa	acc	576
Phe	Gly	Lys	Thr	Ser	Thr	Lys	Asn	Phe	Leu	Leu	Gln	Ile	Leu	Gln	Thr	
			180					185					190			
aca	ttc	aac	gcg	cat	gca	agc	ccc	aaa	agc	gtc	aat	acc	ctt	tta	ggg	624
Thr	Phe	Asn	Ala	His	Ala	Ser	Pro	Lys	Ser	Val	Asn	Thr	Leu	Leu	Gly	
		195					200					205				
ctt	gcg	aat	gat	att	aat	cag	aat	tta	gac	gat	agg	agt	gaa	atc	tat	672
Leu	Ala	Asn	Asp	Ile	Asn	Gln	Asn	Leu	Asp	Asp	Arg	Ser	Glu	Ile	Tyr	
	210					215					220					
atc	gct	gaa	gcc	ggg	gca	agg	aat	aag	ggc	gat	att	aaa	gaa	atc	acc	720
Ile	Ala	Glu	Ala	Gly	Ala	Arg	Asn	Lys	Gly	Asp	Ile	Lys	Glu	Ile	Thr	
225					230					235					240	
tgt	ctc	att	gaa	ccg	cac	ctt	gtt	gtg	gtt	gca	gaa	gtg	ggc	gaa	cag	768
Cys	Leu	Ile	Glu	Pro	His	Leu	Val	Val	Val	Ala	Glu	Val	Gly	Glu	Gln	
				245					250					255		
cat	tta	gaa	tac	ttt	aaa	act	tta	gaa	aat	att	tgc	gag	act	aaa	gcg	816
His	Leu	Glu	Tyr	Phe	Lys	Thr	Leu	Glu	Asn	Ile	Cys	Glu	Thr	Lys	Ala	
			260					265					270			
gaa	tta	ttg	gat	tcc	aaa	cgc	tta	gaa	aaa	gcc	ttt	tgt	tac	tcg	gtg	864
Glu	Leu	Leu	Asp	Ser	Lys	Arg	Leu	Glu	Lys	Ala	Phe	Cys	Tyr	Ser	Val	
		275					280					285				
gaa	aag	atc	aag	ccc	tat	gcc	cct	aaa	gat	agc	cct	tta	ata	gac	tat	912
Glu	Lys	Ile	Lys	Pro	Tyr	Ala	Pro	Lys	Asp	Ser	Pro	Leu	Ile	Asp	Tyr	
	290					295					300					
tct	agc	ctg	gtt	aaa	aac	atc	caa	tcc	act	tta	aaa	ggc	act	tct	ttt	960
Ser	Ser	Leu	Val	Lys	Asn	Ile	Gln	Ser	Thr	Leu	Lys	Gly	Thr	Ser	Phe	
305					310					315					320	
gaa	atg	ctt	ata	ggg	agc	gtt	tgg	gaa	aga	ttt	gaa	aca	aag	gtt	cta	1008
Glu	Met	Leu	Ile	Gly	Ser	Val	Trp	Glu	Arg	Phe	Glu	Thr	Lys	Val	Leu	

325								330				335				
ggg	gag	ttt	agc	gct	tat	aat	atc	gct	tca	gcc	att	tta	atc	gct	aag	1056
Gly	Glu	Phe	Ser	Ala	Tyr	Asn	Ile	Ala	Ser	Ala	Ile	Leu	Ile	Ala	Lys	
			340					345					350			
cat	tta	ggc	tta	gag	acc	gaa	agg	atc	aaa	cgg	ctt	gtt	tta	gaa	ctc	1104
His	Leu	Gly	Leu	Glu	Thr	Glu	Arg	Ile	Lys	Arg	Leu	Val	Leu	Glu	Leu	
		355					360					365				
aac	cct	att	gct	cat	cgt	ttg	caa	ctt	ttg	gaa	gtg	aat	caa	aaa	atc	1152
Asn	Pro	Ile	Ala	His	Arg	Leu	Gln	Leu	Leu	Glu	Val	Asn	Gln	Lys	Ile	
	370					375					380					
atc	ata	gac	gat	agc	ttt	aat	ggg	aat	tta	aag	ggc	atg	tta	gag	ggc	1200
Ile	Ile	Asp	Asp	Ser	Phe	Asn	Gly	Asn	Leu	Lys	Gly	Met	Leu	Glu	Gly	
385					390					395					400	
att	cgt	tta	gcg	agt	ttg	cac	aaa	ggg	cgt	aaa	gtc	att	gta	aca	ccg	1248
Ile	Arg	Leu	Ala	Ser	Leu	His	Lys	Gly	Arg	Lys	Val	Ile	Val	Thr	Pro	
				405					410					415		
ggc	tta	gtg	gaa	agc	aat	aca	gaa	agt	aat	gag	gct	tta	gcg	caa	aaa	1296
Gly	Leu	Val	Glu	Ser	Asn	Thr	Glu	Ser	Asn	Glu	Ala	Leu	Ala	Gln	Lys	
			420					425					430			
ata	gac	ggg	gtt	ttt	gat	gtc	gct	atc	atc	aca	ggg	gag	ttg	aat	tcc	1344
Ile	Asp	Gly	Val	Phe	Asp	Val	Ala	Ile	Ile	Thr	Gly	Glu	Leu	Asn	Ser	
		435					440					445				
aaa	acg	att	gct	tca	caa	ttg	aaa	acc	ccc	caa	aaa	atc	tta	ctc	aag	1392
Lys	Thr	Ile	Ala	Ser	Gln	Leu	Lys	Thr	Pro	Gln	Lys	Ile	Leu	Leu	Lys	
	450					455					460					
gat	aag	gcg	caa	ttg	gaa	aat	atc	tta	caa	gcc	acc	acg	att	caa	ggc	1440
Asp	Lys	Ala	Gln	Leu	Glu	Asn	Ile	Leu	Gln	Ala	Thr	Thr	Ile	Gln	Gly	
465					470				475						480	
gat	ttg	att	tta	ttc	gct	aat	gac	gcc	cct	aat	tac	att	tag			1482
Asp	Leu	Ile	Leu	Phe	Ala	Asn	Asp	Ala	Pro	Asn	Tyr	Ile				
				485				490								

<210> 40  
 <211> 493  
 <212> PRT  
 <213> Helicobacter pylori

<400> 40

Met	Gln	Ser	Leu	Ser	Trp	Leu	Asn	Leu	Ala	Phe	Arg	Trp	Leu	Phe	Ile
1				5					10					15	

Thr Gly Leu Gly Tyr Tyr Ile Met Thr Leu Leu Gln Trp Tyr His Tyr

20

25

30

Ser Val Phe Arg Ile Leu Thr Lys His His Lys Met Arg Trp His Gly  
 35 40 45

Ile Tyr Phe Leu Leu Pro Leu Gly Val Phe Ile Leu Ser Tyr Ala Phe  
 50 55 60

Thr Met Pro Phe Val Phe Asp Phe Phe Cys Gly Val Ile Gln Met Pro  
 65 70 75 80

Met Leu Ile Val Trp Ala Lys Arg Asn Asp Lys Pro Leu Val Phe Thr  
 85 90 95

Pro Arg Val Lys Arg Phe Phe Ile Phe Leu Leu Leu Phe Leu Ile Leu  
 100 105 110

His Glu Ile Leu Asn Ile Glu Leu Val Pro Leu Asp Gly Ile Ser Leu  
 115 120 125

Ala Leu Gly Tyr Leu Cys Leu Phe Ile Phe Val Leu Ser Ala Ser Leu  
 130 135 140

Ile Ser Glu Lys Ala Leu Ser Lys Gln Tyr Leu Gln Thr Ala Lys Asp  
 145 150 155 160

Lys Ile Thr Ser Leu Lys Asn Leu Lys Val Ile Ala Ile Thr Gly Ser  
 165 170 175

Phe Gly Lys Thr Ser Thr Lys Asn Phe Leu Leu Gln Ile Leu Gln Thr  
 180 185 190

Thr Phe Asn Ala His Ala Ser Pro Lys Ser Val Asn Thr Leu Leu Gly  
 195 200 205

Leu Ala Asn Asp Ile Asn Gln Asn Leu Asp Asp Arg Ser Glu Ile Tyr  
 210 215 220

Ile Ala Glu Ala Gly Ala Arg Asn Lys Gly Asp Ile Lys Glu Ile Thr  
 225 230 235 240

Cys Leu Ile Glu Pro His Leu Val Val Val Ala Glu Val Gly Glu Gln  
 245 250 255  
 His Leu Glu Tyr Phe Lys Thr Leu Glu Asn Ile Cys Glu Thr Lys Ala  
 260 265 270  
 Glu Leu Leu Asp Ser Lys Arg Leu Glu Lys Ala Phe Cys Tyr Ser Val  
 275 280 285  
 Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser Pro Leu Ile Asp Tyr  
 290 295 300  
 Ser Ser Leu Val Lys Asn Ile Gln Ser Thr Leu Lys Gly Thr Ser Phe  
 305 310 315 320  
 Glu Met Leu Ile Gly Ser Val Trp Glu Arg Phe Glu Thr Lys Val Leu  
 325 330 335  
 Gly Glu Phe Ser Ala Tyr Asn Ile Ala Ser Ala Ile Leu Ile Ala Lys  
 340 345 350  
 His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val Leu Glu Leu  
 355 360 365  
 Asn Pro Ile Ala His Arg Leu Gln Leu Leu Glu Val Asn Gln Lys Ile  
 370 375 380  
 Ile Ile Asp Asp Ser Phe Asn Gly Asn Leu Lys Gly Met Leu Glu Gly  
 385 390 395 400  
 Ile Arg Leu Ala Ser Leu His Lys Gly Arg Lys Val Ile Val Thr Pro  
 405 410 415  
 Gly Leu Val Glu Ser Asn Thr Glu Ser Asn Glu Ala Leu Ala Gln Lys  
 420 425 430  
 Ile Asp Gly Val Phe Asp Val Ala Ile Ile Thr Gly Glu Leu Asn Ser  
 435 440 445  
 Lys Thr Ile Ala Ser Gln Leu Lys Thr Pro Gln Lys Ile Leu Leu Lys  
 450 455 460

Asp Lys Ala Gln Leu Glu Asn Ile Leu Gln Ala Thr Thr Ile Gln Gly  
 465 470 475 480

Asp Leu Ile Leu Phe Ala Asn Asp Ala Pro Asn Tyr Ile  
 485 490

<210> 41  
 <211> 600  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 41  
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 Met Ser Ser Ala Leu Leu Gly Leu Gln Ile Val Leu Ala Val Leu Ile  
 1 5 10 15  
 gtg gtg gtg gtt ttg ttg caa aaa agt tct agc atc ggc tta ggg act 96  
 Val Val Val Val Leu Leu Gln Lys Ser Ser Ser Ile Gly Leu Gly Thr  
 20 25 30  
 tat agc ggg agt aat gag tct tta ttt ggc gct aaa ggg ccc gcg tgc 144  
 Tyr Ser Gly Ser Asn Glu Ser Leu Phe Gly Ala Lys Gly Pro Ala Cys  
 35 40 45  
 ttt atg gcg aaa ttg acc atg ttt tta ggg ctg tta ttt gtt atc aac 192  
 Phe Met Ala Lys Leu Thr Met Phe Leu Gly Leu Leu Phe Val Ile Asn  
 50 55 60  
 acc atc gct ttg ggc tat ttt tac aac aaa gaa tac ggc aaa agc att 240  
 Thr Ile Ala Leu Gly Tyr Phe Tyr Asn Lys Glu Tyr Gly Lys Ser Ile  
 65 70 75 80  
 tta gat gaa act aaa acc aac aaa gag ctt tcg ccc tta gtc cct gcc 288  
 Leu Asp Glu Thr Lys Thr Asn Lys Glu Leu Ser Pro Leu Val Pro Ala  
 85 90 95  
 acc ggc acg ctc aac cct aca ctc aat ccc acg ctc aac cct acg ctc 336  
 Thr Gly Thr Leu Asn Pro Thr Leu Asn Pro Thr Leu Asn Pro Thr Leu  
 100 105 110  
 aac cct tta gag caa gcc cca act aat cct tta atg cca aaa caa acg 384  
 Asn Pro Leu Glu Gln Ala Pro Thr Asn Pro Leu Met Pro Lys Gln Thr  
 115 120 125  
 cct aac gaa ctc cct aaa gag cca gcc aaa gcg cct tct gtt gaa agc 432

Pro	Asn	Glu	Leu	Pro	Lys	Glu	Pro	Ala	Lys	Ala	Pro	Ser	Val	Glu	Ser	
130						135					140					
ccc	aaa	cag	aat	gaa	aaa	aat	gaa	aaa	aat	gac	gcc	aaa	gag	aat	ggt	480
Pro	Lys	Gln	Asn	Glu	Lys	Asn	Glu	Lys	Asn	Asp	Ala	Lys	Glu	Asn	Gly	
145					150					155					160	
ata	aag	ggt	gtt	gaa	aaa	act	aaa	gag	aac	gcc	aaa	acg	ccc	cca	acc	528
Ile	Lys	Gly	Val	Glu	Lys	Thr	Lys	Glu	Asn	Ala	Lys	Thr	Pro	Pro	Thr	
				165					170						175	
acc	cac	caa	aag	cct	aaa	acg	cat	gcg	aca	caa	acc	aac	gcc	cat	acc	576
Thr	His	Gln	Lys	Pro	Lys	Thr	His	Ala	Thr	Gln	Thr	Asn	Ala	His	Thr	
			180					185					190			
aac	caa	aaa	aag	gat	gaa	aaa	taa									600
Asn	Gln	Lys	Lys	Asp	Glu	Lys										
			195													

<210> 42  
 <211> 199  
 <212> PRT  
 <213> Helicobacter pylori

<400> 42

Met	Ser	Ser	Ala	Leu	Leu	Gly	Leu	Gln	Ile	Val	Leu	Ala	Val	Leu	Ile	
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Val	Val	Val	Val	Leu	Leu	Gln	Lys	Ser	Ser	Ser	Ile	Gly	Leu	Gly	Thr	
			20					25					30			
Tyr	Ser	Gly	Ser	Asn	Glu	Ser	Leu	Phe	Gly	Ala	Lys	Gly	Pro	Ala	Cys	
		35					40					45				
Phe	Met	Ala	Lys	Leu	Thr	Met	Phe	Leu	Gly	Leu	Leu	Phe	Val	Ile	Asn	
	50					55					60					
Thr	Ile	Ala	Leu	Gly	Tyr	Phe	Tyr	Asn	Lys	Glu	Tyr	Gly	Lys	Ser	Ile	
65					70					75					80	
Leu	Asp	Glu	Thr	Lys	Thr	Asn	Lys	Glu	Leu	Ser	Pro	Leu	Val	Pro	Ala	
				85					90					95		
Thr	Gly	Thr	Leu	Asn	Pro	Thr	Leu	Asn	Pro	Thr	Leu	Asn	Pro	Thr	Leu	
			100					105					110			



Asn Pro Leu Glu Gln Ala Pro Thr Asn Pro Leu Met Pro Lys Gln Thr  
115 120 125

Pro Asn Glu Leu Pro Lys Glu Pro Ala Lys Ala Pro Ser Val Glu Ser  
130 135 140

Pro Lys Gln Asn Glu Lys Asn Glu Lys Asn Asp Ala Lys Glu Asn Gly  
145 150 155 160

Ile Lys Gly Val Glu Lys Thr Lys Glu Asn Ala Lys Thr Pro Pro Thr  
165 170 175

Thr His Gln Lys Pro Lys Thr His Ala Thr Gln Thr Asn Ala His Thr  
180 185 190

Asn Gln Lys Lys Asp Glu Lys  
195

<210> 43  
<211> 1536  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(1536)

<400> 43  
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Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu Leu Leu Ile Gly Leu  
1 5 10 15  
tta aca atc tat ctc atc ctt ttt aca gaa tgg ggg aat aag atc atc 96  
Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp Gly Asn Lys Ile Ile  
20 25 30  
gct tcg tat ata gag aaa aaa atc aac ccg aac gag cac tac ttg agc 144  
Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn Glu His Tyr Leu Ser  
35 40 45  
gtt aaa acc ttt aaa ttg aga ttc aac tct ttg gat ttt aaa gct caa 192  
Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu Asp Phe Lys Ala Gln  
50 55 60  
gcc aac gat gat tcc acg ctc att ctt aag ggg gat ttt tca ctt tta 240  
Ala Asn Asp Asp Ser Thr Leu Ile Leu Lys Gly Asp Phe Ser Leu Leu  
65 70 75 80

aag	caa	agc	gta	aat	ttg	aat	tac	cat	ata	gat	att	aaa	gat	tta	cgc	288
Lys	Gln	Ser	Val	Asn	Leu	Asn	Tyr	His	Ile	Asp	Ile	Lys	Asp	Leu	Arg	
				85					90					95		
tct	ttc	aaa	gaa	tg	ata	ccc	tac	cct	tta	agg	ggg	gct	gtt	atc	act	336
Ser	Phe	Lys	Glu	Trp	Ile	Pro	Tyr	Pro	Leu	Arg	Gly	Ala	Val	Ile	Thr	
			100					105					110			
tct	ggg	aat	att	aaa	ggg	cat	aga	aaa	gcc	ctt	atg	att	caa	ggc	gtc	384
Ser	Gly	Asn	Ile	Lys	Gly	His	Arg	Lys	Ala	Leu	Met	Ile	Gln	Gly	Val	
		115					120					125				
tct	aat	gtg	gct	caa	tcc	cac	act	gcc	tac	aat	gcc	ctt	tta	gat	gat	432
Ser	Asn	Val	Ala	Gln	Ser	His	Thr	Ala	Tyr	Asn	Ala	Leu	Leu	Asp	Asp	
	130					135					140					
ttc	aag	ctt	tct	cgc	tta	aat	ttg	aac	gca	caa	gac	gcc	aat	tta	gaa	480
Phe	Lys	Leu	Ser	Arg	Leu	Asn	Leu	Asn	Ala	Gln	Asp	Ala	Asn	Leu	Glu	
145					150					155					160	
gat	ttg	ctt	tat	tta	atc	aat	cgc	ccc	gct	tat	gcg	aac	gca	aaa	gtg	528
Asp	Leu	Leu	Tyr	Leu	Ile	Asn	Arg	Pro	Ala	Tyr	Ala	Asn	Ala	Lys	Val	
				165					170					175		
tcc	tta	cag	gcg	gat	ttt	aac	tct	cta	aag	cct	tta	gag	ggg	cat	ttg	576
Ser	Leu	Gln	Ala	Asp	Phe	Asn	Ser	Leu	Lys	Pro	Leu	Glu	Gly	His	Leu	
			180					185					190			
atc	cta	aca	gct	aat	aac	gct	tta	atc	aat	aac	gcc	cta	atc	aat	caa	624
Ile	Leu	Thr	Ala	Asn	Asn	Ala	Leu	Ile	Asn	Asn	Ala	Leu	Ile	Asn	Gln	
		195					200					205				
att	ttt	cat	tta	aac	ctt	aaa	gac	acg	ctt	gtt	ttc	agc	ctc	tcg	cat	672
Ile	Phe	His	Leu	Asn	Leu	Lys	Asp	Thr	Leu	Val	Phe	Ser	Leu	Ser	His	
	210					215					220					
tca	agc	gac	ttt	aaa	gga	aac	aaa	gcc	atc	agc	gat	acc	acc	ctg	act	720
Ser	Ser	Asp	Phe	Lys	Gly	Asn	Lys	Ala	Ile	Ser	Asp	Thr	Thr	Leu	Thr	
225					230					235				240		
agc	cct	tta	gcc	aat	ttc	aaa	gcc	cta	aaa	agc	gaa	tac	ctt	ttc	tct	768
Ser	Pro	Leu	Ala	Asn	Phe	Lys	Ala	Leu	Lys	Ser	Glu	Tyr	Leu	Phe	Ser	
				245					250					255		
att	tta	aaa	ctc	aac	gcc	ccc	tac	act	tta	gaa	atc	ccc	aat	cta	gcc	816
Ile	Leu	Lys	Leu	Asn	Ala	Pro	Tyr	Thr	Leu	Glu	Ile	Pro	Asn	Leu	Ala	
			260					265					270			
aaa	ctc	tat	aac	att	acc	aac	cac	ccc	tta	aaa	ggg	agc	ttg	act	tta	864
Lys	Leu	Tyr	Asn	Ile	Thr	Asn	His	Pro	Leu	Lys	Gly	Ser	Leu	Thr	Leu	
		275					280					285				
aaa	ggc	gct	ata	gaa	caa	agc	ccc	aaa	ctt	tta	aaa	gtc	agc	ggc	cat	912
Lys	Gly	Ala	Ile	Glu	Gln	Ser	Pro	Lys	Leu	Leu	Lys	Val	Ser	Gly	His	
	290					295					300					

tca	aat	tta	cta	gac	ggc	gcg	ctg	gat	ttc	acg	ctt	tta	aat	aaa	gat	960
Ser	Asn	Leu	Leu	Asp	Gly	Ala	Leu	Asp	Phe	Thr	Leu	Leu	Asn	Lys	Asp	
305					310					315					320	
ttg	aaa	ggg	cgt	ttt	tcc	aat	att	tcc	act	tta	aaa	gct	tta	gat	tta	1008
Leu	Lys	Gly	Arg	Phe	Ser	Asn	Ile	Ser	Thr	Leu	Lys	Ala	Leu	Asp	Leu	
				325					330					335		
ttc	cat	tac	cct	aag	ttt	ttc	caa	tcc	ggt	gca	gac	gct	aat	ttg	gat	1056
Phe	His	Tyr	Pro	Lys	Phe	Phe	Gln	Ser	Val	Ala	Asp	Ala	Asn	Leu	Asp	
			340					345					350			
tat	gat	ctt	atc	gct	aag	caa	ggc	gta	ttg	aaa	gcc	cgc	cta	aaa	aac	1104
Tyr	Asp	Leu	Ile	Ala	Lys	Gln	Gly	Val	Leu	Lys	Ala	Arg	Leu	Lys	Asn	
		355					360					365				
gca	aga	ttc	ctc	aaa	aat	gca	ttc	agc	gat	ttt	ctc	tac	tcc	att	tct	1152
Ala	Arg	Phe	Leu	Lys	Asn	Ala	Phe	Ser	Asp	Phe	Leu	Tyr	Ser	Ile	Ser	
	370					375					380					
aaa	ttt	gat	att	aca	aaa	gaa	att	tat	aac	gat	gcc	aat	ctg	gta	agc	1200
Lys	Phe	Asp	Ile	Thr	Lys	Glu	Ile	Tyr	Asn	Asp	Ala	Asn	Leu	Val	Ser	
385					390					395					400	
caa	atc	aac	cag	caa	cgc	ctg	ctc	tct	gat	ctg	agt	tta	aaa	agc	ccc	1248
Gln	Ile	Asn	Gln	Gln	Arg	Leu	Leu	Ser	Asp	Leu	Ser	Leu	Lys	Ser	Pro	
			405						410					415		
aaa	acc	caa	ttg	aaa	atc	cat	aac	ggt	ttg	ttg	gat	tta	aac	acc	aaa	1296
Lys	Thr	Gln	Leu	Lys	Ile	His	Asn	Gly	Leu	Leu	Asp	Leu	Asn	Thr	Lys	
			420					425					430			
caa	atg	aac	atg	ctc	atg	gat	gcg	gaa	att	tta	aaa	ttc	att	ttt	aaa	1344
Gln	Met	Asn	Met	Leu	Met	Asp	Ala	Glu	Ile	Leu	Lys	Phe	Ile	Phe	Lys	
		435					440					445				
atg	aaa	ctt	caa	ggc	aac	atg	cac	cag	cca	aaa	ttt	tct	ctc	att	tta	1392
Met	Lys	Leu	Gln	Gly	Asn	Met	His	Gln	Pro	Lys	Phe	Ser	Leu	Ile	Leu	
	450				455						460					
aac	gaa	aaa	gcc	att	cag	caa	aac	ttg	caa	caa	ggc	ttg	aaa	gaa	atc	1440
Asn	Glu	Lys	Ala	Ile	Gln	Gln	Asn	Leu	Gln	Gln	Gly	Leu	Lys	Glu	Ile	
465					470					475					480	
tta	aaa	aac	gac	acc	ctt	aaa	aaa	ggt	tta	gat	cat	ttg	ctt	aaa	gat	1488
Leu	Lys	Asn	Asp	Thr	Leu	Lys	Lys	Gly	Leu	Asp	His	Leu	Leu	Lys	Asp	
				485				490						495		
gat	aag	ctc	aaa	gaa	aag	ctt	gaa	aaa	ggg	ctt	aag	ggg	ctt	ttt	taa	1536
Asp	Lys	Leu	Lys	Glu	Lys	Leu	Glu	Lys	Gly	Leu	Lys	Gly	Leu	Phe		
			500					505					510			

<210> 44

<211> 511  
 <212> PRT  
 <213> Helicobacter pylori

<400> 44

Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu Leu Leu Ile Gly Leu  
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Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp Gly Asn Lys Ile Ile  
 20 25 30

Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn Glu His Tyr Leu Ser  
 35 40 45

Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu Asp Phe Lys Ala Gln  
 50 55 60

Ala Asn Asp Asp Ser Thr Leu Ile Leu Lys Gly Asp Phe Ser Leu Leu  
 65 70 75 80

Lys Gln Ser Val Asn Leu Asn Tyr His Ile Asp Ile Lys Asp Leu Arg  
 85 90 95

Ser Phe Lys Glu Trp Ile Pro Tyr Pro Leu Arg Gly Ala Val Ile Thr  
 100 105 110

Ser Gly Asn Ile Lys Gly His Arg Lys Ala Leu Met Ile Gln Gly Val  
 115 120 125

Ser Asn Val Ala Gln Ser His Thr Ala Tyr Asn Ala Leu Leu Asp Asp  
 130 135 140

Phe Lys Leu Ser Arg Leu Asn Leu Asn Ala Gln Asp Ala Asn Leu Glu  
 145 150 155 160

Asp Leu Leu Tyr Leu Ile Asn Arg Pro Ala Tyr Ala Asn Ala Lys Val  
 165 170 175

Ser Leu Gln Ala Asp Phe Asn Ser Leu Lys Pro Leu Glu Gly His Leu  
 180 185 190

Ile Leu Thr Ala Asn Asn Ala Leu Ile Asn Asn Ala Leu Ile Asn Gln

195					200					205					
Ile	Phe	His	Leu	Asn	Leu	Lys	Asp	Thr	Leu	Val	Phe	Ser	Leu	Ser	His
	210					215					220				
Ser	Ser	Asp	Phe	Lys	Gly	Asn	Lys	Ala	Ile	Ser	Asp	Thr	Thr	Leu	Thr
225					230					235					240
Ser	Pro	Leu	Ala	Asn	Phe	Lys	Ala	Leu	Lys	Ser	Glu	Tyr	Leu	Phe	Ser
				245					250					255	
Ile	Leu	Lys	Leu	Asn	Ala	Pro	Tyr	Thr	Leu	Glu	Ile	Pro	Asn	Leu	Ala
			260					265					270		
Lys	Leu	Tyr	Asn	Ile	Thr	Asn	His	Pro	Leu	Lys	Gly	Ser	Leu	Thr	Leu
		275					280					285			
Lys	Gly	Ala	Ile	Glu	Gln	Ser	Pro	Lys	Leu	Leu	Lys	Val	Ser	Gly	His
	290					295					300				
Ser	Asn	Leu	Leu	Asp	Gly	Ala	Leu	Asp	Phe	Thr	Leu	Leu	Asn	Lys	Asp
305					310					315					320
Leu	Lys	Gly	Arg	Phe	Ser	Asn	Ile	Ser	Thr	Leu	Lys	Ala	Leu	Asp	Leu
				325					330					335	
Phe	His	Tyr	Pro	Lys	Phe	Phe	Gln	Ser	Val	Ala	Asp	Ala	Asn	Leu	Asp
			340					345					350		
Tyr	Asp	Leu	Ile	Ala	Lys	Gln	Gly	Val	Leu	Lys	Ala	Arg	Leu	Lys	Asn
		355					360					365			
Ala	Arg	Phe	Leu	Lys	Asn	Ala	Phe	Ser	Asp	Phe	Leu	Tyr	Ser	Ile	Ser
	370					375					380				
Lys	Phe	Asp	Ile	Thr	Lys	Glu	Ile	Tyr	Asn	Asp	Ala	Asn	Leu	Val	Ser
385						390					395				400
Gln	Ile	Asn	Gln	Gln	Arg	Leu	Leu	Ser	Asp	Leu	Ser	Leu	Lys	Ser	Pro
				405					410					415	

Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu Asp Leu Asn Thr Lys  
420 425 430

Gln Met Asn Met Leu Met Asp Ala Glu Ile Leu Lys Phe Ile Phe Lys  
435 440 445

Met Lys Leu Gln Gly Asn Met His Gln Pro Lys Phe Ser Leu Ile Leu  
450 455 460

Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln Gly Leu Lys Glu Ile  
465 470 475 480

Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp His Leu Leu Lys Asp  
485 490 495

Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu Lys Gly Leu Phe  
500 505 510

<210> 45  
<211> 540  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(540)

<400> 45  
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Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val  
1 5 10 15  
gct ggc tgt agt cat aaa atg gat aat aag act gtg gcc ggc gat gtg 96  
Ala Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala Gly Asp Val  
20 25 30  
agt gct aaa acg gtt cag act gca cct gtt act aca gaa cca gct cca 144  
Ser Ala Lys Thr Val Gln Thr Ala Pro Val Thr Thr Glu Pro Ala Pro  
35 40 45  
gag aaa gaa gag cct aaa caa gag cca gct cca gtg gtt gaa gaa aaa 192  
Glu Lys Glu Glu Pro Lys Gln Glu Pro Ala Pro Val Val Glu Glu Lys  
50 55 60  
ccg gct gtt gag agc ggg act atc atc gct tct att tat ttt gat ttt 240  
Pro Ala Val Glu Ser Gly Thr Ile Ile Ala Ser Ile Tyr Phe Asp Phe  
65 70 75 80

gac aag tat gaa atc aaa gaa tcc gat caa gag act tta gat gag atc	288
Asp Lys Tyr Glu Ile Lys Glu Ser Asp Gln Glu Thr Leu Asp Glu Ile	
85 90 95	
gtg caa aaa gct aaa gaa aac cac atg caa gtg ctt ttg gaa ggc aat	336
Val Gln Lys Ala Lys Glu Asn His Met Gln Val Leu Leu Glu Gly Asn	
100 105 110	
acc gat gaa ttt ggc tct agc gaa tac aac caa gcg ctt ggc gtt aaa	384
Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys	
115 120 125	
agg act ttg agc gtg aaa aac gct tta gtc att aaa ggg gta gaa aaa	432
Arg Thr Leu Ser Val Lys Asn Ala Leu Val Ile Lys Gly Val Glu Lys	
130 135 140	
gat atg atc aaa acc atc agt ttt ggt gaa acc aaa ccc aaa tgc gcc	480
Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Thr Lys Pro Lys Cys Ala	
145 150 155 160	
caa aaa act aga gag tgt tat aaa gaa aac aga aga gtg gat gtc aaa	528
Gln Lys Thr Arg Glu Cys Tyr Lys Glu Asn Arg Arg Val Asp Val Lys	
165 170 175	
tta atg aag taa	540
Leu Met Lys	

<210> 46  
 <211> 179  
 <212> PRT  
 <213> Helicobacter pylori

<400> 46

Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val	
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Ala Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala Gly Asp Val	
20 25 30	
Ser Ala Lys Thr Val Gln Thr Ala Pro Val Thr Thr Glu Pro Ala Pro	
35 40 45	
Glu Lys Glu Glu Pro Lys Gln Glu Pro Ala Pro Val Val Glu Glu Lys	
50 55 60	
Pro Ala Val Glu Ser Gly Thr Ile Ile Ala Ser Ile Tyr Phe Asp Phe	
65 70 75 80	

Asp Lys Tyr Glu Ile Lys Glu Ser Asp Gln Glu Thr Leu Asp Glu Ile  
85 90 95

Val Gln Lys Ala Lys Glu Asn His Met Gln Val Leu Leu Glu Gly Asn  
100 105 110

Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys  
115 120 125

Arg Thr Leu Ser Val Lys Asn Ala Leu Val Ile Lys Gly Val Glu Lys  
130 135 140

Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Thr Lys Pro Lys Cys Ala  
145 150 155 160

Gln Lys Thr Arg Glu Cys Tyr Lys Glu Asn Arg Arg Val Asp Val Lys  
165 170 175

Leu Met Lys

<210> 47  
<211> 1557  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(1557)

<400> 47  
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Met Ile Lys Lys Asn Arg Thr Leu Phe Leu Ser Leu Ala Leu Cys Ala  
1 5 10 15  
agc ata agt tat gcc gaa gat gat gga ggg ttt ttc acc gtc ggt tat 96  
Ser Ile Ser Tyr Ala Glu Asp Asp Gly Gly Phe Phe Thr Val Gly Tyr  
20 25 30  
cag ctc ggg caa gtc atg caa gat gtc caa aac cca ggc ggc gct aaa 144  
Gln Leu Gly Gln Val Met Gln Asp Val Gln Asn Pro Gly Gly Ala Lys  
35 40 45  
agc gac gaa ctc gcc aga gag ctt aac gct gat gta acg aac aac att 192



Ser	Asp	Glu	Leu	Ala	Arg	Glu	Leu	Asn	Ala	Asp	Val	Thr	Asn	Asn	Ile	
50						55					60					
tta	aac	aac	aac	acc	gga	ggc	aac	atc	gca	ggg	gcg	ttg	agt	aac	gct	240
Leu	Asn	Asn	Asn	Thr	Gly	Gly	Asn	Ile	Ala	Gly	Ala	Leu	Ser	Asn	Ala	
65					70					75					80	
ttc	tcc	caa	tac	ctt	tat	tcg	ctt	tta	ggg	gct	tac	ccc	aca	aaa	ctc	288
Phe	Ser	Gln	Tyr	Leu	Tyr	Ser	Leu	Leu	Gly	Ala	Tyr	Pro	Thr	Lys	Leu	
				85					90					95		
aat	ggt	agc	gat	gtg	tct	gcg	aac	gct	ctt	tta	agt	ggt	gcg	gta	ggc	336
Asn	Gly	Ser	Asp	Val	Ser	Ala	Asn	Ala	Leu	Leu	Ser	Gly	Ala	Val	Gly	
			100					105					110			
tct	ggg	act	tgt	gcg	gct	gca	ggg	acg	gct	ggg	ggc	act	tct	ctt	aac	384
Ser	Gly	Thr	Cys	Ala	Ala	Ala	Gly	Thr	Ala	Gly	Gly	Thr	Ser	Leu	Asn	
		115					120					125				
act	caa	agc	act	tgc	acc	ggt	gcg	ggc	tat	tac	tgg	ctc	cct	agc	ttg	432
Thr	Gln	Ser	Thr	Cys	Thr	Val	Ala	Gly	Tyr	Tyr	Trp	Leu	Pro	Ser	Leu	
	130					135					140					
act	gac	agg	att	tta	agc	acg	atc	ggc	agc	cag	act	aac	tac	ggc	acg	480
Thr	Asp	Arg	Ile	Leu	Ser	Thr	Ile	Gly	Ser	Gln	Thr	Asn	Tyr	Gly	Thr	
145					150					155					160	
aac	acc	aat	ttc	ccc	aac	atg	caa	caa	cag	ctc	acc	tac	ttg	aat	gcg	528
Asn	Thr	Asn	Phe	Pro	Asn	Met	Gln	Gln	Gln	Leu	Thr	Tyr	Leu	Asn	Ala	
				165					170					175		
ggg	aat	gtg	ttt	ttt	aat	gcg	atg	aat	aag	gct	tta	gag	aat	aag	aat	576
Gly	Asn	Val	Phe	Phe	Asn	Ala	Met	Asn	Lys	Ala	Leu	Glu	Asn	Lys	Asn	
			180					185					190			
gga	act	agt	agt	gct	agt	gga	act	agt	ggt	gcg	act	ggt	tca	gat	ggt	624
Gly	Thr	Ser	Ser	Ala	Ser	Gly	Thr	Ser	Gly	Ala	Thr	Gly	Ser	Asp	Gly	
		195				200						205				
caa	act	tac	tcc	aca	caa	gct	atc	caa	tac	ctt	caa	ggc	caa	caa	aat	672
Gln	Thr	Tyr	Ser	Thr	Gln	Ala	Ile	Gln	Tyr	Leu	Gln	Gly	Gln	Gln	Asn	
	210					215					220					
atc	tta	aat	aac	gca	gcg	aac	ttg	ctc	aag	caa	gat	gaa	ttg	ctc	tta	720
Ile	Leu	Asn	Asn	Ala	Ala	Asn	Leu	Leu	Lys	Gln	Asp	Glu	Leu	Leu	Leu	
225					230					235					240	
gaa	gct	ttc	aac	tct	gcc	gta	gcc	gcc	aac	att	ggg	aat	aag	gaa	ttc	768
Glu	Ala	Phe	Asn	Ser	Ala	Val	Ala	Ala	Asn	Ile	Gly	Asn	Lys	Glu	Phe	
				245					250					255		
aat	tca	gcc	gct	ttt	aca	ggt	ttg	gtg	caa	ggc	att	att	gat	caa	tct	816
Asn	Ser	Ala	Ala	Phe	Thr	Gly	Leu	Val	Gln	Gly	Ile	Ile	Asp	Gln	Ser	
			260					265					270			

caa gcg gtt tat aac gag ctc act aaa aac acc att agc ggg agt gcg Gln Ala Val Tyr Asn Glu Leu Thr Lys Asn Thr Ile Ser Gly Ser Ala 275 280 285	864
gtt att agc gct ggg ata aac tcc aac caa gct aac gct gtg caa ggg Val Ile Ser Ala Gly Ile Asn Ser Asn Gln Ala Asn Ala Val Gln Gly 290 295 300	912
cgc gct agt cag ctc cct aac gct ctt tat aac gcg caa gta act ttg Arg Ala Ser Gln Leu Pro Asn Ala Leu Tyr Asn Ala Gln Val Thr Leu 305 310 315 320	960
gat aaa atc aat gcg ctc aat aat caa gtg aga agc atg cct tac ttg Asp Lys Ile Asn Ala Leu Asn Asn Gln Val Arg Ser Met Pro Tyr Leu 325 330 335	1008
ccc caa ttc aga gcc ggg aac agc cgt tca acg aat att tta aac ggg Pro Gln Phe Arg Ala Gly Asn Ser Arg Ser Thr Asn Ile Leu Asn Gly 340 345 350	1056
ttt tac acc aaa ata ggc tat aag caa ttc ttc ggg aag aaa agg aat Phe Tyr Thr Lys Ile Gly Tyr Lys Gln Phe Phe Gly Lys Lys Arg Asn 355 360 365	1104
atc ggt ttg cgc tat tat ggt ttc ttt tct tat aac gga gcg agc gtg Ile Gly Leu Arg Tyr Tyr Gly Phe Phe Ser Tyr Asn Gly Ala Ser Val 370 375 380	1152
ggc ttt aga tcc act caa aat aat gta ggg tta tac act tat ggg gtg Gly Phe Arg Ser Thr Gln Asn Asn Val Gly Leu Tyr Thr Tyr Gly Val 385 390 395 400	1200
ggg act gat gtg ttg tat aac atc ttt agc cgc tcc tat caa aac cgc Gly Thr Asp Val Leu Tyr Asn Ile Phe Ser Arg Ser Tyr Gln Asn Arg 405 410 415	1248
tct gtg gat atg ggc ttt ttt agc ggt atc caa tta gcc ggt gag acc Ser Val Asp Met Gly Phe Phe Ser Gly Ile Gln Leu Ala Gly Glu Thr 420 425 430	1296
ttc caa tcc acg ctc aga gat gac ccc aat gtg aaa ttg cat ggg aaa Phe Gln Ser Thr Leu Arg Asp Asp Pro Asn Val Lys Leu His Gly Lys 435 440 445	1344
atc aat aac acg cac ttc cag ttc ctc ttt gac ttc ggt atg agg atg Ile Asn Asn Thr His Phe Gln Phe Leu Phe Asp Phe Gly Met Arg Met 450 455 460	1392
aac ttc ggt aag ttg gac ggg aaa tcc aac cgc cac aac cag cac acg Asn Phe Gly Lys Leu Asp Gly Lys Ser Asn Arg His Asn Gln His Thr 465 470 475 480	1440
gtg gaa ttt ggc gta gtg gtg cct acg att tat aac act tat tac aaa Val Glu Phe Gly Val Val Val Pro Thr Ile Tyr Asn Thr Tyr Tyr Lys 485 490 495	1488

tca gca ggg act acc gtg aag tat ttc cgt cct tat agc gtt tat tgg	1536
Ser Ala Gly Thr Thr Val Lys Tyr Phe Arg Pro Tyr Ser Val Tyr Trp	
500 505 510	

tct tat ggg tat tca ttc taa	1557
Ser Tyr Gly Tyr Ser Phe	
515	

<210> 48  
 <211> 518  
 <212> PRT  
 <213> *Helicobacter pylori*

<400> 48

Met Ile Lys Lys Asn Arg Thr Leu Phe Leu Ser Leu Ala Leu Cys Ala
1 5 10 15

Ser Ile Ser Tyr Ala Glu Asp Asp Gly Gly Phe Phe Thr Val Gly Tyr
20 25 30

Gln Leu Gly Gln Val Met Gln Asp Val Gln Asn Pro Gly Gly Ala Lys
35 40 45

Ser Asp Glu Leu Ala Arg Glu Leu Asn Ala Asp Val Thr Asn Asn Ile
50 55 60

Leu Asn Asn Asn Thr Gly Gly Asn Ile Ala Gly Ala Leu Ser Asn Ala
65 70 75 80

Phe Ser Gln Tyr Leu Tyr Ser Leu Leu Gly Ala Tyr Pro Thr Lys Leu
85 90 95

Asn Gly Ser Asp Val Ser Ala Asn Ala Leu Leu Ser Gly Ala Val Gly
100 105 110

Ser Gly Thr Cys Ala Ala Ala Gly Thr Ala Gly Gly Thr Ser Leu Asn
115 120 125

Thr Gln Ser Thr Cys Thr Val Ala Gly Tyr Tyr Trp Leu Pro Ser Leu
130 135 140

Thr Asp Arg Ile Leu Ser Thr Ile Gly Ser Gln Thr Asn Tyr Gly Thr
145 150 155 160

Asn	Thr	Asn	Phe	Pro	Asn	Met	Gln	Gln	Gln	Leu	Thr	Tyr	Leu	Asn	Ala	165	170	175
Gly	Asn	Val	Phe	Phe	Asn	Ala	Met	Asn	Lys	Ala	Leu	Glu	Asn	Lys	Asn	180	185	190
Gly	Thr	Ser	Ser	Ala	Ser	Gly	Thr	Ser	Gly	Ala	Thr	Gly	Ser	Asp	Gly	195	200	205
Gln	Thr	Tyr	Ser	Thr	Gln	Ala	Ile	Gln	Tyr	Leu	Gln	Gly	Gln	Gln	Asn	210	215	220
Ile	Leu	Asn	Asn	Ala	Ala	Asn	Leu	Leu	Lys	Gln	Asp	Glu	Leu	Leu	Leu	225	230	235
Glu	Ala	Phe	Asn	Ser	Ala	Val	Ala	Ala	Asn	Ile	Gly	Asn	Lys	Glu	Phe	245	250	255
Asn	Ser	Ala	Ala	Phe	Thr	Gly	Leu	Val	Gln	Gly	Ile	Ile	Asp	Gln	Ser	260	265	270
Gln	Ala	Val	Tyr	Asn	Glu	Leu	Thr	Lys	Asn	Thr	Ile	Ser	Gly	Ser	Ala	275	280	285
Val	Ile	Ser	Ala	Gly	Ile	Asn	Ser	Asn	Gln	Ala	Asn	Ala	Val	Gln	Gly	290	295	300
Arg	Ala	Ser	Gln	Leu	Pro	Asn	Ala	Leu	Tyr	Asn	Ala	Gln	Val	Thr	Leu	305	310	315
Asp	Lys	Ile	Asn	Ala	Leu	Asn	Asn	Gln	Val	Arg	Ser	Met	Pro	Tyr	Leu	325	330	335
Pro	Gln	Phe	Arg	Ala	Gly	Asn	Ser	Arg	Ser	Thr	Asn	Ile	Leu	Asn	Gly	340	345	350
Phe	Tyr	Thr	Lys	Ile	Gly	Tyr	Lys	Gln	Phe	Phe	Gly	Lys	Lys	Arg	Asn	355	360	365

Ile Gly Leu Arg Tyr Tyr Gly Phe Phe Ser Tyr Asn Gly Ala Ser Val  
 370 375 380

Gly Phe Arg Ser Thr Gln Asn Asn Val Gly Leu Tyr Thr Tyr Gly Val  
 385 390 395 400

Gly Thr Asp Val Leu Tyr Asn Ile Phe Ser Arg Ser Tyr Gln Asn Arg  
 405 410 415

Ser Val Asp Met Gly Phe Phe Ser Gly Ile Gln Leu Ala Gly Glu Thr  
 420 425 430

Phe Gln Ser Thr Leu Arg Asp Asp Pro Asn Val Lys Leu His Gly Lys  
 435 440 445

Ile Asn Asn Thr His Phe Gln Phe Leu Phe Asp Phe Gly Met Arg Met  
 450 455 460

Asn Phe Gly Lys Leu Asp Gly Lys Ser Asn Arg His Asn Gln His Thr  
 465 470 475 480

Val Glu Phe Gly Val Val Val Pro Thr Ile Tyr Asn Thr Tyr Tyr Lys  
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Ser Ala Gly Thr Thr Val Lys Tyr Phe Arg Pro Tyr Ser Val Tyr Trp  
 500 505 510

Ser Tyr Gly Tyr Ser Phe  
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<210> 49  
 <211> 1062  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1062)

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48

cta ggc aca gcc tta agt gca tct tta agt tta gcc gca aca gaa agc	96
Leu Gly Thr Ala Leu Ser Ala Ser Leu Ser Leu Ala Ala Thr Glu Ser	
20 25 30	
ccc act aaa aca gag cct aag ccc gct aaa ggg gtt aaa aac aag ccc	144
Pro Thr Lys Thr Glu Pro Lys Pro Ala Lys Gly Val Lys Asn Lys Pro	
35 40 45	
aaa tcg ccc gtt act aaa gtc atg atg acc aat tgc gac aat att aaa	192
Lys Ser Pro Val Thr Lys Val Met Met Thr Asn Cys Asp Asn Ile Lys	
50 55 60	
gat ttt aac gct aag caa aaa gaa gtc tta aaa gcc gct tat caa ttc	240
Asp Phe Asn Ala Lys Gln Lys Glu Val Leu Lys Ala Ala Tyr Gln Phe	
65 70 75 80	
ggc tct aaa gaa aat tta ggc tat gaa atg gca ggc att gca tgg aaa	288
Gly Ser Lys Glu Asn Leu Gly Tyr Glu Met Ala Gly Ile Ala Trp Lys	
85 90 95	
gag tca tgc gca ggg gtt tat aaa atc aat ttt tcg gat ccg agc gcg	336
Glu Ser Cys Ala Gly Val Tyr Lys Ile Asn Phe Ser Asp Pro Ser Ala	
100 105 110	
ggc gtg tat cat tct tat atc cca agc gtt cta aaa agc tat ggg cat	384
Gly Val Tyr His Ser Tyr Ile Pro Ser Val Leu Lys Ser Tyr Gly His	
115 120 125	
aat gat agc ccc ttt ttg cgt aat gtg atg ggg gaa ttg ctc att aaa	432
Asn Asp Ser Pro Phe Leu Arg Asn Val Met Gly Glu Leu Leu Ile Lys	
130 135 140	
gac gat gcg ttt gct tct gaa gtg gct tta aaa gag ttg ctc tat tgg	480
Asp Asp Ala Phe Ala Ser Glu Val Ala Leu Lys Glu Leu Leu Tyr Trp	
145 150 155 160	
aaa aca cgc tac cat gac aat tta aaa gac atg att aaa tct tac aac	528
Lys Thr Arg Tyr His Asp Asn Leu Lys Asp Met Ile Lys Ser Tyr Asn	
165 170 175	
aag ggc agt cgt tgg gaa agg agc gaa aaa tct aac gct gat gct gaa	576
Lys Gly Ser Arg Trp Glu Arg Ser Glu Lys Ser Asn Ala Asp Ala Glu	
180 185 190	
aaa tat tac gaa gag ata caa gac aga atc agg cgt ttg aaa gaa tct	624
Lys Tyr Tyr Glu Glu Ile Gln Asp Arg Ile Arg Arg Leu Lys Glu Ser	
195 200 205	
aaa atc ttt gat tcg cag tct agt aat gac caa gaa ttg caa aaa agc	672
Lys Ile Phe Asp Ser Gln Ser Ser Asn Asp Gln Glu Leu Gln Lys Ser	
210 215 220	
gct aat agc aac ctg gat tta gac cct atc ggc aac gcc atg ccc caa	720
Ala Asn Ser Asn Leu Asp Leu Asp Pro Ile Gly Asn Ala Met Pro Gln	
225 230 235 240	

gcc tta att gcc aaa gaa act aaa ata gaa gaa acc caa gca gaa aaa	768
Ala Leu Ile Ala Lys Glu Thr Lys Ile Glu Glu Thr Gln Ala Glu Lys	
245 250 255	
tcc caa gaa atg aaa gag aca act agc gag caa aca aaa agt aag cca	816
Ser Gln Glu Met Lys Glu Thr Thr Ser Glu Gln Thr Lys Ser Lys Pro	
260 265 270	
gaa aaa gca aaa gat aaa ccc atg tat ttg gcg caa atc aac agc act	864
Glu Lys Ala Lys Asp Lys Pro Met Tyr Leu Ala Gln Ile Asn Ser Thr	
275 280 285	
gat ttc aca ccc gtt aaa aaa agc ccc aaa aaa ccg gct aaa gtg agc	912
Asp Phe Thr Pro Val Lys Lys Ser Pro Lys Lys Pro Ala Lys Val Ser	
290 295 300	
caa aaa cac tcc ttt aag aat aac att aaa aat aat gta aaa aac aac	960
Gln Lys His Ser Phe Lys Asn Asn Ile Lys Asn Asn Val Lys Asn Asn	
305 310 315 320	
gcc aaa acc gct tcc aaa aaa caa gaa atg tgc aaa aat tgc tct cca	1008
Ala Lys Thr Ala Ser Lys Lys Gln Glu Met Cys Lys Asn Cys Ser Pro	
325 330 335	
ggg caa agg aat gcg att tta gct aac cac atc act ctc atg caa gag	1056
Gly Gln Arg Asn Ala Ile Leu Ala Asn His Ile Thr Leu Met Gln Glu	
340 345 350	
ctt taa	1062
Leu	

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 <211> 353  
 <212> PRT  
 <213> Helicobacter pylori

<400> 50

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20 25 30	
Pro Thr Lys Thr Glu Pro Lys Pro Ala Lys Gly Val Lys Asn Lys Pro	
35 40 45	
Lys Ser Pro Val Thr Lys Val Met Met Thr Asn Cys Asp Asn Ile Lys	
50 55 60	

Asp	Phe	Asn	Ala	Lys	Gln	Lys	Glu	Val	Leu	Lys	Ala	Ala	Tyr	Gln	Phe	65	70	75	80
Gly	Ser	Lys	Glu	Asn	Leu	Gly	Tyr	Glu	Met	Ala	Gly	Ile	Ala	Trp	Lys	85	90	95	
Glu	Ser	Cys	Ala	Gly	Val	Tyr	Lys	Ile	Asn	Phe	Ser	Asp	Pro	Ser	Ala	100	105	110	
Gly	Val	Tyr	His	Ser	Tyr	Ile	Pro	Ser	Val	Leu	Lys	Ser	Tyr	Gly	His	115	120	125	
Asn	Asp	Ser	Pro	Phe	Leu	Arg	Asn	Val	Met	Gly	Glu	Leu	Leu	Ile	Lys	130	135	140	
Asp	Asp	Ala	Phe	Ala	Ser	Glu	Val	Ala	Leu	Lys	Glu	Leu	Leu	Tyr	Trp	145	150	155	160
Lys	Thr	Arg	Tyr	His	Asp	Asn	Leu	Lys	Asp	Met	Ile	Lys	Ser	Tyr	Asn	165	170	175	
Lys	Gly	Ser	Arg	Trp	Glu	Arg	Ser	Glu	Lys	Ser	Asn	Ala	Asp	Ala	Glu	180	185	190	
Lys	Tyr	Tyr	Glu	Glu	Ile	Gln	Asp	Arg	Ile	Arg	Arg	Leu	Lys	Glu	Ser	195	200	205	
Lys	Ile	Phe	Asp	Ser	Gln	Ser	Ser	Asn	Asp	Gln	Glu	Leu	Gln	Lys	Ser	210	215	220	
Ala	Asn	Ser	Asn	Leu	Asp	Leu	Asp	Pro	Ile	Gly	Asn	Ala	Met	Pro	Gln	225	230	235	240
Ala	Leu	Ile	Ala	Lys	Glu	Thr	Lys	Ile	Glu	Glu	Thr	Gln	Ala	Glu	Lys	245	250	255	
Ser	Gln	Glu	Met	Lys	Glu	Thr	Thr	Ser	Glu	Gln	Thr	Lys	Ser	Lys	Pro	260	265	270	



Glu Lys Ala Lys Asp Lys Pro Met Tyr Leu Ala Gln Ile Asn Ser Thr  
 275 280 285

Asp Phe Thr Pro Val Lys Lys Ser Pro Lys Lys Pro Ala Lys Val Ser  
 290 295 300

Gln Lys His Ser Phe Lys Asn Asn Ile Lys Asn Asn Val Lys Asn Asn  
 305 310 315 320

Ala Lys Thr Ala Ser Lys Lys Gln Glu Met Cys Lys Asn Cys Ser Pro  
 325 330 335

Gly Gln Arg Asn Ala Ile Leu Ala Asn His Ile Thr Leu Met Gln Glu  
 340 345 350

Leu

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 <212> DNA  
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<220>  
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 ttt aaa cgc ttt ttg caa tcc aaa gac tta gcc ctt gtg gtc ttt gtg 96  
 Phe Lys Arg Phe Leu Gln Ser Lys Asp Leu Ala Leu Val Val Phe Val  
 20 25 30  
 atc gct att ttg gcg atc att atc gtg ccg tta ccg cct ttt gtg ttg 144  
 Ile Ala Ile Leu Ala Ile Ile Ile Val Pro Leu Pro Pro Phe Val Leu  
 35 40 45  
 gat ttt tta ctc acg att tct atc gcg ctg tcg gtg ttg att att tta 192  
 Asp Phe Leu Leu Thr Ile Ser Ile Ala Leu Ser Val Leu Ile Ile Leu  
 50 55 60  
 att ggg ctt tat att gac aag ccg act gat ttt agc gct ttc ccc act 240  
 Ile Gly Leu Tyr Ile Asp Lys Pro Thr Asp Phe Ser Ala Phe Pro Thr  
 65 70 75 80

tta	ttg	ctc	att	gta	acc	ttg	tat	cgc	ttg	gct	tta	aat	gtc	gcc	acc	288
Leu	Leu	Leu	Ile	Val	Thr	Leu	Tyr	Arg	Leu	Ala	Leu	Asn	Val	Ala	Thr	
			85						90					95		
act	aga	atg	att	tta	acg	caa	ggc	tat	aaa	ggg	cct	agt	gcg	gtg	agc	336
Thr	Arg	Met	Ile	Leu	Thr	Gln	Gly	Tyr	Lys	Gly	Pro	Ser	Ala	Val	Ser	
			100					105					110			
gat	att	atc	acg	gcg	ttt	ggg	gaa	ttt	agc	gtg	agc	ggg	aat	tat	gtg	384
Asp	Ile	Ile	Thr	Ala	Phe	Gly	Glu	Phe	Ser	Val	Ser	Gly	Asn	Tyr	Val	
		115				120						125				
att	ggg	gcg	att	atc	ttt	agt	att	tta	gtg	cta	gtg	aat	cta	tta	gtg	432
Ile	Gly	Ala	Ile	Ile	Phe	Ser	Ile	Leu	Val	Leu	Val	Asn	Leu	Leu	Val	
	130					135					140					
gtt	act	aat	ggc	tct	act	agg	gtt	act	gaa	gtg	agg	gcg	cga	ttt	gcc	480
Val	Thr	Asn	Gly	Ser	Thr	Arg	Val	Thr	Glu	Val	Arg	Ala	Arg	Phe	Ala	
145					150					155					160	
cta	gat	gct	atg	cca	gga	aag	caa	atg	gcg	att	gat	gcg	gat	tta	aac	528
Leu	Asp	Ala	Met	Pro	Gly	Lys	Gln	Met	Ala	Ile	Asp	Ala	Asp	Leu	Asn	
				165					170					175		
tca	gga	ctt	att	gac	gat	aag	gaa	gcc	aaa	aaa	cgg	cgc	gcc	gct	cta	576
Ser	Gly	Leu	Ile	Asp	Asp	Lys	Glu	Ala	Lys	Lys	Arg	Arg	Ala	Ala	Leu	
			180					185					190			
agc	caa	gaa	gcg	gat	ttt	tat	ggc	gcg	atg	gat	ggc	gca	tct	aaa	ttc	624
Ser	Gln	Glu	Ala	Asp	Phe	Tyr	Gly	Ala	Met	Asp	Gly	Ala	Ser	Lys	Phe	
		195					200					205				
gtc	aaa	ggc	gat	gcg	atc	gct	tct	atc	atc	atc	acg	ctt	atc	aat	atc	672
Val	Lys	Gly	Asp	Ala	Ile	Ala	Ser	Ile	Ile	Ile	Thr	Leu	Ile	Asn	Ile	
	210					215					220					
att	gga	ggg	ttt	tta	gtg	ggc	gtg	ttt	caa	agg	gat	atg	agc	ttg	agc	720
Ile	Gly	Gly	Phe	Leu	Val	Gly	Val	Phe	Gln	Arg	Asp	Met	Ser	Leu	Ser	
225					230					235					240	
ttt	agc	gct	agc	act	ttc	act	atc	tta	acc	att	ggc	gat	ggg	ctt	gtg	768
Phe	Ser	Ala	Ser	Thr	Phe	Thr	Ile	Leu	Thr	Ile	Gly	Asp	Gly	Leu	Val	
				245					250					255		
ggg	caa	atc	cct	gcc	tta	atc	att	gcg	aca	gcg	acc	ggt	att	gtc	gcc	816
Gly	Gln	Ile	Pro	Ala	Leu	Ile	Ile	Ala	Thr	Ala	Thr	Gly	Ile	Val	Ala	
			260					265					270			
act	cgc	acc	acg	caa	aat	gaa	gaa	gag	gac	ttt	gct	tcc	aaa	ctc	atc	864
Thr	Arg	Thr	Thr	Gln	Asn	Glu	Glu	Glu	Asp	Phe	Ala	Ser	Lys	Leu	Ile	
			275				280					285				
aca	cag	ctc	acc	aat	aaa	agc	aaa	act	tta	gtg	att	gtg	gga	gcg	att	912
Thr	Gln	Leu	Thr	Asn	Lys	Ser	Lys	Thr	Leu	Val	Ile	Val	Gly	Ala	Ile	
	290					295					300					

tta	ttg	ctt	ttt	gcc	acc	att	cct	gga	ctc	cct	acc	ttt	tct	tta	gcg	960
Leu	Leu	Leu	Phe	Ala	Thr	Ile	Pro	Gly	Leu	Pro	Thr	Phe	Ser	Leu	Ala	
305					310					315					320	
ttt	gta	ggg	act	ctc	ttt	tta	ttc	atc	gca	tgg	ctg	att	agc	agg	gag	1008
Phe	Val	Gly	Thr	Leu	Phe	Leu	Phe	Ile	Ala	Trp	Leu	Ile	Ser	Arg	Glu	
				325					330					335		
ggg	aaa	gac	ggg	ctg	ctc	act	aaa	tta	gaa	aat	tat	ttg	agt	caa	aaa	1056
Gly	Lys	Asp	Gly	Leu	Leu	Thr	Lys	Leu	Glu	Asn	Tyr	Leu	Ser	Gln	Lys	
			340					345					350			
ttc	ggc	ttg	gat	ttg	agc	gaa	aaa	ccc	cac	agc	tcc	aaa	atc	aaa	ccc	1104
Phe	Gly	Leu	Asp	Leu	Ser	Glu	Lys	Pro	His	Ser	Ser	Lys	Ile	Lys	Pro	
		355					360					365				
cac	acc	cca	acc	aca	agg	gct	aaa	acc	caa	gaa	gag	ctt	aaa	aga	gaa	1152
His	Thr	Pro	Thr	Thr	Arg	Ala	Lys	Thr	Gln	Glu	Glu	Leu	Lys	Arg	Glu	
	370					375					380					
gaa	gag	caa	gcg	att	gat	gaa	gtg	tta	aaa	att	gaa	ttt	tta	gaa	ctg	1200
Glu	Glu	Gln	Ala	Ile	Asp	Glu	Val	Leu	Lys	Ile	Glu	Phe	Leu	Glu	Leu	
385					390					395					400	
gct	tta	ggc	tat	caa	ctc	atc	agt	ctt	gcg	gac	atg	aaa	caa	ggg	ggc	1248
Ala	Leu	Gly	Tyr	Gln	Leu	Ile	Ser	Leu	Ala	Asp	Met	Lys	Gln	Gly	Gly	
				405					410					415		
gat	ttg	tta	gaa	agg	att	agg	ggt	att	aga	aaa	aag	ata	gcg	agc	gat	1296
Asp	Leu	Leu	Glu	Arg	Ile	Arg	Gly	Ile	Arg	Lys	Lys	Ile	Ala	Ser	Asp	
			420				425						430			
tat	ggt	ttt	ttg	atg	cct	caa	atc	cgg	atc	agg	gat	aat	ttg	cag	ctc	1344
Tyr	Gly	Phe	Leu	Met	Pro	Gln	Ile	Arg	Ile	Arg	Asp	Asn	Leu	Gln	Leu	
		435					440					445				
ccc	cca	acg	cat	tat	gaa	atc	aaa	ctt	aaa	ggc	att	gtg	att	ggt	gag	1392
Pro	Pro	Thr	His	Tyr	Glu	Ile	Lys	Leu	Lys	Gly	Ile	Val	Ile	Gly	Glu	
	450					455					460					
ggc	atg	gtg	atg	cca	gac	aag	ttt	tta	gcc	atg	aat	acc	ggt	ttt	gtg	1440
Gly	Met	Val	Met	Pro	Asp	Lys	Phe	Leu	Ala	Met	Asn	Thr	Gly	Phe	Val	
465					470					475					480	
aat	aaa	gaa	att	gaa	ggc	att	cct	act	aaa	gag	ccg	gct	ttt	gga	atg	1488
Asn	Lys	Glu	Ile	Glu	Gly	Ile	Pro	Thr	Lys	Glu	Pro	Ala	Phe	Gly	Met	
				485					490					495		
gac	gct	tta	tgg	att	gaa	act	aaa	aat	aaa	gaa	gaa	gcc	att	att	caa	1536
Asp	Ala	Leu	Trp	Ile	Glu	Thr	Lys	Asn	Lys	Glu	Glu	Ala	Ile	Ile	Gln	
			500					505					510			
ggc	tat	acc	att	att	gat	cca	agc	acc	ggt	att	gcg	acg	cac	acc	agc	1584
Gly	Tyr	Thr	Ile	Ile	Asp	Pro	Ser	Thr	Val	Ile	Ala	Thr	His	Thr	Ser	

515						520						525							
gaa	tta	gtg	aaa	aaa	tac	gct	gaa	gat	ttt	atc	act	aaa	gat	gaa	gtg	1632			
Glu	Leu	Val	Lys	Lys	Tyr	Ala	Glu	Asp	Phe	Ile	Thr	Lys	Asp	Glu	Val				
530						535						540							
aaa	tcc	ctt	tta	gag	cgc	ttg	gcc	aaa	gat	tat	cct	acg	att	gta	gaa	1680			
Lys	Ser	Leu	Leu	Glu	Arg	Leu	Ala	Lys	Asp	Tyr	Pro	Thr	Ile	Val	Glu				
545						550						555						560	
gag	agt	aaa	aaa	atc	ccc	acc	ggt	gcg	atc	cga	tca	gtc	ttg	caa	gcc	1728			
Glu	Ser	Lys	Lys	Ile	Pro	Thr	Gly	Ala	Ile	Arg	Ser	Val	Leu	Gln	Ala				
565						570						575							
ttg	tta	cat	gaa	aaa	atc	ccc	att	aaa	gac	atg	ctc	act	att	tta	gaa	1776			
Leu	Leu	His	Glu	Lys	Ile	Pro	Ile	Lys	Asp	Met	Leu	Thr	Ile	Leu	Glu				
580						585						590							
acg	att	acc	gat	att	gcc	cca	ttg	gtt	caa	aac	gat	gtg	aat	atc	tta	1824			
Thr	Ile	Thr	Asp	Ile	Ala	Pro	Leu	Val	Gln	Asn	Asp	Val	Asn	Ile	Leu				
595						600						605							
acc	gaa	caa	gtg	agg	gcg	agg	ctt	tct	agg	gtg	atc	act	aac	gct	ttt	1872			
Thr	Glu	Gln	Val	Arg	Ala	Arg	Leu	Ser	Arg	Val	Ile	Thr	Asn	Ala	Phe				
610						615						620							
aaa	tct	gaa	gac	ggg	cgt	ttg	aaa	ttt	tta	acc	ttt	tct	acc	gat	agc	1920			
Lys	Ser	Glu	Asp	Gly	Arg	Leu	Lys	Phe	Leu	Thr	Phe	Ser	Thr	Asp	Ser				
625						630						635						640	
gaa	caa	ttt	ttg	ctt	aat	aaa	ttg	cga	gaa	aat	ggc	act	tct	aaa	agt	1968			
Glu	Gln	Phe	Leu	Leu	Asn	Lys	Leu	Arg	Glu	Asn	Gly	Thr	Ser	Lys	Ser				
645						650						655							
ttg	ctg	ctc	aat	gtg	ggc	gaa	ttg	caa	aaa	ctc	att	gaa	gtg	gtc	tct	2016			
Leu	Leu	Leu	Asn	Val	Gly	Glu	Leu	Gln	Lys	Leu	Ile	Glu	Val	Val	Ser				
660						665						670							
gaa	gag	gcc	atg	aaa	gtc	ttg	caa	aaa	ggg	atc	gct	ccg	gtg	att	ttg	2064			
Glu	Glu	Ala	Met	Lys	Val	Leu	Gln	Lys	Gly	Ile	Ala	Pro	Val	Ile	Leu				
675						680						685							
atc	gta	gag	cct	aat	tta	aga	aaa	gct	ctt	tcc	aat	caa	atg	gag	caa	2112			
Ile	Val	Glu	Pro	Asn	Leu	Arg	Lys	Ala	Leu	Ser	Asn	Gln	Met	Glu	Gln				
690						695						700							
gcc	agg	att	gat	gtg	atc	gtg	cta	agc	cat	gcg	gaa	tta	gat	cct	aac	2160			
Ala	Arg	Ile	Asp	Val	Ile	Val	Leu	Ser	His	Ala	Glu	Leu	Asp	Pro	Asn				
705						710						715						720	
tct	aat	ttt	gaa	gct	tta	ggc	acg	atc	cat	att	aac	ttt	taa			2202			
Ser	Asn	Phe	Glu	Ala	Leu	Gly	Thr	Ile	His	Ile	Asn	Phe							
725						730													

<210> 52  
 <211> 733  
 <212> PRT  
 <213> Helicobacter pylori

<400> 52

Met Ala Asn Glu Arg Ser Lys Leu Ala Phe Lys Lys Thr Phe Pro Val  
 1 5 10 15

Phe Lys Arg Phe Leu Gln Ser Lys Asp Leu Ala Leu Val Val Phe Val  
 20 25 30

Ile Ala Ile Leu Ala Ile Ile Ile Val Pro Leu Pro Pro Phe Val Leu  
 35 40 45

Asp Phe Leu Leu Thr Ile Ser Ile Ala Leu Ser Val Leu Ile Ile Leu  
 50 55 60

Ile Gly Leu Tyr Ile Asp Lys Pro Thr Asp Phe Ser Ala Phe Pro Thr  
 65 70 75 80

Leu Leu Leu Ile Val Thr Leu Tyr Arg Leu Ala Leu Asn Val Ala Thr  
 85 90 95

Thr Arg Met Ile Leu Thr Gln Gly Tyr Lys Gly Pro Ser Ala Val Ser  
 100 105 110

Asp Ile Ile Thr Ala Phe Gly Glu Phe Ser Val Ser Gly Asn Tyr Val  
 115 120 125

Ile Gly Ala Ile Ile Phe Ser Ile Leu Val Leu Val Asn Leu Leu Val  
 130 135 140

Val Thr Asn Gly Ser Thr Arg Val Thr Glu Val Arg Ala Arg Phe Ala  
 145 150 155 160

Leu Asp Ala Met Pro Gly Lys Gln Met Ala Ile Asp Ala Asp Leu Asn  
 165 170 175

Ser Gly Leu Ile Asp Asp Lys Glu Ala Lys Lys Arg Arg Ala Ala Leu  
 180 185 190

Ser Gln Glu Ala Asp Phe Tyr Gly Ala Met Asp Gly Ala Ser Lys Phe  
195 200 205

Val Lys Gly Asp Ala Ile Ala Ser Ile Ile Ile Thr Leu Ile Asn Ile  
210 215 220

Ile Gly Gly Phe Leu Val Gly Val Phe Gln Arg Asp Met Ser Leu Ser  
225 230 235 240

Phe Ser Ala Ser Thr Phe Thr Ile Leu Thr Ile Gly Asp Gly Leu Val  
245 250 255

Gly Gln Ile Pro Ala Leu Ile Ile Ala Thr Ala Thr Gly Ile Val Ala  
260 265 270

Thr Arg Thr Thr Gln Asn Glu Glu Glu Asp Phe Ala Ser Lys Leu Ile  
275 280 285

Thr Gln Leu Thr Asn Lys Ser Lys Thr Leu Val Ile Val Gly Ala Ile  
290 295 300

Leu Leu Leu Phe Ala Thr Ile Pro Gly Leu Pro Thr Phe Ser Leu Ala  
305 310 315 320

Phe Val Gly Thr Leu Phe Leu Phe Ile Ala Trp Leu Ile Ser Arg Glu  
325 330 335

Gly Lys Asp Gly Leu Leu Thr Lys Leu Glu Asn Tyr Leu Ser Gln Lys  
340 345 350

Phe Gly Leu Asp Leu Ser Glu Lys Pro His Ser Ser Lys Ile Lys Pro  
355 360 365

His Thr Pro Thr Thr Arg Ala Lys Thr Gln Glu Glu Leu Lys Arg Glu  
370 375 380

Glu Glu Gln Ala Ile Asp Glu Val Leu Lys Ile Glu Phe Leu Glu Leu  
385 390 395 400

Ala Leu Gly Tyr Gln Leu Ile Ser Leu Ala Asp Met Lys Gln Gly Gly  
405 410 415

Asp Leu Leu Glu Arg Ile Arg Gly Ile Arg Lys Lys Ile Ala Ser Asp  
420 425 430

Tyr Gly Phe Leu Met Pro Gln Ile Arg Ile Arg Asp Asn Leu Gln Leu  
435 440 445

Pro Pro Thr His Tyr Glu Ile Lys Leu Lys Gly Ile Val Ile Gly Glu  
450 455 460

Gly Met Val Met Pro Asp Lys Phe Leu Ala Met Asn Thr Gly Phe Val  
465 470 475 480

Asn Lys Glu Ile Glu Gly Ile Pro Thr Lys Glu Pro Ala Phe Gly Met  
485 490 495

Asp Ala Leu Trp Ile Glu Thr Lys Asn Lys Glu Glu Ala Ile Ile Gln  
500 505 510

Gly Tyr Thr Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser  
515 520 525

Glu Leu Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val  
530 535 540

Lys Ser Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu  
545 550 555 560

Glu Ser Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala  
565 570 575

Leu Leu His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu  
580 585 590

Thr Ile Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu  
595 600 605

Thr Glu Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe  
610 615 620

Lys Ser Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Ser

625		630		635		640
Glu Gln Phe Leu Leu Asn Lys Leu Arg Glu Asn Gly Thr Ser Lys Ser						
	645			650		655
Leu Leu Leu Asn Val Gly Glu Leu Gln Lys Leu Ile Glu Val Val Ser						
	660			665		670
Glu Glu Ala Met Lys Val Leu Gln Lys Gly Ile Ala Pro Val Ile Leu						
	675			680		685
Ile Val Glu Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln						
	690			695		700
Ala Arg Ile Asp Val Ile Val Leu Ser His Ala Glu Leu Asp Pro Asn						
705		710		715		720
Ser Asn Phe Glu Ala Leu Gly Thr Ile His Ile Asn Phe						
	725			730		

<210> 53  
 <211> 189  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(189)

<400> 53	
atg caa aaa gaa caa gaa gcc cga gaa atc gct aaa aaa gcc gtt caa	48
Met Gln Lys Glu Gln Glu Ala Arg Glu Ile Ala Lys Lys Ala Val Gln	
1 5 10 15	
atc gtg ttt ttt tta ggg att gtg gtg gtg ctt ttg atg atg ata aac	96
Ile Val Phe Phe Leu Gly Ile Val Val Val Leu Leu Met Met Ile Asn	
20 25 30	
ctt tac atg ctc atc aat caa atc aac gcg agc gct aaa atg agc caa	144
Leu Tyr Met Leu Ile Asn Gln Ile Asn Ala Ser Ala Lys Met Ser Gln	
35 40 45	
caa atc aaa aaa ata gaa gaa agg ctt aac caa ggg caa aaa tag	189
Gln Ile Lys Lys Ile Glu Glu Arg Leu Asn Gln Gly Gln Lys	
50 55 60	



<210> 54  
 <211> 62  
 <212> PRT  
 <213> Helicobacter pylori

<400> 54

Met Gln Lys Glu Gln Glu Ala Arg Glu Ile Ala Lys Lys Ala Val Gln  
 1 5 10 15

Ile Val Phe Phe Leu Gly Ile Val Val Val Leu Leu Met Met Ile Asn  
 20 25 30

Leu Tyr Met Leu Ile Asn Gln Ile Asn Ala Ser Ala Lys Met Ser Gln  
 35 40 45

Gln Ile Lys Lys Ile Glu Glu Arg Leu Asn Gln Gly Gln Lys  
 50 55 60

<210> 55  
 <211> 1008  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1008)

<400> 55

atg tta gtt act cgc ttt aaa aaa gct ttc att tct tat tct tta ggc 48  
 Met Leu Val Thr Arg Phe Lys Lys Ala Phe Ile Ser Tyr Ser Leu Gly  
 1 5 10 15

gtg ctt gtc gct tca tta tgg ttg aac gtg tgc aac gct tca gcg caa 96  
 Val Leu Val Ala Ser Leu Trp Leu Asn Val Cys Asn Ala Ser Ala Gln  
 20 25 30

gaa gtc aaa gtc aag gat tat ttc ggg gag caa acc atc aag ctt cct 144  
 Glu Val Lys Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile Lys Leu Pro  
 35 40 45

gtt tct aaa ata gcc tat ata ggg agc tat gta gaa gtg cct gcc atg 192  
 Val Ser Lys Ile Ala Tyr Ile Gly Ser Tyr Val Glu Val Pro Ala Met  
 50 55 60

ctt aat gtt tgg aat agg gtt gta ggc gtt tcg gat tac gct ttt aaa 240  
 Leu Asn Val Trp Asn Arg Val Val Gly Val Ser Asp Tyr Ala Phe Lys  
 65 70 75 80

gac gat att gtc aaa gcc act ctc aaa ggc gaa gat ctt aaa cgc gtc Asp Asp Ile Val Lys Ala Thr Leu Lys Gly Glu Asp Leu Lys Arg Val 85 90 95	288
aaa cac atg agc act gat cat aca gcc gcg cta aat gta gag ctt tta Lys His Met Ser Thr Asp His Thr Ala Ala Leu Asn Val Glu Leu Leu 100 105 110	336
aaa aag ctt agc cct gat ctt gtg gta acc ttt gtg ggc aac cct aaa Lys Lys Leu Ser Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro Lys 115 120 125	384
gcg gta gag cat gcg aaa aaa ttt ggt ata tca ttt ctt tct ttt caa Ala Val Glu His Ala Lys Lys Phe Gly Ile Ser Phe Leu Ser Phe Gln 130 135 140	432
gag aca acg att gca gag gcc atg cag gcc atg caa gct caa gcc acg Glu Thr Thr Ile Ala Glu Ala Met Gln Ala Met Gln Ala Gln Ala Thr 145 150 155 160	480
gtt tta gag att gac gct tcc aaa aaa ttc gcc aaa atg caa gaa act Val Leu Glu Ile Asp Ala Ser Lys Lys Phe Ala Lys Met Gln Glu Thr 165 170 175	528
ttg gat ttt att gct gag cgt ttg aaa aat gtc aaa aag aaa aag ggg Leu Asp Phe Ile Ala Glu Arg Leu Lys Asn Val Lys Lys Lys Lys Gly 180 185 190	576
gtg gag ctt ttc cat aaa gcc aat aaa atc agc ggc cat caa gcc att Val Glu Leu Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Ile 195 200 205	624
agc tca gac att tta gaa aaa ggg ggc ata gac aat ttt ggc ttg aaa Ser Ser Asp Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys 210 215 220	672
tat gtc aaa ttt ggg cgt gct gac att agc gtg gaa aaa atc gtt aaa Tyr Val Lys Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys 225 230 235 240	720
gaa aac cct gag att atc ttt att tgg tgg ata agc cca ctc acg cct Glu Asn Pro Glu Ile Ile Phe Ile Trp Trp Ile Ser Pro Leu Thr Pro 245 250 255	768
gaa gat gtg tta aac aac ccc aaa ttt gct acc atc aaa gcc att aaa Glu Asp Val Leu Asn Asn Pro Lys Phe Ala Thr Ile Lys Ala Ile Lys 260 265 270	816
aac aag cag gtt tat aaa ctc ccc aca atg gat att ggc ggg cct aga Asn Lys Gln Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro Arg 275 280 285	864
gcc cca ctc ata agt ctt ttt atc gct cta aaa gcc cac cct gaa gcc Ala Pro Leu Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala 290 295 300	912

t	t	a	a	g	c	c	a	a	t	t	a	a	t	t	a	a		960
Phe	Lys	Gly	Val	Asp	Ile	Asn	Ala	Met	Val	Lys	Asp	Tyr	Tyr	Lys	Val			
305					310					315					320			

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<210> 56
<211> 335
<212> PRT
<213> Helicobacter pylori
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Met Leu Val Thr Arg Phe Lys Lys Ala Phe Ile Ser Tyr Ser Leu Gly  
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Glu Val Lys Val Lys Asp Tyr Phe Gly Glu Gln Thr Ile Lys Leu Pro  
35 40 45

Leu Asn Val Trp Asn Arg Val Val Gly Val Ser Asp Tyr Ala Phe Lys  
65 70 75 80

Lys His Met Ser Thr Asp His Thr Ala Ala Leu Asn Val Glu Leu Leu  
100 105 110

Ala Val Glu His Ala Lys Lys Phe Gly Ile Ser Phe Leu Ser Phe Gln  
130 135 140

Val Leu Glu Ile Asp Ala Ser Lys Lys Phe Ala Lys Met Gln Glu Thr  
165 170 175

Leu Asp Phe Ile Ala Glu Arg Leu Lys Asn Val Lys Lys Lys Lys Gly  
180 185 190

Val Glu Leu Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Ile  
195 200 205

Ser Ser Asp Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys  
210 215 220

Tyr Val Lys Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys  
225 230 235 240

Glu Asn Pro Glu Ile Ile Phe Ile Trp Trp Ile Ser Pro Leu Thr Pro  
245 250 255

Glu Asp Val Leu Asn Asn Pro Lys Phe Ala Thr Ile Lys Ala Ile Lys  
260 265 270

Asn Lys Gln Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro Arg  
275 280 285

Ala Pro Leu Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala  
290 295 300

Phe Lys Gly Val Asp Ile Asn Ala Met Val Lys Asp Tyr Tyr Lys Val  
305 310 315 320

Val Phe Asp Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His  
325 330 335

<210> 57  
<211> 240  
<212> DNA  
<213> Helicobacter pylori

<220> .  
<221> CDS  
<222> (1)..(240)

<400> 57  
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 Met Gly Gly Phe Thr Ser Ile Trp His Trp Val Ile Val Leu Leu Val  
 1 5 10 15  
 att gtg ttg tta ttt ggg gct aaa aag atc cca gaa ttg gct aaa ggt 96  
 Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Glu Leu Ala Lys Gly  
 20 25 30  
 tta ggc agt ggg att aag aat ttc aaa aaa gcc gtg aaa gac gat gaa 144  
 Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp Glu  
 35 40 45  
 gaa gag gct aaa aac gag cca aaa acc cta gac gct caa gca acg caa 192  
 Glu Glu Ala Lys Asn Glu Pro Lys Thr Leu Asp Ala Gln Ala Thr Gln  
 50 55 60  
 acc aaa gtg cat gag agt agc gag att aaa agc aaa caa gaa agt taa 240  
 Thr Lys Val His Glu Ser Ser Glu Ile Lys Ser Lys Gln Glu Ser  
 65 70 75

<210> 58  
 <211> 79  
 <212> PRT  
 <213> Helicobacter pylori

<400> 58  
 Met Gly Gly Phe Thr Ser Ile Trp His Trp Val Ile Val Leu Leu Val  
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 Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Glu Leu Ala Lys Gly  
 20 25 30  
 Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp Glu  
 35 40 45  
 Glu Glu Ala Lys Asn Glu Pro Lys Thr Leu Asp Ala Gln Ala Thr Gln  
 50 55 60  
 Thr Lys Val His Glu Ser Ser Glu Ile Lys Ser Lys Gln Glu Ser  
 65 70 75

<210> 59  
 <211> 1764  
 <212> DNA  
 <213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1764)

<400> 59

atg	aaa	aac	ttt	tcc	cca	ctt	tgt	tgt	ttt	aaa	aag	ctc	aaa	aaa	cgc	48
Met	Lys	Asn	Phe	Ser	Pro	Leu	Cys	Cys	Phe	Lys	Lys	Leu	Lys	Lys	Arg	
1				5					10					15		

cat	tta	atc	gct	ttg	agc	ctg	ccc	ttg	ctt	tct	tat	gct	aat	ggc	ttt	96
His	Leu	Ile	Ala	Leu	Ser	Leu	Pro	Leu	Leu	Ser	Tyr	Ala	Asn	Gly	Phe	
			20					25					30			

aaa	atc	caa	gag	caa	agc	ctg	aat	ggc	acg	gct	tta	ggc	tcg	gcg	tat	144
Lys	Ile	Gln	Glu	Gln	Ser	Leu	Asn	Gly	Thr	Ala	Leu	Gly	Ser	Ala	Tyr	
		35					40					45				

gtc	gct	ggg	gct	agg	ggg	gct	gat	gct	tcc	ttt	tat	aac	ccg	gcg	aat	192
Val	Ala	Gly	Ala	Arg	Gly	Ala	Asp	Ala	Ser	Phe	Tyr	Asn	Pro	Ala	Asn	
	50					55					60					

atg	ggc	ttt	act	aac	gat	tgg	gat	gaa	aac	aga	agc	gaa	ttt	gaa	atg	240
Met	Gly	Phe	Thr	Asn	Asp	Trp	Asp	Glu	Asn	Arg	Ser	Glu	Phe	Glu	Met	
65					70					75					80	

acc	acc	acc	gtg	att	aat	atc	ccg	gcc	ttt	aag	ttt	caa	gtc	cct	acg	288
Thr	Thr	Thr	Val	Ile	Asn	Ile	Pro	Ala	Phe	Lys	Phe	Gln	Val	Pro	Thr	
				85					90					95		

act	aat	caa	ggc	ttg	tat	tcg	gtt	acg	agc	tta	caa	att	gat	aaa	agc	336
Thr	Asn	Gln	Gly	Leu	Tyr	Ser	Val	Thr	Ser	Leu	Gln	Ile	Asp	Lys	Ser	
			100					105					110			

caa	caa	aat	att	tta	ggc	atc	atc	aac	act	ata	ggg	ctt	agc	aat	atc	384
Gln	Gln	Asn	Ile	Leu	Gly	Ile	Ile	Asn	Thr	Ile	Gly	Leu	Ser	Asn	Ile	
		115					120					125				

ctt	aaa	gcg	ctt	ggc	aat	acg	gcc	gct	acc	aat	ggc	tta	tca	caa	gca	432
Leu	Lys	Ala	Leu	Gly	Asn	Thr	Ala	Ala	Thr	Asn	Gly	Leu	Ser	Gln	Ala	
	130					135					140					

atc	aat	cgg	gtt	caa	ggg	ctt	atg	aat	cta	acc	aat	caa	aaa	gtc	gta	480
Ile	Asn	Arg	Val	Gln	Gly	Leu	Met	Asn	Leu	Thr	Asn	Gln	Lys	Val	Val	
145					150					155					160	

acc	ctc	gct	tca	aaa	cct	gac	acc	caa	atc	gtg	aat	ggc	tgg	acg	gga	528
Thr	Leu	Ala	Ser	Lys	Pro	Asp	Thr	Gln	Ile	Val	Asn	Gly	Trp	Thr	Gly	
				165					170					175		

acg	act	aat	ttt	gtt	tta	ccc	aaa	ttc	ttt	tat	aaa	acg	cgc	acg	cat	576
Thr	Thr	Asn	Phe	Val	Leu	Pro	Lys	Phe	Phe	Tyr	Lys	Thr	Arg	Thr	His	
			180					185					190			

aac	ggc	ttc	act	ttt	ggg	ggg	agt	ttt	acc	gct	cct	agc	ggg	ttg	ggc	624
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Asn	Gly	Phe	Thr	Phe	Gly	Gly	Ser	Phe	Thr	Ala	Pro	Ser	Gly	Leu	Gly	
		195					200					205				
atg	aaa	tgg	aat	ggg	aaa	ggg	ggg	gaa	ttt	ttg	cat	gac	gtg	ttt	atc	672
Met	Lys	Trp	Asn	Gly	Lys	Gly	Gly	Glu	Phe	Leu	His	Asp	Val	Phe	Ile	
	210					215				220						
atg	atg	gta	gag	ctt	gcc	cct	agc	atg	agc	tat	act	ggt	aat	aag	cac	720
Met	Met	Val	Glu	Leu	Ala	Pro	Ser	Met	Ser	Tyr	Thr	Val	Asn	Lys	His	
	225				230					235					240	
ttt	tcc	gtg	ggc	gtg	ggc	tta	agg	ggg	ctt	tat	gcg	acc	ggg	agc	ttt	768
Phe	Ser	Val	Gly	Val	Gly	Leu	Arg	Gly	Leu	Tyr	Ala	Thr	Gly	Ser	Phe	
				245					250					255		
aat	aac	acc	ggt	tat	gtg	cct	tta	gag	ggc	gct	tcg	ggt	ttg	agc	gcg	816
Asn	Asn	Thr	Val	Tyr	Val	Pro	Leu	Glu	Gly	Ala	Ser	Val	Leu	Ser	Ala	
		260						265					270			
gag	caa	att	tta	aat	tta	ccc	aac	aat	ggt	ttt	gcc	gat	caa	gtg	cca	864
Glu	Gln	Ile	Leu	Asn	Leu	Pro	Asn	Asn	Val	Phe	Ala	Asp	Gln	Val	Pro	
	275						280					285				
agt	aac	atg	atg	act	tta	tta	ggc	aat	att	ggc	tac	caa	cca	gcg	ctt	912
Ser	Asn	Met	Met	Thr	Leu	Leu	Gly	Asn	Ile	Gly	Tyr	Gln	Pro	Ala	Leu	
	290					295					300					
aat	tgc	caa	aaa	gcc	ggt	ggg	gat	atg	agc	gat	cag	agc	tgt	caa	gag	960
Asn	Cys	Gln	Lys	Ala	Gly	Gly	Asp	Met	Ser	Asp	Gln	Ser	Cys	Gln	Glu	
	305				310					315					320	
ttt	tat	aac	ggc	ttg	aaa	aaa	atc	atg	ggc	tat	agc	ggc	tta	atc	aaa	1008
Phe	Tyr	Asn	Gly	Leu	Lys	Lys	Ile	Met	Gly	Tyr	Ser	Gly	Leu	Ile	Lys	
				325					330					335		
gcg	agc	gcg	aat	ctt	tat	ggc	acg	act	caa	gtc	gtg	caa	aaa	tct	aac	1056
Ala	Ser	Ala	Asn	Leu	Tyr	Gly	Thr	Thr	Gln	Val	Val	Gln	Lys	Ser	Asn	
			340					345					350			
ggg	caa	ggc	gta	tcg	ggg	ggc	tat	aga	gtg	ggg	tcg	agt	ttg	cgt	gtg	1104
Gly	Gln	Gly	Val	Ser	Gly	Gly	Tyr	Arg	Val	Gly	Ser	Ser	Leu	Arg	Val	
		355					360					365				
ttt	gat	cat	ggc	atg	ttt	tcg	gtg	gtg	tat	aat	tct	tca	ggt	aca	ttc	1152
Phe	Asp	His	Gly	Met	Phe	Ser	Val	Val	Tyr	Asn	Ser	Ser	Val	Thr	Phe	
	370					375					380					
aat	atg	aaa	ggc	gct	cta	gtg	gct	atc	acc	gag	ctt	ggc	cct	tct	tta	1200
Asn	Met	Lys	Gly	Ala	Leu	Val	Ala	Ile	Thr	Glu	Leu	Gly	Pro	Ser	Leu	
	385				390					395					400	
ggg	agc	ggt	ttg	act	aaa	ggc	agc	ttg	aat	atc	aat	ggt	tca	ctc	ccc	1248
Gly	Ser	Val	Leu	Thr	Lys	Gly	Ser	Leu	Asn	Ile	Asn	Val	Ser	Leu	Pro	
				405					410					415		

caa acc cta agc cta gcc tac gcc cac caa ttt ttt aaa gac cat tta	1296
Gln Thr Leu Ser Leu Ala Tyr Ala His Gln Phe Phe Lys Asp His Leu	
420 425 430	
aga ata gag ggg gtg ttt gag cgt acc ttt tgg agt caa ggg aat aaa	1344
Arg Ile Glu Gly Val Phe Glu Arg Thr Phe Trp Ser Gln Gly Asn Lys	
435 440 445	
ttt tta gta acc cct gat ttt gcg aac gct act tac aag ggc ttg agc	1392
Phe Leu Val Thr Pro Asp Phe Ala Asn Ala Thr Tyr Lys Gly Leu Ser	
450 455 460	
gga acg gtg gct tca cta gac tct gag acg ctt aaa aaa atg gta ggc	1440
Gly Thr Val Ala Ser Leu Asp Ser Glu Thr Leu Lys Lys Met Val Gly	
465 470 475 480	
tta gcg aat ttt aaa agc gtg atg aac atg ggg gct ggc tgg aga gac	1488
Leu Ala Asn Phe Lys Ser Val Met Asn Met Gly Ala Gly Trp Arg Asp	
485 490 495	
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Ile Gly Ile Pro Asp Ser Asn Gly Tyr Thr Val Ala Phe Gly Thr Lys	
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Tyr Asn Phe Arg Gly Phe Asp Leu Gly Val Ala Gly Ser Phe Thr Phe	
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Lys Ser Asn Arg Ser Ser Leu Tyr Gln Ser Pro Asn Ile Gly Gln Leu	
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Gln Gln Asn Ile Leu Gly Ile Ile Asn Thr Ile Gly Leu Ser Asn Ile  
 115 120 125

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 130 135 140

Ile Asn Arg Val Gln Gly Leu Met Asn Leu Thr Asn Gln Lys Val Val  
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Asn Gly Phe Thr Phe Gly Gly Ser Phe Thr Ala Pro Ser Gly Leu Gly  
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Phe Leu Val Thr Pro Asp Phe Ala Asn Ala Thr Tyr Lys Gly Leu Ser  
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Leu Ala Asn Phe Lys Ser Val Met Asn Met Gly Ala Gly Trp Arg Asp  
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Leu Met Gly Ala Ile Asp Tyr Asp Gln Ala Pro Ser Pro Gln Asp Ala  
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Asn Phe Leu Asp Leu Val Leu Arg His Tyr Ser Asn His Asn Phe Tyr
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Ile Glu Ile Phe Gln Thr Asp Ile Arg Asn Pro Ile Met Tyr Leu Asn  
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Ser Leu Arg Asn Pro Ile Leu His Phe Met Pro Phe Glu Glu Cys Ile  
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Thr His Thr Arg Phe Trp Trp Phe Leu Ser Thr Lys Val Glu Lys Leu  
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His Glu Ile Ile Arg Leu Gln Val Lys Thr Asp Glu Thr Leu Lys Leu  
65 70 75 80  
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Ser	Lys	Glu	Ala	Phe	Tyr	Phe	Leu	Phe	Gln	Asn	Lys	Leu	Asn	Pro	Met		
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His	Glu	Ile	Ile	Arg	Leu	Gln	Val	Lys	Thr	Asp	Glu	Thr	Leu	Lys	Leu		
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Ile Lys Glu Ala Lys Lys Arg Leu Asn Tyr Asn Asp Asp Ile Arg Asp  
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Val Leu Gln Gly Leu Leu Asn Ile Val Pro Asp Ser Ile Thr Ile Asn  
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Ser Ile Glu Ile Asp Gln Gln Ser Val Val Val Ser Gly Lys Thr Pro  
115 120 125

Ser Lys Glu Ala Phe Tyr Phe Leu Phe Gln Asn Lys Leu Asn Pro Met  
130 135 140

Phe Asp Tyr Ser Arg Ala Glu Phe Phe Pro Leu Ser Asp Gly Trp Phe  
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Asn Phe Val Ser Thr Asn Phe Ser Asn Ser Leu Leu Ile Lys Asn Pro  
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Ser	Ala	Glu	Leu	Phe	Asn	Asp	Glu	Pro	Ile	His	Pro	Leu	Val	Arg	Ala	
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Glu	Asn	Asp	Leu	Lys	Phe	Asp	Ile	Arg	Val	Leu	Gly	Asn	His	Glu	Phe	
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Val	Gly	Tyr	Val	Val	Ala	His	Ile	Pro	Thr	Trp	Glu	Ala	Ser	Thr	Pro	
				165				170						175		
gaa	cat	ttt	gca	gga	ttg	aag	ttt	ttg	gac	gct	gaa	gaa	gcg	tta	aaa	576
Glu	His	Phe	Ala	Gly	Leu	Lys	Phe	Leu	Asp	Ala	Glu	Glu	Ala	Leu	Lys	
			180					185					190			
aag	acc	tta	aaa	gag	ttg	aaa	ggg	aag	tat	gat	att	ttg	att	ggc	gct	624
Lys	Thr	Leu	Lys	Glu	Leu	Lys	Gly	Lys	Tyr	Asp	Ile	Leu	Ile	Gly	Ala	
		195					200					205				
ttt	cat	ttg	ggg	cga	gaa	gat	gag	aaa	ggg	ggc	gac	ggg	ata	ccg	gat	672
Phe	His	Leu	Gly	Arg	Glu	Asp	Glu	Lys	Gly	Gly	Asp	Gly	Ile	Pro	Asp	
	210					215					220					
tta	gcg	aaa	aaa	ttc	ccg	caa	ttt	gac	atc	att	ttt	gca	ggg	cat	gag	720
Leu	Ala	Lys	Lys	Phe	Pro	Gln	Phe	Asp	Ile	Ile	Phe	Ala	Gly	His	Glu	
225					230					235					240	
cat	gcg	gtt	tat	aac	acc	aaa	gta	ggg	aaa	gtg	cat	acc	att	gag	cct	768
His	Ala	Val	Tyr	Asn	Thr	Lys	Val	Gly	Lys	Val	His	Thr	Ile	Glu	Pro	
				245					250					255		
gga	gcg	tat	ggg	gct	tat	ctg	gca	aag	ggc	gtg	gtg	gta	ttt	gac	act	816
Gly	Ala	Tyr	Gly	Ala	Tyr	Leu	Ala	Lys	Gly	Val	Val	Val	Phe	Asp	Thr	
			260					265					270			
aaa	acg	aag	aaa	aaa	att	ata	acg	act	gaa	aat	tta	ccc	aca	aaa	gat	864
Lys	Thr	Lys	Lys	Lys	Ile	Ile	Thr	Thr	Glu	Asn	Leu	Pro	Thr	Lys	Asp	
		275					280					285				

gtg cca gaa gat gaa gaa tta gcg aaa aaa tac gaa tat gtg gat aaa Val Pro Glu Asp Glu Glu Leu Ala Lys Lys Tyr Glu Tyr Val Asp Lys 290 295 300	912
aaa tca aaa gaa tac gct aat gaa gtg gtt ggc gaa gtt aca aaa acc Lys Ser Lys Glu Tyr Ala Asn Glu Val Val Gly Glu Val Thr Lys Thr 305 310 315 320	960
ttt att gac agg cct gat ttt atc aca gga gaa gaa aaa atc acc acg Phe Ile Asp Arg Pro Asp Phe Ile Thr Gly Glu Glu Lys Ile Thr Thr 325 330 335	1008
atg ccc acc gcc gcc ttg caa gaa aca ccg gtg ata gaa ttg att aat Met Pro Thr Ala Ala Leu Gln Glu Thr Pro Val Ile Glu Leu Ile Asn 340 345 350	1056
aaa gtg caa aaa tat tac gca aaa gcc gat gtt tca gcg gca gcc tta Lys Val Gln Lys Tyr Tyr Ala Lys Ala Asp Val Ser Ala Ala Leu 355 360 365	1104
ttc aat ttt ggg gcg aat ttg aaa aaa ggg cct ttc aaa aga aaa gat Phe Asn Phe Gly Ala Asn Leu Lys Lys Gly Pro Phe Lys Arg Lys Asp 370 375 380	1152
gtc act tat att tac aag ttc gct aat acg ctc att gga gtg cgt ata Val Thr Tyr Ile Tyr Lys Phe Ala Asn Thr Leu Ile Gly Val Arg Ile 385 390 395 400	1200
acg ggt gaa aat ctg ttg aaa tac atg gaa tgg tca tac cga ttt tac Thr Gly Glu Asn Leu Leu Lys Tyr Met Glu Trp Ser Tyr Arg Phe Tyr 405 410 415	1248
aat cag ttg caa cca gga gat ttg acg atc agt ttt aat gaa aac att Asn Gln Leu Gln Pro Gly Asp Leu Thr Ile Ser Phe Asn Glu Asn Ile 420 425 430	1296
cgc ggc tat aac ttt gat atg ttt tct ggc gtg aaa tac cag gtt gat Arg Gly Tyr Asn Phe Asp Met Phe Ser Gly Val Lys Tyr Gln Val Asp 435 440 445	1344
gtt aca aaa ccc gcc gga caa agg att atc aat ccg aca atc aac aac Val Thr Lys Pro Ala Gly Gln Arg Ile Ile Asn Pro Thr Ile Asn Asn 450 455 460	1392
aaa ccc att gac ccc aaa gcc atc tat aaa tta gcg atc aac aat tac Lys Pro Ile Asp Pro Lys Ala Ile Tyr Lys Leu Ala Ile Asn Asn Tyr 465 470 475 480	1440
cga ttc gga aca tta tcc acg aca ttg aat ttg gtt aca gac gct gat Arg Phe Gly Thr Leu Ser Thr Thr Leu Asn Leu Val Thr Asp Ala Asp 485 490 495	1488
agg tat tat aat tct tac gat gaa ctg caa gat aat ggg caa ata cga Arg Tyr Tyr Asn Ser Tyr Asp Glu Leu Gln Asp Asn Gly Gln Ile Arg	1536

500							505							510							
gat	ttg	atc	atc	aaa	tac	atc	acg	gaa	gaa	aaa	ggg	ggg	aag	gta	acc	1584					
Asp	Leu	Ile	Ile	Lys	Tyr	Ile	Thr	Glu	Glu	Lys	Gly	Gly	Lys	Val	Thr						
	515						520					525									
cct	gaa	ttg	gag	ggg	aat	tgg	gaa	atc	atc	aac	tac	gat	ttc	aaa	aac	1632					
Pro	Glu	Leu	Glu	Gly	Asn	Trp	Glu	Ile	Ile	Asn	Tyr	Asp	Phe	Lys	Asn						
	530					535					540										
ccg	ttg	ttg	gaa	aaa	ttg	aga	gaa	aaa	tta	aaa	gag	ggg	agc	atc	aaa	1680					
Pro	Leu	Leu	Glu	Lys	Leu	Arg	Glu	Lys	Leu	Lys	Glu	Gly	Ser	Ile	Lys						
545					550					555					560						
atc	ccc	acc	tca	aag	gat	ggg	agg	act	ttg	aat	gtc	aaa	tcc	att	aaa	1728					
Ile	Pro	Thr	Ser	Lys	Asp	Gly	Arg	Thr	Leu	Asn	Val	Lys	Ser	Ile	Lys						
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Glu	Ser	Glu	Val	Lys																	
			580																		

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 <212> PRT  
 <213> Helicobacter pylori

<400> 66

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			20					25					30		
Gly	Arg	Leu	Phe	Ser	Tyr	Asp	Tyr	Ala	Ile	Gly	Glu	Gln	Lys	Pro	Asn
		35					40					45			
Asn	Gly	Leu	Thr	Arg	Ile	Ala	Thr	Leu	Ile	Lys	Lys	Gln	Arg	Ala	Glu
	50					55					60				
Asn	Lys	Asn	Val	Val	Leu	Ile	Asp	Ser	Gly	Asp	Leu	Leu	Gln	Gly	Asn
65					70					75					80
Ser	Ala	Glu	Leu	Phe	Asn	Asp	Glu	Pro	Ile	His	Pro	Leu	Val	Arg	Ala
				85					90					95	

Glu	Asn	Asp	Leu	Lys	Phe	Asp	Ile	Arg	Val	Leu	Gly	Asn	His	Glu	Phe	100	105	110
Asn	Phe	Ser	Lys	Asp	Phe	Leu	Glu	Lys	Asn	Ile	Lys	Gly	Phe	Asn	Gly	115	120	125
Asp	Val	Met	Asn	Ala	Asn	Ile	Ile	Lys	Ile	Ala	Asp	Asn	Lys	Pro	Phe	130	135	140
Val	Lys	Pro	Tyr	Ile	Ile	Lys	Lys	Ile	Asp	Gly	Val	Arg	Val	Ala	Val	145	150	155
Val	Gly	Tyr	Val	Val	Ala	His	Ile	Pro	Thr	Trp	Glu	Ala	Ser	Thr	Pro	165	170	175
Glu	His	Phe	Ala	Gly	Leu	Lys	Phe	Leu	Asp	Ala	Glu	Glu	Ala	Leu	Lys	180	185	190
Lys	Thr	Leu	Lys	Glu	Leu	Lys	Gly	Lys	Tyr	Asp	Ile	Leu	Ile	Gly	Ala	195	200	205
Phe	His	Leu	Gly	Arg	Glu	Asp	Glu	Lys	Gly	Gly	Asp	Gly	Ile	Pro	Asp	210	215	220
Leu	Ala	Lys	Lys	Phe	Pro	Gln	Phe	Asp	Ile	Ile	Phe	Ala	Gly	His	Glu	225	230	235
His	Ala	Val	Tyr	Asn	Thr	Lys	Val	Gly	Lys	Val	His	Thr	Ile	Glu	Pro	245	250	255
Gly	Ala	Tyr	Gly	Ala	Tyr	Leu	Ala	Lys	Gly	Val	Val	Val	Phe	Asp	Thr	260	265	270
Lys	Thr	Lys	Lys	Lys	Ile	Ile	Thr	Thr	Glu	Asn	Leu	Pro	Thr	Lys	Asp	275	280	285
Val	Pro	Glu	Asp	Glu	Glu	Leu	Ala	Lys	Lys	Tyr	Glu	Tyr	Val	Asp	Lys	290	295	300
Lys	Ser	Lys	Glu	Tyr	Ala	Asn	Glu	Val	Val	Gly	Glu	Val	Thr	Lys	Thr	305	310	315

Phe	Ile	Asp	Arg	Pro	Asp	Phe	Ile	Thr	Gly	Glu	Glu	Lys	Ile	Thr	Thr	325	330	335	
Met	Pro	Thr	Ala	Ala	Leu	Gln	Glu	Thr	Pro	Val	Ile	Glu	Leu	Ile	Asn	340	345	350	
Lys	Val	Gln	Lys	Tyr	Tyr	Ala	Lys	Ala	Asp	Val	Ser	Ala	Ala	Ala	Leu	355	360	365	
Phe	Asn	Phe	Gly	Ala	Asn	Leu	Lys	Lys	Gly	Pro	Phe	Lys	Arg	Lys	Asp	370	375	380	
Val	Thr	Tyr	Ile	Tyr	Lys	Phe	Ala	Asn	Thr	Leu	Ile	Gly	Val	Arg	Ile	385	390	395	400
Thr	Gly	Glu	Asn	Leu	Leu	Lys	Tyr	Met	Glu	Trp	Ser	Tyr	Arg	Phe	Tyr	405	410	415	
Asn	Gln	Leu	Gln	Pro	Gly	Asp	Leu	Thr	Ile	Ser	Phe	Asn	Glu	Asn	Ile	420	425	430	
Arg	Gly	Tyr	Asn	Phe	Asp	Met	Phe	Ser	Gly	Val	Lys	Tyr	Gln	Val	Asp	435	440	445	
Val	Thr	Lys	Pro	Ala	Gly	Gln	Arg	Ile	Ile	Asn	Pro	Thr	Ile	Asn	Asn	450	455	460	
Lys	Pro	Ile	Asp	Pro	Lys	Ala	Ile	Tyr	Lys	Leu	Ala	Ile	Asn	Asn	Tyr	465	470	475	480
Arg	Phe	Gly	Thr	Leu	Ser	Thr	Thr	Leu	Asn	Leu	Val	Thr	Asp	Ala	Asp	485	490	495	
Arg	Tyr	Tyr	Asn	Ser	Tyr	Asp	Glu	Leu	Gln	Asp	Asn	Gly	Gln	Ile	Arg	500	505	510	
Asp	Leu	Ile	Ile	Lys	Tyr	Ile	Thr	Glu	Glu	Lys	Gly	Gly	Lys	Val	Thr	515	520	525	
Pro	Glu	Leu	Glu	Gly	Asn	Trp	Glu	Ile	Ile	Asn	Tyr	Asp	Phe	Lys	Asn	530	535	540	

Pro Leu Leu Glu Lys Leu Arg Glu Lys Leu Lys Glu Gly Ser Ile Lys  
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Ile Pro Thr Ser Lys Asp Gly Arg Thr Leu Asn Val Lys Ser Ile Lys  
 565 570 575

Glu Ser Glu Val Lys  
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 gtc gtg tta gcc gct ctt tta ggt tta ggg ggg ctt ttt att ggt ttt 96  
 Val Val Leu Ala Ala Leu Leu Gly Leu Gly Gly Leu Phe Ile Gly Phe  
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 gta aag gtt atg caa aaa gat gtg tta gcg caa ctc atg gag cat tta 144  
 Val Lys Val Met Gln Lys Asp Val Leu Ala Gln Leu Met Glu His Leu  
 35 40 45  
 gaa acc ggg caa tac aaa aag cgt gaa aaa acg ctc gct tac atg aca 192  
 Glu Thr Gly Gln Tyr Lys Lys Arg Glu Lys Thr Leu Ala Tyr Met Thr  
 50 55 60  
 aaa att att gaa cag ggc att cat gag tat tac aaa aat ttt gac aat 240  
 Lys Ile Ile Glu Gln Gly Ile His Glu Tyr Tyr Lys Asn Phe Asp Asn  
 65 70 75 80  
 gct act gca aga aaa atg gcg tta gat tat ttc aaa cgc atc aac gac 288  
 Ala Thr Ala Arg Lys Met Ala Leu Asp Tyr Phe Lys Arg Ile Asn Asp  
 85 90 95  
 gat aag ggc atg att tat atg gtg gtg gtg gat aaa aac ggg gtg gta 336  
 Asp Lys Gly Met Ile Tyr Met Val Val Val Asp Lys Asn Gly Val Val  
 100 105 110  
 ttg ttt gat ccg gtc aat cct aaa acc gta ggc caa tca ggg ctt gac 384  
 Leu Phe Asp Pro Val Asn Pro Lys Thr Val Gly Gln Ser Gly Leu Asp



115					120					125						
gct	cag	agc	gtt	gat	ggg	gtg	tat	tat	gtt	agg	ggg	tat	ttg	gag	gcg	432
Ala	Gln	Ser	Val	Asp	Gly	Val	Tyr	Tyr	Val	Arg	Gly	Tyr	Leu	Glu	Ala	
	130					135					140					
gcc	aaa	aaa	ggg	gga	ggc	tac	act	tat	tat	aaa	atg	cct	aaa	tac	gat	480
Ala	Lys	Lys	Gly	Gly	Gly	Tyr	Thr	Tyr	Tyr	Lys	Met	Pro	Lys	Tyr	Asp	
	145				150					155					160	
gga	ggc	gta	ccg	gag	aaa	aaa	ttc	gcc	tac	tcg	cat	tat	gat	gaa	gtt	528
Gly	Gly	Val	Pro	Glu	Lys	Lys	Phe	Ala	Tyr	Ser	His	Tyr	Asp	Glu	Val	
				165					170					175		
tct	caa	atg	gtg	atc	gca	acg	act	tcc	tat	tac	act	gac	att	aac	aca	576
Ser	Gln	Met	Val	Ile	Ala	Thr	Thr	Ser	Tyr	Tyr	Thr	Asp	Ile	Asn	Thr	
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gaa	aat	aaa	gcg	atc	aaa	gaa	ggc	gtg	aat	aag	gtt	ttt	gat	gaa	aac	624
Glu	Asn	Lys	Ala	Ile	Lys	Glu	Gly	Val	Asn	Lys	Val	Phe	Asp	Glu	Asn	
		195					200					205				
acc	acg	aaa	tta	ttc	ctt	tgg	ata	ctg	aca	gcg	acg	ata	gcg	cta	gtg	672
Thr	Thr	Lys	Leu	Phe	Leu	Trp	Ile	Leu	Thr	Ala	Thr	Ile	Ala	Leu	Val	
	210					215					220					
gtt	ttg	acg	ctc	ata	tac	gct	aaa	tta	agg	atc	gtg	aaa	cgc	att	gat	720
Val	Leu	Thr	Leu	Ile	Tyr	Ala	Lys	Leu	Arg	Ile	Val	Lys	Arg	Ile	Asp	
	225				230					235					240	
gaa	ctg	gtc	ctt	aaa	atc	aac	gct	ttt	agc	cgt	ggg	gat	aag	gat	ttg	768
Glu	Leu	Val	Leu	Lys	Ile	Asn	Ala	Phe	Ser	Arg	Gly	Asp	Lys	Asp	Leu	
				245					250					255		
aga	gcc	aaa	att	gat	gtg	ggt	gat	cgc	aac	gat	gaa	atc	tcg	caa	gtg	816
Arg	Ala	Lys	Ile	Asp	Val	Gly	Asp	Arg	Asn	Asp	Glu	Ile	Ser	Gln	Val	
			260					265					270			
ggc	cgt	ggg	atc	aat	ttg	ttt	gtg	gaa	aac	gcc	cgc	ttg	att	atg	gaa	864
Gly	Arg	Gly	Ile	Asn	Leu	Phe	Val	Glu	Asn	Ala	Arg	Leu	Ile	Met	Glu	
		275					280					285				
gag	att	aaa	ggg	att	tcc	acc	ctc	aat	aaa	act	tca	atg	gat	aaa	tta	912
Glu	Ile	Lys	Gly	Ile	Ser	Thr	Leu	Asn	Lys	Thr	Ser	Met	Asp	Lys	Leu	
	290					295					300					
gtc	caa	atc	acg	caa	gaa	acc	caa	aag	agc	atg	aaa	gat	tcc	tca	acc	960
Val	Gln	Ile	Thr	Gln	Glu	Thr	Gln	Lys	Ser	Met	Lys	Asp	Ser	Ser	Thr	
	305				310					315					320	
acc	cta	aat	tcc	gtg	aaa	aat	aaa	gcc	act	gat	ata	gcg	agc	atg	atg	1008
Thr	Leu	Asn	Ser	Val	Lys	Asn	Lys	Ala	Thr	Asp	Ile	Ala	Ser	Met	Met	
				325					330					335		
aat	gct	tcc	ata	gag	caa	tct	caa	ggg	tta	agg	aag	cgt	ttg	att	gaa	1056

Asn	Ala	Ser	Ile	Glu	Gln	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Leu	Ile	Glu		
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acg	caa	ggg	ctg	gtc	aaa	gag	agc	aag	gat	gcg	atc	ggg	gat	tta	ttt	1104	
Thr	Gln	Gly	Leu	Val	Lys	Glu	Ser	Lys	Asp	Ala	Ile	Gly	Asp	Leu	Phe		
		355					360					365					
tct	caa	atc	aca	gag	agc	gcg	cac	act	gaa	gag	gaa	ctc	tct	agc	aaa	1152	
Ser	Gln	Ile	Thr	Glu	Ser	Ala	His	Thr	Glu	Glu	Glu	Leu	Ser	Ser	Lys		
	370					375					380						
gtg	gag	cag	cta	agc	cgt	aac	gct	gat	gat	gtc	aaa	tcc	att	ctg	gat	1200	
Val	Glu	Gln	Leu	Ser	Arg	Asn	Ala	Asp	Asp	Val	Lys	Ser	Ile	Leu	Asp		
385					390					395					400		
att	atc	aat	gat	att	gcc	gat	caa	acg	aat	tta	tta	gcc	cta	aac	gct	1248	
Ile	Ile	Asn	Asp	Ile	Ala	Asp	Gln	Thr	Asn	Leu	Leu	Ala	Leu	Asn	Ala		
				405					410					415			
gct	att	gaa	gcc	gca	agg	gct	ggc	gag	cat	ggc	aga	ggc	ttt	gcg	gtg	1296	
Ala	Ile	Glu	Ala	Ala	Arg	Ala	Gly	Glu	His	Gly	Arg	Gly	Phe	Ala	Val		
			420					425					430				
gtg	gct	gat	gaa	gtt	agg	aat	tta	gcc	ggg	cgc	act	caa	aag	tct	tta	1344	
Val	Ala	Asp	Glu	Val	Arg	Asn	Leu	Ala	Gly	Arg	Thr	Gln	Lys	Ser	Leu		
		435					440					445					
gcc	gaa	atc	aat	tcc	act	atc	atg	gtg	att	gtc	caa	gaa	atc	aat	gcc	1392	
Ala	Glu	Ile	Asn	Ser	Thr	Ile	Met	Val	Ile	Val	Gln	Glu	Ile	Asn	Ala		
	450					455					460						
gtg	agt	tcg	caa	atg	aat	ctc	aat	tcg	caa	aaa	atg	gag	cgt	ttg	agc	1440	
Val	Ser	Ser	Gln	Met	Asn	Leu	Asn	Ser	Gln	Lys	Met	Glu	Arg	Leu	Ser		
465					470					475				480			
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Asp	Met	Ser	Lys	Ser	Val	Gln	Glu	Thr	Tyr	Glu	Lys	Met	Ser	Ser	Asn		
				485				490						495			
tta	agc	tca	gtc	gtg	tca	gac	agc	aat	caa	agc	atg	gac	gat	tac	gcc	1536	
Leu	Ser	Ser	Val	Val	Ser	Asp	Ser	Asn	Gln	Ser	Met	Asp	Asp	Tyr	Ala		
			500					505					510				
aaa	tcc	gga	cac	caa	att	gaa	gtt	atg	gta	agc	gat	ttt	gca	gag	gtg	1584	
Lys	Ser	Gly	His	Gln	Ile	Glu	Val	Met	Val	Ser	Asp	Phe	Ala	Glu	Val		
		515					520					525					
gaa	aaa	gtg	gct	tct	aag	act	tta	gcg	gat	tct	tca	gat	att	tta	aac	1632	
Glu	Lys	Val	Ala	Ser	Lys	Thr	Leu	Ala	Asp	Ser	Ser	Asp	Ile	Leu	Asn		
	530					535					540						
atc	gct	acg	cat	gtg	agt	gga	acg	acc	atg	aat	tta	gac	aaa	caa	gtg	1680	
Ile	Ala	Thr	His	Val	Ser	Gly	Thr	Thr	Met	Asn	Leu	Asp	Lys	Gln	Val		
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 Asn Leu Phe Lys Thr  
 565

1698

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Val Lys Val Met Gln Lys Asp Val Leu Ala Gln Leu Met Glu His Leu  
 35 40 45

Glu Thr Gly Gln Tyr Lys Lys Arg Glu Lys Thr Leu Ala Tyr Met Thr  
 50 55 60

Lys Ile Ile Glu Gln Gly Ile His Glu Tyr Tyr Lys Asn Phe Asp Asn  
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Ala Thr Ala Arg Lys Met Ala Leu Asp Tyr Phe Lys Arg Ile Asn Asp  
 85 90 95

Asp Lys Gly Met Ile Tyr Met Val Val Val Asp Lys Asn Gly Val Val  
 100 105 110

Leu Phe Asp Pro Val Asn Pro Lys Thr Val Gly Gln Ser Gly Leu Asp  
 115 120 125

Ala Gln Ser Val Asp Gly Val Tyr Tyr Val Arg Gly Tyr Leu Glu Ala  
 130 135 140

Ala Lys Lys Gly Gly Gly Tyr Thr Tyr Tyr Lys Met Pro Lys Tyr Asp  
 145 150 155 160

Gly Gly Val Pro Glu Lys Lys Phe Ala Tyr Ser His Tyr Asp Glu Val  
 165 170 175

Ser Gln Met Val Ile Ala Thr Thr Ser Tyr Tyr Thr Asp Ile Asn Thr  
 180 185 190

Glu Asn Lys Ala Ile Lys Glu Gly Val Asn Lys Val Phe Asp Glu Asn  
 195 200 205

Thr Thr Lys Leu Phe Leu Trp Ile Leu Thr Ala Thr Ile Ala Leu Val  
 210 215 220

Val Leu Thr Leu Ile Tyr Ala Lys Leu Arg Ile Val Lys Arg Ile Asp  
 225 230 235 240

Glu Leu Val Leu Lys Ile Asn Ala Phe Ser Arg Gly Asp Lys Asp Leu  
 245 250 255

Arg Ala Lys Ile Asp Val Gly Asp Arg Asn Asp Glu Ile Ser Gln Val  
 260 265 270

Gly Arg Gly Ile Asn Leu Phe Val Glu Asn Ala Arg Leu Ile Met Glu  
 275 280 285

Glu Ile Lys Gly Ile Ser Thr Leu Asn Lys Thr Ser Met Asp Lys Leu  
 290 295 300

Val Gln Ile Thr Gln Glu Thr Gln Lys Ser Met Lys Asp Ser Ser Thr  
 305 310 315 320

Thr Leu Asn Ser Val Lys Asn Lys Ala Thr Asp Ile Ala Ser Met Met  
 325 330 335

Asn Ala Ser Ile Glu Gln Ser Gln Gly Leu Arg Lys Arg Leu Ile Glu  
 340 345 350

Thr Gln Gly Leu Val Lys Glu Ser Lys Asp Ala Ile Gly Asp Leu Phe  
 355 360 365

Ser Gln Ile Thr Glu Ser Ala His Thr Glu Glu Glu Leu Ser Ser Lys  
 370 375 380

Val Glu Gln Leu Ser Arg Asn Ala Asp Asp Val Lys Ser Ile Leu Asp

385		390		395		400
Ile Ile Asn Asp	Ile Ala Asp Gln Thr	Asn Leu Leu Ala Leu	Asn Ala			
	405	410	415			
Ala Ile Glu Ala	Ala Arg Ala Gly Glu	His Gly Arg Gly	Phe Ala Val			
	420	425	430			
Val Ala Asp Glu	Val Arg Asn Leu Ala Gly	Arg Thr Gln Lys Ser Leu				
	435	440	445			
Ala Glu Ile Asn Ser Thr	Ile Met Val Ile Val	Gln Glu Ile Asn Ala				
	450	455	460			
Val Ser Ser Gln Met	Asn Leu Asn Ser Gln	Lys Met Glu Arg Leu Ser				
465	470	475	480			
Asp Met Ser Lys Ser	Val Gln Glu Thr Tyr	Glu Lys Met Ser Ser Asn				
	485	490	495			
Leu Ser Ser Val Val	Ser Asp Ser Asn Gln Ser Met Asp	Asp Tyr Ala				
	500	505	510			
Lys Ser Gly His Gln Ile Glu	Val Met Val Ser Asp Phe Ala Glu Val					
	515	520	525			
Glu Lys Val Ala Ser Lys Thr	Leu Ala Asp Ser Ser Asp Ile Leu Asn					
	530	535	540			
Ile Ala Thr His Val Ser Gly Thr Thr	Met Asn Leu Asp Lys Gln Val					
545	550	555	560			
Asn Leu Phe Lys Thr						
	565					

<210> 69  
 <211> 855  
 <212> DNA  
 <213> Helicobacter pylori

<220>

<221> CDS  
 <222> (1)..(855)

<400> 69

ttg ggt atc aat atg tgt tct aaa aaa ata aga aat ctc att tta tgc	48
Leu Gly Ile Asn Met Cys Ser Lys Lys Ile Arg Asn Leu Ile Leu Cys	
1 5 10 15	
ttt ggt ttt atg ttg ggc ttg cac gct gaa gaa aat acg act gaa gga	96
Phe Gly Phe Met Leu Gly Leu His Ala Glu Glu Asn Thr Thr Glu Gly	
20 25 30	
aat atg act gaa gaa aat atc tct aaa gac gct ccc att ctt ttg gaa	144
Asn Met Thr Glu Glu Asn Ile Ser Lys Asp Ala Pro Ile Leu Leu Glu	
35 40 45	
gaa aaa cgc gcc caa acg cta gaa ttt aaa gaa gaa aag gaa gct aaa	192
Glu Lys Arg Ala Gln Thr Leu Glu Phe Lys Glu Glu Lys Glu Ala Lys	
50 55 60	
aag aat att gat gaa aaa agc ctg ctt gaa gaa atc cat aag aaa aaa	240
Lys Asn Ile Asp Glu Lys Ser Leu Leu Glu Glu Ile His Lys Lys Lys	
65 70 75 80	
cgc caa ctt tac atg ctc aaa ggg gaa ttg cat gaa aaa aat gaa tct	288
Arg Gln Leu Tyr Met Leu Lys Gly Glu Leu His Glu Lys Asn Glu Ser	
85 90 95	
ctc ttg ttc caa cga atg gct aaa aat aag agc ggt ttt ttt ata ggc	336
Leu Leu Phe Gln Arg Met Ala Lys Asn Lys Ser Gly Phe Phe Ile Gly	
100 105 110	
gta atc ctt ggc gat ata ggg gtt agc gct cat tct tat gag aag ttt	384
Val Ile Leu Gly Asp Ile Gly Val Ser Ala His Ser Tyr Glu Lys Phe	
115 120 125	
gaa ctt tta agc aat att caa gct tct cct ttg ttg tat ggc tta agg	432
Glu Leu Leu Ser Asn Ile Gln Ala Ser Pro Leu Leu Tyr Gly Leu Arg	
130 135 140	
agc ggg tat caa aag tat ttt gct aac ggg att agc gcc tta cgc ttt	480
Ser Gly Tyr Gln Lys Tyr Phe Ala Asn Gly Ile Ser Ala Leu Arg Phe	
145 150 155 160	
tat ggg gag tat tta ggg ggg gcg atg aaa gga ttt aaa agc gat tct	528
Tyr Gly Glu Tyr Leu Gly Gly Ala Met Lys Gly Phe Lys Ser Asp Ser	
165 170 175	
tta gcc tct tat caa acc gca agc ttg aac att gat ttg ttg atg gat	576
Leu Ala Ser Tyr Gln Thr Ala Ser Leu Asn Ile Asp Leu Leu Met Asp	
180 185 190	
aag cct att gac aaa gaa aaa agg ttt gcg tta ggg ata ttt gga ggc	624
Lys Pro Ile Asp Lys Glu Lys Arg Phe Ala Leu Gly Ile Phe Gly Gly	
195 200 205	

gtt gga gtg ggg tgg aat ggg atg tat caa aat tta aaa gag gtt aaa	672
Val Gly Val Gly Trp Asn Gly Met Tyr Gln Asn Leu Lys Glu Val Lys	
210 215 220	
ggg tat tca cag cct aac gct ttt gga tta gtg cta aat tta ggg gtg	720
Gly Tyr Ser Gln Pro Asn Ala Phe Gly Leu Val Leu Asn Leu Gly Val	
225 230 235 240	
agc atg acg ctt aac ctc aaa cac cgc ttt gaa tta gcc tta aaa atg	768
Ser Met Thr Leu Asn Leu Lys His Arg Phe Glu Leu Ala Leu Lys Met	
245 250 255	
cct ccc tta aaa gaa act tcg caa acc ttt tta tat tat ttt aaa agc	816
Pro Pro Leu Lys Glu Thr Ser Gln Thr Phe Leu Tyr Tyr Phe Lys Ser	
260 265 270	
act aat att tat tat att agt tac aac tat tta ttg taa	855
Thr Asn Ile Tyr Tyr Ile Ser Tyr Asn Tyr Leu Leu	
275 280	

<210> 70  
 <211> 284  
 <212> PRT  
 <213> *Helicobacter pylori*

<400> 70

Leu Gly Ile Asn Met Cys Ser Lys Lys Ile Arg Asn Leu Ile Leu Cys	
1 5 10 15	
Phe Gly Phe Met Leu Gly Leu His Ala Glu Glu Asn Thr Thr Glu Gly	
20 25 30	
Asn Met Thr Glu Glu Asn Ile Ser Lys Asp Ala Pro Ile Leu Leu Glu	
35 40 45	
Glu Lys Arg Ala Gln Thr Leu Glu Phe Lys Glu Glu Lys Glu Ala Lys	
50 55 60	
Lys Asn Ile Asp Glu Lys Ser Leu Leu Glu Glu Ile His Lys Lys Lys	
65 70 75 80	
Arg Gln Leu Tyr Met Leu Lys Gly Glu Leu His Glu Lys Asn Glu Ser	
85 90 95	
Leu Leu Phe Gln Arg Met Ala Lys Asn Lys Ser Gly Phe Phe Ile Gly	
100 105 110	

Val Ile Leu Gly Asp Ile Gly Val Ser Ala His Ser Tyr Glu Lys Phe  
115 120 125

Glu Leu Leu Ser Asn Ile Gln Ala Ser Pro Leu Leu Tyr Gly Leu Arg  
130 135 140

Ser Gly Tyr Gln Lys Tyr Phe Ala Asn Gly Ile Ser Ala Leu Arg Phe  
145 150 155 160

Tyr Gly Glu Tyr Leu Gly Gly Ala Met Lys Gly Phe Lys Ser Asp Ser  
165 170 175

Leu Ala Ser Tyr Gln Thr Ala Ser Leu Asn Ile Asp Leu Leu Met Asp  
180 185 190

Lys Pro Ile Asp Lys Glu Lys Arg Phe Ala Leu Gly Ile Phe Gly Gly  
195 200 205

Val Gly Val Gly Trp Asn Gly Met Tyr Gln Asn Leu Lys Glu Val Lys  
210 215 220

Gly Tyr Ser Gln Pro Asn Ala Phe Gly Leu Val Leu Asn Leu Gly Val  
225 230 235 240

Ser Met Thr Leu Asn Leu Lys His Arg Phe Glu Leu Ala Leu Lys Met  
245 250 255

Pro Pro Leu Lys Glu Thr Ser Gln Thr Phe Leu Tyr Tyr Phe Lys Ser  
260 265 270

Thr Asn Ile Tyr Tyr Ile Ser Tyr Asn Tyr Leu Leu  
275 280

<210> 71  
<211> 669  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(669)



<400> 71																	
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Met	Ala	Glu	Asn	Ser	Phe	Lys	Asn	Val	Ser	Thr	Gln	Pro	Lys	Val	Phe		
1				5				10						15			
ttc	tta	ttg	cca	gct	aaa	acc	ctg	ttt	ctt	tta	gga	ggc	ggt	ttt	agc		96
Phe	Leu	Leu	Pro	Ala	Lys	Thr	Leu	Phe	Leu	Leu	Gly	Gly	Val	Phe	Ser		
			20				25						30				
gcg	ttt	ttt	atc	ctt	att	gct	ggc	ttg	ggt	ttt	ttt	gat	tat	gct	cat		144
Ala	Phe	Phe	Ile	Leu	Ile	Ala	Gly	Leu	Val	Phe	Phe	Asp	Tyr	Ala	His		
		35					40					45					
ttg	atg	gac	aat	gcc	att	ttt	aat	ttt	gcg	cgt	tca	acc	ccc	ttt	aat		192
Leu	Met	Asp	Asn	Ala	Ile	Phe	Asn	Phe	Ala	Arg	Ser	Thr	Pro	Phe	Asn		
	50					55					60						
tcc	agc	cct	att	tta	act	cta	atc	ctc	caa	aat	atc	gct	aat	tta	ggc		240
Ser	Ser	Pro	Ile	Leu	Thr	Leu	Ile	Leu	Gln	Asn	Ile	Ala	Asn	Leu	Gly		
65					70					75					80		
tct	tct	caa	ttc	gtg	ttg	cct	ttg	agt	ttg	ttg	gtg	ggg	gtg	ttt	tta		288
Ser	Ser	Gln	Phe	Val	Leu	Pro	Leu	Ser	Leu	Leu	Val	Gly	Val	Phe	Leu		
			85						90					95			
agc	ctt	tat	cgc	aga	aac	tta	gtg	ctt	ggg	gtg	tgg	ttt	gtg	tta	agc		336
Ser	Leu	Tyr	Arg	Arg	Asn	Leu	Val	Leu	Gly	Val	Trp	Phe	Val	Leu	Ser		
			100					105					110				
gtg	atc	ttg	ttt	gaa	gcc	ctt	tta	gaa	tct	tta	aaa	cac	ctt	ttt	gca		384
Val	Ile	Leu	Phe	Glu	Ala	Leu	Leu	Glu	Ser	Leu	Lys	His	Leu	Phe	Ala		
		115					120					125					
tat	tcc	att	cag	tgg	ctt	tcg	cgc	agc	gct	aat	ttc	cct	aac	gct	act		432
Tyr	Ser	Ile	Gln	Trp	Leu	Ser	Arg	Ser	Ala	Asn	Phe	Pro	Asn	Ala	Thr		
	130					135					140						
gcg	ctt	tct	tta	gtg	cta	ttt	tat	ggg	ttg	ctt	att	tta	ttg	ata	ccc		480
Ala	Leu	Ser	Leu	Val	Leu	Phe	Tyr	Gly	Leu	Leu	Ile	Leu	Leu	Ile	Pro		
145					150					155					160		
cat	tta	atc	acg	cat	caa	acg	ctt	aaa	aat	ggt	ctt	ttt	tat	agc	tta		528
His	Leu	Ile	Thr	His	Gln	Thr	Leu	Lys	Asn	Val	Leu	Phe	Tyr	Ser	Leu		
				165					170					175			
ttt	ggt	ttg	att	ttt	tta	ata	ggg	tta	gca	ctg	att	ggt	tta	ggg	ggt		576
Phe	Gly	Leu	Ile	Phe	Leu	Ile	Gly	Leu	Ala	Leu	Ile	Val	Leu	Gly	Val		
			180					185					190				
tct	ttc	agt	agt	ggt	tta	gga	ggg	ttt	tgt	tta	ggg	gcg	tta	ggg	gct		624
Ser	Phe	Ser	Ser	Val	Leu	Gly	Gly	Phe	Cys	Leu	Gly	Ala	Leu	Gly	Ala		
		195					200					205					

tgt ttt tcc ata ggg att tat ttg agc gtg ttt caa aag atc taa  
 Cys Phe Ser Ile Gly Ile Tyr Leu Ser Val Phe Gln Lys Ile  
       210                              215                              220

669

<210> 72  
 <211> 222  
 <212> PRT  
 <213> Helicobacter pylori

<400> 72

Met Ala Glu Asn Ser Phe Lys Asn Val Ser Thr Gln Pro Lys Val Phe  
 1                              5                              10                              15

Phe Leu Leu Pro Ala Lys Thr Leu Phe Leu Leu Gly Gly Val Phe Ser  
                               20                              25                              30

Ala Phe Phe Ile Leu Ile Ala Gly Leu Val Phe Phe Asp Tyr Ala His  
                               35                              40                              45

Leu Met Asp Asn Ala Ile Phe Asn Phe Ala Arg Ser Thr Pro Phe Asn  
       50                              55                              60

Ser Ser Pro Ile Leu Thr Leu Ile Leu Gln Asn Ile Ala Asn Leu Gly  
 65                              70                              75                              80

Ser Ser Gln Phe Val Leu Pro Leu Ser Leu Leu Val Gly Val Phe Leu  
                               85                              90                              95

Ser Leu Tyr Arg Arg Asn Leu Val Leu Gly Val Trp Phe Val Leu Ser  
                               100                              105                              110

Val Ile Leu Phe Glu Ala Leu Leu Glu Ser Leu Lys His Leu Phe Ala  
                               115                              120                              125

Tyr Ser Ile Gln Trp Leu Ser Arg Ser Ala Asn Phe Pro Asn Ala Thr  
       130                              135                              140

Ala Leu Ser Leu Val Leu Phe Tyr Gly Leu Leu Ile Leu Leu Ile Pro  
 145                              150                              155                              160

His Leu Ile Thr His Gln Thr Leu Lys Asn Val Leu Phe Tyr Ser Leu  
                               165                              170                              175

Phe Gly Leu Ile Phe Leu Ile Gly Leu Ala Leu Ile Val Leu Gly Val  
180 185 190

Ser Phe Ser Ser Val Leu Gly Gly Phe Cys Leu Gly Ala Leu Gly Ala  
195 200 205

Cys Phe Ser Ile Gly Ile Tyr Leu Ser Val Phe Gln Lys Ile  
210 215 220

<210> 73  
<211> 804  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(804)

<400> 73  
atg tca gaa aaa gaa aga ctg aat gaa gtg atc tta gaa gaa gaa aat 48  
Met Ser Glu Lys Glu Arg Leu Asn Glu Val Ile Leu Glu Glu Glu Asn  
1 5 10 15  
aat ggg agc ggc act aaa aag gtg ttt ttg atc gtg gct ata gcc att 96  
Asn Gly Ser Gly Thr Lys Lys Val Phe Leu Ile Val Ala Ile Ala Ile  
20 25 30  
atc att tta gcg gtg ctt tta atg gtg ttt tgg aaa agc acg aga gtc 144  
Ile Ile Leu Ala Val Leu Leu Met Val Phe Trp Lys Ser Thr Arg Val  
35 40 45  
gct cct aaa gag act ttt tta caa acc gat agc ggc atg caa aaa ata 192  
Ala Pro Lys Glu Thr Phe Leu Gln Thr Asp Ser Gly Met Gln Lys Ile  
50 55 60  
ggc aac act aaa gac gag aaa aaa gac gat gag ttt gaa agc ttg aat 240  
Gly Asn Thr Lys Asp Glu Lys Lys Asp Asp Glu Phe Glu Ser Leu Asn  
65 70 75 80  
ttg gat cct tcc aag caa gaa gac aag cta gac aaa gtg gcg gat aat 288  
Leu Asp Pro Ser Lys Gln Glu Asp Lys Leu Asp Lys Val Ala Asp Asn  
85 90 95  
gtt aag aag caa gaa aat gat gcg ttt aac atg ccc act caa acc gat 336  
Val Lys Lys Gln Glu Asn Asp Ala Phe Asn Met Pro Thr Gln Thr Asp  
100 105 110  
caa act caa acg gag atg aaa aca aca gaa gaa acg caa gaa gct caa 384  
Gln Thr Gln Thr Glu Met Lys Thr Thr Glu Glu Thr Gln Glu Ala Gln

115						120						125						
aaa	gga	tta	aaa	gtt	gtt	gag	cac	act	agc	act	caa	aaa	gaa	tct	caa	432		
Lys	Gly	Leu	Lys	Val	Val	Glu	His	Thr	Ser	Thr	Gln	Lys	Glu	Ser	Gln			
	130						135				140							
gct	gtg	gct	aaa	aaa	gaa	atc	tcc	cat	aaa	aag	cct	aaa	gca	acc	cct	480		
Ala	Val	Ala	Lys	Lys	Glu	Ile	Ser	His	Lys	Lys	Pro	Lys	Ala	Thr	Pro			
	145					150					155				160			
aaa	gat	aag	gaa	gcc	cat	aaa	gat	aaa	gat	aag	cat	gcg	gtt	aaa	gag	528		
Lys	Asp	Lys	Glu	Ala	His	Lys	Asp	Lys	Asp	Lys	His	Ala	Val	Lys	Glu			
				165					170					175				
cta	aaa	gtc	aaa	aaa	gaa	gct	cat	aaa	gaa	gtt	cct	aaa	aaa	gcc	aat	576		
Leu	Lys	Val	Lys	Lys	Glu	Ala	His	Lys	Glu	Val	Pro	Lys	Lys	Ala	Asn			
			180					185						190				
tct	aaa	acc	act	ctt	act	aaa	ggg	cat	tat	ttg	caa	gtg	ggg	gtt	ttt	624		
Ser	Lys	Thr	Thr	Leu	Thr	Lys	Gly	His	Tyr	Leu	Gln	Val	Gly	Val	Phe			
		195					200					205						
gcg	cac	acg	ccc	aat	aaa	gcc	ttt	ttg	caa	gcg	ttt	aac	caa	ttc	ccc	672		
Ala	His	Thr	Pro	Asn	Lys	Ala	Phe	Leu	Gln	Ala	Phe	Asn	Gln	Phe	Pro			
	210					215					220							
cat	aag	att	gaa	gat	agg	ggg	tct	act	aaa	cgc	tat	ctc	ata	ggc	cct	720		
His	Lys	Ile	Glu	Asp	Arg	Gly	Ser	Thr	Lys	Arg	Tyr	Leu	Ile	Gly	Pro			
	225				230					235					240			
tat	aag	aat	aag	caa	gaa	gcc	tta	atg	cat	gct	gat	gaa	gtc	agc	aaa	768		
Tyr	Lys	Asn	Lys	Gln	Glu	Ala	Leu	Met	His	Ala	Asp	Glu	Val	Ser	Lys			
				245					250					255				
aag	atg	act	aaa	ccg	gtt	gtc	ata	gaa	gcg	cgg	tag					804		
Lys	Met	Thr	Lys	Pro	Val	Val	Ile	Glu	Ala	Arg								
			260					265										

<210> 74  
 <211> 267  
 <212> PRT  
 <213> Helicobacter pylori

<400> 74

Met	Ser	Glu	Lys	Glu	Arg	Leu	Asn	Glu	Val	Ile	Leu	Glu	Glu	Glu	Asn
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Asn	Gly	Ser	Gly	Thr	Lys	Lys	Val	Phe	Leu	Ile	Val	Ala	Ile	Ala	Ile
				20				25				30			

Ile	Ile	Leu	Ala	Val	Leu	Leu	Met	Val	Phe	Trp	Lys	Ser	Thr	Arg	Val	
		35					40					45				
Ala	Pro	Lys	Glu	Thr	Phe	Leu	Gln	Thr	Asp	Ser	Gly	Met	Gln	Lys	Ile	
	50					55					60					
Gly	Asn	Thr	Lys	Asp	Glu	Lys	Lys	Asp	Asp	Glu	Phe	Glu	Ser	Leu	Asn	
65					70					75					80	
Leu	Asp	Pro	Ser	Lys	Gln	Glu	Asp	Lys	Leu	Asp	Lys	Val	Ala	Asp	Asn	
				85					90					95		
Val	Lys	Lys	Gln	Glu	Asn	Asp	Ala	Phe	Asn	Met	Pro	Thr	Gln	Thr	Asp	
			100					105					110			
Gln	Thr	Gln	Thr	Glu	Met	Lys	Thr	Thr	Glu	Glu	Thr	Gln	Glu	Ala	Gln	
		115					120					125				
Lys	Gly	Leu	Lys	Val	Val	Glu	His	Thr	Ser	Thr	Gln	Lys	Glu	Ser	Gln	
	130					135					140					
Ala	Val	Ala	Lys	Lys	Glu	Ile	Ser	His	Lys	Lys	Pro	Lys	Ala	Thr	Pro	
145					150					155					160	
Lys	Asp	Lys	Glu	Ala	His	Lys	Asp	Lys	Asp	Lys	His	Ala	Val	Lys	Glu	
				165					170					175		
Leu	Lys	Val	Lys	Lys	Glu	Ala	His	Lys	Glu	Val	Pro	Lys	Lys	Ala	Asn	
			180					185					190			
Ser	Lys	Thr	Thr	Leu	Thr	Lys	Gly	His	Tyr	Leu	Gln	Val	Gly	Val	Phe	
		195					200					205				
Ala	His	Thr	Pro	Asn	Lys	Ala	Phe	Leu	Gln	Ala	Phe	Asn	Gln	Phe	Pro	
	210					215					220					
His	Lys	Ile	Glu	Asp	Arg	Gly	Ser	Thr	Lys	Arg	Tyr	Leu	Ile	Gly	Pro	
225					230					235					240	
Tyr	Lys	Asn	Lys	Gln	Glu	Ala	Leu	Met	His	Ala	Asp	Glu	Val	Ser	Lys	
				245					250					255		

Lys Met Thr Lys Pro Val Val Ile Glu Ala Arg  
 260 265

<210> 75  
 <211> 1545  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1545)

<400> 75  
 gtg agg caa gaa aag tat ttt ctg act tct tct tta tcg ctt tta tcg 48  
 Val Arg Gln Glu Lys Tyr Phe Leu Thr Ser Ser Leu Ser Leu Ser  
 1 5 10 15  
 ttt tta tta tgt cct gca gaa gct ttt gat tat cgc ttt agc ggt cgt 96  
 Phe Leu Leu Cys Pro Ala Glu Ala Phe Asp Tyr Arg Phe Ser Gly Arg  
 20 25 30  
 gtg gag aac ttt tct aag att ggt ttt aac aat tct caa atc aat act 144  
 Val Glu Asn Phe Ser Lys Ile Gly Phe Asn Asn Ser Gln Ile Asn Thr  
 35 40 45  
 aaa aaa ggg att tat cct act gaa agt ttt ata gat att gta act tta 192  
 Lys Lys Gly Ile Tyr Pro Thr Glu Ser Phe Ile Asp Ile Val Thr Leu  
 50 55 60  
 gcg caa gtc aaa gtc aat tta ctc cct aaa ggc acc gaa aac cat agg 240  
 Ala Gln Val Lys Val Asn Leu Leu Pro Lys Gly Thr Glu Asn His Arg  
 65 70 75 80  
 ctc tct gtc tct ttg ggt ggg gcg att gca gcc att cct tat gat aag 288  
 Leu Ser Val Ser Leu Gly Gly Ala Ile Ala Ala Ile Pro Tyr Asp Lys  
 85 90 95  
 act aaa tat gat att aac caa gct aac ggg aag att ttt ggc tca att 336  
 Thr Lys Tyr Asp Ile Asn Gln Ala Asn Gly Lys Ile Phe Gly Ser Ile  
 100 105 110  
 gta gag aat ttc att ggg ggc tat cat gga tac ttt ttt aat aag tat 384  
 Val Glu Asn Phe Ile Gly Gly Tyr His Gly Tyr Phe Phe Asn Lys Tyr  
 115 120 125  
 ctt ggc cct gct tat gcg ggg act tct caa tca gcg agc tat cat gca 432  
 Leu Gly Pro Ala Tyr Ala Gly Thr Ser Gln Ser Ala Ser Tyr His Ala  
 130 135 140  
 agg cct tat gtg gtg gat acc gct ttt tta cga tac gat tac aaa gat 480  
 Arg Pro Tyr Val Val Asp Thr Ala Phe Leu Arg Tyr Asp Tyr Lys Asp  
 145 150 155 160

gtt ttt ggg ttt aag gcg ggg cgc tat gaa gcg aat att gat ttc atg	528
Val Phe Gly Phe Lys Ala Gly Arg Tyr Glu Ala Asn Ile Asp Phe Met	
165 170 175	
agc gga tcg aat caa ggg tgg gaa gtg tat tat cag ccc tat aag act	576
Ser Gly Ser Asn Gln Gly Trp Glu Val Tyr Tyr Gln Pro Tyr Lys Thr	
180 185 190	
gaa acg caa agg tta agg ttt tgg tgg tgg agt tct ttt ggg aga ggt	624
Glu Thr Gln Arg Leu Arg Phe Trp Trp Trp Ser Ser Phe Gly Arg Gly	
195 200 205	
tta gcg ttc aac tct tgg att tat gag ttt ttt gcg acg gtg cct tat	672
Leu Ala Phe Asn Ser Trp Ile Tyr Glu Phe Phe Ala Thr Val Pro Tyr	
210 215 220	
ttg aaa aag gga ggc aat cct aat aac agc aac gat ttc atc aat tat	720
Leu Lys Lys Gly Gly Asn Pro Asn Asn Ser Asn Asp Phe Ile Asn Tyr	
225 230 235 240	
ggc tgg cat gga atc acc aca acc tat tct tat aaa ggt tta gac gct	768
Gly Trp His Gly Ile Thr Thr Thr Tyr Ser Tyr Lys Gly Leu Asp Ala	
245 250 255	
caa ttt ttt tat tat ttt gcg cct aag act tat aac gct cct ggc ttt	816
Gln Phe Phe Tyr Tyr Phe Ala Pro Lys Thr Tyr Asn Ala Pro Gly Phe	
260 265 270	
aag ctg gtc tat gac acg aat agg aat ttt caa aat gta ggc ttt cgc	864
Lys Leu Val Tyr Asp Thr Asn Arg Asn Phe Gln Asn Val Gly Phe Arg	
275 280 285	
tct caa agc atg atc atg aca acc ttt cct tta tac tat aga ggg tgg	912
Ser Gln Ser Met Ile Met Thr Thr Phe Pro Leu Tyr Tyr Arg Gly Trp	
290 295 300	
tat aac cca gag aca aac act tat agt tta gaa gac agc acg cct cat	960
Tyr Asn Pro Glu Thr Asn Thr Tyr Ser Leu Glu Asp Ser Thr Pro His	
305 310 315 320	
ggc tcg ttg ttg ggg agg aat ggc gtt act tta aat atc cgc cag gtt	1008
Gly Ser Leu Leu Gly Arg Asn Gly Val Thr Leu Asn Ile Arg Gln Val	
325 330 335	
ttt tgg tgg gat aat ttc aac tgg tcc att ggc ttt tat aac acc ttt	1056
Phe Trp Trp Asp Asn Phe Asn Trp Ser Ile Gly Phe Tyr Asn Thr Phe	
340 345 350	
ggc aat tcg gac gct ttt tta ggc tct cac acg atg cca agg ggt aat	1104
Gly Asn Ser Asp Ala Phe Leu Gly Ser His Thr Met Pro Arg Gly Asn	
355 360 365	
aac act tcc tat atc ggt agt gaa atc tcc ata acg act agg cat gcc	1152
Asn Thr Ser Tyr Ile Gly Ser Glu Ile Ser Ile Thr Thr Arg His Ala	

370	375	380	
gga atg att ggc tat gat ttt tgg gat aat acg gct tat gat ggg cta			1200
Gly Met Ile Gly Tyr Asp Phe Trp Asp Asn Thr Ala Tyr Asp Gly Leu			
385	390	395	400
gct gat gcg atc act aac gct aac act ttc act ttt tac act tct gtt			1248
Ala Asp Ala Ile Thr Asn Ala Asn Thr Phe Thr Phe Tyr Thr Ser Val			
	405	410	415
gga ggg atc cat aag cgt ttt gca tgg cat gtt ttt ggg cgc gtc tct			1296
Gly Gly Ile His Lys Arg Phe Ala Trp His Val Phe Gly Arg Val Ser			
	420	425	430
cat gcg aat aaa aac gcg tta ggg caa gtg ggg agg gct aat gaa tat			1344
His Ala Asn Lys Asn Ala Leu Gly Gln Val Gly Arg Ala Asn Glu Tyr			
	435	440	445
tcc ttg caa ttc aac gcg agc tat gcg ttc act gaa tca atc ctt ctt			1392
Ser Leu Gln Phe Asn Ala Ser Tyr Ala Phe Thr Glu Ser Ile Leu Leu			
	450	455	460
aac ttt agg atc act tat tat ggg gct agg atc aat aaa ggg tat caa			1440
Asn Phe Arg Ile Thr Tyr Tyr Gly Ala Arg Ile Asn Lys Gly Tyr Gln			
465	470	475	480
gcg ggg tat ttt gga gcg ccc aaa ttc aat aac cct gat ggc gat ttt			1488
Ala Gly Tyr Phe Gly Ala Pro Lys Phe Asn Asn Pro Asp Gly Asp Phe			
	485	490	495
agc gct aat tac caa gac aga agt tac atg atg acc aac ctc acg ctg			1536
Ser Ala Asn Tyr Gln Asp Arg Ser Tyr Met Met Thr Asn Leu Thr Leu			
	500	505	510
aag ttt tga			1545
Lys Phe			

<210> 76  
 <211> 514  
 <212> PRT  
 <213> Helicobacter pylori

<400> 76

Val Arg Gln Glu Lys Tyr Phe Leu Thr Ser Ser Leu Ser Leu Leu Ser
1 5 10 15
Phe Leu Leu Cys Pro Ala Glu Ala Phe Asp Tyr Arg Phe Ser Gly Arg
20 25 30



Val	Glu	Asn	Phe	Ser	Lys	Ile	Gly	Phe	Asn	Asn	Ser	Gln	Ile	Asn	Thr	
		35					40					45				
Lys	Lys	Gly	Ile	Tyr	Pro	Thr	Glu	Ser	Phe	Ile	Asp	Ile	Val	Thr	Leu	
	50					55					60					
Ala	Gln	Val	Lys	Val	Asn	Leu	Leu	Pro	Lys	Gly	Thr	Glu	Asn	His	Arg	
65					70					75					80	
Leu	Ser	Val	Ser	Leu	Gly	Gly	Ala	Ile	Ala	Ala	Ile	Pro	Tyr	Asp	Lys	
				85					90					95		
Thr	Lys	Tyr	Asp	Ile	Asn	Gln	Ala	Asn	Gly	Lys	Ile	Phe	Gly	Ser	Ile	
			100					105					110			
Val	Glu	Asn	Phe	Ile	Gly	Gly	Tyr	His	Gly	Tyr	Phe	Phe	Asn	Lys	Tyr	
		115					120					125				
Leu	Gly	Pro	Ala	Tyr	Ala	Gly	Thr	Ser	Gln	Ser	Ala	Ser	Tyr	His	Ala	
	130					135					140					
Arg	Pro	Tyr	Val	Val	Asp	Thr	Ala	Phe	Leu	Arg	Tyr	Asp	Tyr	Lys	Asp	
145					150					155					160	
Val	Phe	Gly	Phe	Lys	Ala	Gly	Arg	Tyr	Glu	Ala	Asn	Ile	Asp	Phe	Met	
				165					170					175		
Ser	Gly	Ser	Asn	Gln	Gly	Trp	Glu	Val	Tyr	Tyr	Gln	Pro	Tyr	Lys	Thr	
			180					185					190			
Glu	Thr	Gln	Arg	Leu	Arg	Phe	Trp	Trp	Trp	Ser	Ser	Phe	Gly	Arg	Gly	
		195					200					205				
Leu	Ala	Phe	Asn	Ser	Trp	Ile	Tyr	Glu	Phe	Phe	Ala	Thr	Val	Pro	Tyr	
	210					215					220					
Leu	Lys	Lys	Gly	Gly	Asn	Pro	Asn	Asn	Ser	Asn	Asp	Phe	Ile	Asn	Tyr	
225					230					235					240	
Gly	Trp	His	Gly	Ile	Thr	Thr	Thr	Tyr	Ser	Tyr	Lys	Gly	Leu	Asp	Ala	
				245					250					255		

Gln Phe Phe Tyr Tyr Phe Ala Pro Lys Thr Tyr Asn Ala Pro Gly Phe  
 260 265 270

Lys Leu Val Tyr Asp Thr Asn Arg Asn Phe Gln Asn Val Gly Phe Arg  
 275 280 285

Ser Gln Ser Met Ile Met Thr Thr Phe Pro Leu Tyr Tyr Arg Gly Trp  
 290 295 300

Tyr Asn Pro Glu Thr Asn Thr Tyr Ser Leu Glu Asp Ser Thr Pro His  
 305 310 315 320

Gly Ser Leu Leu Gly Arg Asn Gly Val Thr Leu Asn Ile Arg Gln Val  
 325 330 335

Phe Trp Trp Asp Asn Phe Asn Trp Ser Ile Gly Phe Tyr Asn Thr Phe  
 340 345 350

Gly Asn Ser Asp Ala Phe Leu Gly Ser His Thr Met Pro Arg Gly Asn  
 355 360 365

Asn Thr Ser Tyr Ile Gly Ser Glu Ile Ser Ile Thr Thr Arg His Ala  
 370 375 380

Gly Met Ile Gly Tyr Asp Phe Trp Asp Asn Thr Ala Tyr Asp Gly Leu  
 385 390 395 400

Ala Asp Ala Ile Thr Asn Ala Asn Thr Phe Thr Phe Tyr Thr Ser Val  
 405 410 415

Gly Gly Ile His Lys Arg Phe Ala Trp His Val Phe Gly Arg Val Ser  
 420 425 430

His Ala Asn Lys Asn Ala Leu Gly Gln Val Gly Arg Ala Asn Glu Tyr  
 435 440 445

Ser Leu Gln Phe Asn Ala Ser Tyr Ala Phe Thr Glu Ser Ile Leu Leu  
 450 455 460

Asn Phe Arg Ile Thr Tyr Tyr Gly Ala Arg Ile Asn Lys Gly Tyr Gln  
 465 470 475 480

Ala Gly Tyr Phe Gly Ala Pro Lys Phe Asn Asn Pro Asp Gly Asp Phe  
485 490 495

Ser Ala Asn Tyr Gln Asp Arg Ser Tyr Met Met Thr Asn Leu Thr Leu  
500 505 510

Lys Phe

<210> 77  
<211> 912  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(912)

<400> 77  
atg aaa aag att att ctt gca tgc ctt atg gct ttt gtg ggt gcc aat 48  
Met Lys Lys Ile Ile Leu Ala Cys Leu Met Ala Phe Val Gly Ala Asn  
1 5 10 15  
tta agc gca gag cct aag tgg tat agc aag gcc tac aac aaa aca aac 96  
Leu Ser Ala Glu Pro Lys Trp Tyr Ser Lys Ala Tyr Asn Lys Thr Asn  
20 25 30  
acc caa aaa ggc tat ctt tat ggg agt ggt tca gcc act tct aaa gag 144  
Thr Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr Ser Lys Glu  
35 40 45  
gct tct aaa caa aaa gcg tta gcg gat tta gtg gcg tct att agc gtg 192  
Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser Ile Ser Val  
50 55 60  
gtg gtt aat tcc caa atc cat att caa aaa agt cgt gtg gac aat aag 240  
Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val Asp Asn Lys  
65 70 75 80  
tta aaa tcc agc gat tcg caa acg att aac tta aag acc gat gac ttg 288  
Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr Asp Asp Leu  
85 90 95  
gaa ttg aat aat gta gaa att gtc aat caa gaa gtg caa aaa ggg atc 336  
Glu Leu Asn Asn Val Glu Ile Val Asn Gln Glu Val Gln Lys Gly Ile  
100 105 110  
tac tac acc aga gta agg atc aat caa aac ttg ttt ttg cag ggt tta 384  
Tyr Tyr Thr Arg Val Arg Ile Asn Gln Asn Leu Phe Leu Gln Gly Leu

115					120					125						
agg	gat	aag	tat	aac	gct	ctt	tat	ggg	cag	ttt	tcc	acc	tta	atg	cct	432
Arg	Asp	Lys	Tyr	Asn	Ala	Leu	Tyr	Gly	Gln	Phe	Ser	Thr	Leu	Met	Pro	
	130					135					140					
aag	gtt	tgt	aaa	ggg	gtt	ttt	tta	cag	caa	tcc	aag	agc	atg	ggg	gat	480
Lys	Val	Cys	Lys	Gly	Val	Phe	Leu	Gln	Gln	Ser	Lys	Ser	Met	Gly	Asp	
	145				150					155					160	
tta	ttg	gct	aaa	gcg	atg	cct	ata	gaa	agg	att	tta	aaa	gcg	tat	tct	528
Leu	Leu	Ala	Lys	Ala	Met	Pro	Ile	Glu	Arg	Ile	Leu	Lys	Ala	Tyr	Ser	
				165					170					175		
gtt	ccg	gtg	ggg	tcg	tta	gaa	aat	tat	gaa	aaa	atc	tat	tat	caa	aac	576
Val	Pro	Val	Gly	Ser	Leu	Glu	Asn	Tyr	Glu	Lys	Ile	Tyr	Tyr	Gln	Asn	
			180					185					190			
gct	ttc	aaa	cct	aaa	gtg	caa	atc	act	ttt	gat	aac	aac	ggc	gat	gcg	624
Ala	Phe	Lys	Pro	Lys	Val	Gln	Ile	Thr	Phe	Asp	Asn	Asn	Gly	Asp	Ala	
		195					200					205				
gaa	atc	aaa	agc	gct	ctc	ata	agc	gct	tat	gcc	aga	gtg	cta	acc	cct	672
Glu	Ile	Lys	Ser	Ala	Leu	Ile	Ser	Ala	Tyr	Ala	Arg	Val	Leu	Thr	Pro	
	210					215					220					
agt	gat	gaa	gaa	aaa	ctc	tat	caa	atc	aaa	aat	gaa	gtt	ttc	aca	gac	720
Ser	Asp	Glu	Glu	Lys	Leu	Tyr	Gln	Ile	Lys	Asn	Glu	Val	Phe	Thr	Asp	
	225				230					235					240	
agt	gct	aat	ggc	atc	acg	cgc	att	aga	gtg	gtt	gtt	agc	gcg	agc	gat	768
Ser	Ala	Asn	Gly	Ile	Thr	Arg	Ile	Arg	Val	Val	Val	Ser	Ala	Ser	Asp	
					245					250				255		
tgt	caa	ggc	acg	cct	gta	ttg	aat	aga	agc	ctt	gaa	gtg	gat	gaa	aag	816
Cys	Gln	Gly	Thr	Pro	Val	Leu	Asn	Arg	Ser	Leu	Glu	Val	Asp	Glu	Lys	
			260					265					270			
aat	aag	aat	ttt	gct	atc	acg	cgc	tta	caa	tct	ttg	ctt	tat	aaa	gaa	864
Asn	Lys	Asn	Phe	Ala	Ile	Thr	Arg	Leu	Gln	Ser	Leu	Leu	Tyr	Lys	Glu	
		275					280					285				
ctg	aaa	gat	tat	gcc	aat	aaa	gaa	ggg	caa	ggc	aat	acg	ggg	tta	taa	912
Leu	Lys	Asp	Tyr	Ala	Asn	Lys	Glu	Gly	Gln	Gly	Asn	Thr	Gly	Leu		
	290					295					300					

<210> 78  
 <211> 303  
 <212> PRT  
 <213> Helicobacter pylori

<400> 78

Met	Lys	Lys	Ile	Ile	Leu	Ala	Cys	Leu	Met	Ala	Phe	Val	Gly	Ala	Asn	1	5	10	15
Leu	Ser	Ala	Glu	Pro	Lys	Trp	Tyr	Ser	Lys	Ala	Tyr	Asn	Lys	Thr	Asn	20	25	30	
Thr	Gln	Lys	Gly	Tyr	Leu	Tyr	Gly	Ser	Gly	Ser	Ala	Thr	Ser	Lys	Glu	35	40	45	
Ala	Ser	Lys	Gln	Lys	Ala	Leu	Ala	Asp	Leu	Val	Ala	Ser	Ile	Ser	Val	50	55	60	
Val	Val	Asn	Ser	Gln	Ile	His	Ile	Gln	Lys	Ser	Arg	Val	Asp	Asn	Lys	65	70	75	80
Leu	Lys	Ser	Ser	Asp	Ser	Gln	Thr	Ile	Asn	Leu	Lys	Thr	Asp	Asp	Leu	85	90	95	
Glu	Leu	Asn	Asn	Val	Glu	Ile	Val	Asn	Gln	Glu	Val	Gln	Lys	Gly	Ile	100	105	110	
Tyr	Tyr	Thr	Arg	Val	Arg	Ile	Asn	Gln	Asn	Leu	Phe	Leu	Gln	Gly	Leu	115	120	125	
Arg	Asp	Lys	Tyr	Asn	Ala	Leu	Tyr	Gly	Gln	Phe	Ser	Thr	Leu	Met	Pro	130	135	140	
Lys	Val	Cys	Lys	Gly	Val	Phe	Leu	Gln	Gln	Ser	Lys	Ser	Met	Gly	Asp	145	150	155	160
Leu	Leu	Ala	Lys	Ala	Met	Pro	Ile	Glu	Arg	Ile	Leu	Lys	Ala	Tyr	Ser	165	170	175	
Val	Pro	Val	Gly	Ser	Leu	Glu	Asn	Tyr	Glu	Lys	Ile	Tyr	Tyr	Gln	Asn	180	185	190	
Ala	Phe	Lys	Pro	Lys	Val	Gln	Ile	Thr	Phe	Asp	Asn	Asn	Gly	Asp	Ala	195	200	205	
Glu	Ile	Lys	Ser	Ala	Leu	Ile	Ser	Ala	Tyr	Ala	Arg	Val	Leu	Thr	Pro				

210	215	220
Ser Asp Glu Glu Lys Leu Tyr Gln Ile Lys Asn Glu Val Phe Thr Asp		
225	230	235 240
Ser Ala Asn Gly Ile Thr Arg Ile Arg Val Val Val Ser Ala Ser Asp		
	245	250 255
Cys Gln Gly Thr Pro Val Leu Asn Arg Ser Leu Glu Val Asp Glu Lys		
	260	265 270
Asn Lys Asn Phe Ala Ile Thr Arg Leu Gln Ser Leu Leu Tyr Lys Glu		
	275	280 285
Leu Lys Asp Tyr Ala Asn Lys Glu Gly Gln Gly Asn Thr Gly Leu		
	290	295 300

<210> 79  
 <211> 834  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(834)

<400> 79	
atg aaa aca aac ggg ctt ttt aaa atg tgg ggg ctg ttt tta gtt tta	48
Met Lys Thr Asn Gly Leu Phe Lys Met Trp Gly Leu Phe Leu Val Leu	
1 5 10 15	
atc gct tta gtc ttt aat gca tgt tct gat agc cat aaa gaa aaa aag	96
Ile Ala Leu Val Phe Asn Ala Cys Ser Asp Ser His Lys Glu Lys Lys	
20 25 30	
gac gct tta gaa gtc att aaa caa aga ggg gtt tta aaa gtg ggg gtt	144
Asp Ala Leu Glu Val Ile Lys Gln Arg Gly Val Leu Lys Val Gly Val	
35 40 45	
ttt agc gat aag cct cct ttt ggc tct gtg gat tct aaa ggg aaa tat	192
Phe Ser Asp Lys Pro Pro Phe Gly Ser Val Asp Ser Lys Gly Lys Tyr	
50 55 60	
caa ggc tat gat gta gtt att gct aaa cgc atg gct ctt gat tta ttg	240
Gln Gly Tyr Asp Val Val Ile Ala Lys Arg Met Ala Leu Asp Leu Leu	
65 70 75 80	
ggc gat gaa aat aag att gag ttt att cct gta gaa gct tca gct agg	288

Gly	Asp	Glu	Asn	Lys	Ile	Glu	Phe	Ile	Pro	Val	Glu	Ala	Ser	Ala	Arg	
				85					90					95		
gtg	gaa	ttt	tta	aaa	gcc	aat	aaa	gtg	gat	att	atc	atg	gct	aat	ttc	336
Val	Glu	Phe	Leu	Lys	Ala	Asn	Lys	Val	Asp	Ile	Ile	Met	Ala	Asn	Phe	
			100					105					110			
acg	cgc	act	aaa	gaa	aga	gaa	aaa	gtc	gtg	gat	ttc	gct	aag	ccg	tat	384
Thr	Arg	Thr	Lys	Glu	Arg	Glu	Lys	Val	Val	Asp	Phe	Ala	Lys	Pro	Tyr	
		115					120					125				
atg	aaa	gtc	gct	tta	ggg	gtg	gtt	tct	aaa	gat	ggg	gtc	att	aaa	aat	432
Met	Lys	Val	Ala	Leu	Gly	Val	Val	Ser	Lys	Asp	Gly	Val	Ile	Lys	Asn	
	130					135					140					
ata	gaa	gag	ttg	aaa	gat	aaa	gag	ttg	att	gtg	aat	aaa	ggc	acg	aca	480
Ile	Glu	Glu	Leu	Lys	Asp	Lys	Glu	Leu	Ile	Val	Asn	Lys	Gly	Thr	Thr	
	145				150					155					160	
gcg	gat	ttt	tat	ttc	act	aaa	aat	tac	ccc	aat	atc	aag	ctt	ttg	aaa	528
Ala	Asp	Phe	Tyr	Phe	Thr	Lys	Asn	Tyr	Pro	Asn	Ile	Lys	Leu	Leu	Lys	
				165					170					175		
ttt	gag	caa	aat	aca	gag	act	ttt	tta	gcc	ctt	tta	aac	aat	aag	gct	576
Phe	Glu	Gln	Asn	Thr	Glu	Thr	Phe	Leu	Ala	Leu	Leu	Asn	Asn	Lys	Ala	
			180					185					190			
acc	gct	cta	gcc	cat	gac	aac	act	tta	ttg	ctc	gct	tgg	acg	aaa	caa	624
Thr	Ala	Leu	Ala	His	Asp	Asn	Thr	Leu	Leu	Leu	Ala	Trp	Thr	Lys	Gln	
		195					200					205				
cac	cct	gaa	ttt	aaa	tta	ggc	att	aca	agc	ctt	ggc	gat	aag	gat	gtg	672
His	Pro	Glu	Phe	Lys	Leu	Gly	Ile	Thr	Ser	Leu	Gly	Asp	Lys	Asp	Val	
	210					215					220					
atc	gct	cca	gcg	att	aaa	aaa	ggc	aac	ccc	aag	ctt	tta	gaa	tgg	ttg	720
Ile	Ala	Pro	Ala	Ile	Lys	Lys	Gly	Asn	Pro	Lys	Leu	Leu	Glu	Trp	Leu	
	225				230					235					240	
aat	aac	gaa	ata	gat	tcc	ctc	att	tct	agc	gac	ttc	tta	aaa	gaa	gct	768
Asn	Asn	Glu	Ile	Asp	Ser	Leu	Ile	Ser	Ser	Asp	Phe	Leu	Lys	Glu	Ala	
				245					250					255		
tat	caa	gag	act	tta	gca	cct	gtt	tat	ggc	gat	gaa	atc	aaa	ccg	gaa	816
Tyr	Gln	Glu	Thr	Leu	Ala	Pro	Val	Tyr	Gly	Asp	Glu	Ile	Lys	Pro	Glu	
			260					265					270			
gaa	att	att	ttt	gaa	tga											834
Glu	Ile	Ile	Phe	Glu												
			275													

<210> 80

<211> 277  
 <212> PRT  
 <213> Helicobacter pylori  
 <400> 80

Met Lys Thr Asn Gly Leu Phe Lys Met Trp Gly Leu Phe Leu Val Leu  
 1 5 10 15

Ile Ala Leu Val Phe Asn Ala Cys Ser Asp Ser His Lys Glu Lys Lys  
 20 25 30

Asp Ala Leu Glu Val Ile Lys Gln Arg Gly Val Leu Lys Val Gly Val  
 35 40 45

Phe Ser Asp Lys Pro Pro Phe Gly Ser Val Asp Ser Lys Gly Lys Tyr  
 50 55 60

Gln Gly Tyr Asp Val Val Ile Ala Lys Arg Met Ala Leu Asp Leu Leu  
 65 70 75 80

Gly Asp Glu Asn Lys Ile Glu Phe Ile Pro Val Glu Ala Ser Ala Arg  
 85 90 95

Val Glu Phe Leu Lys Ala Asn Lys Val Asp Ile Ile Met Ala Asn Phe  
 100 105 110

Thr Arg Thr Lys Glu Arg Glu Lys Val Val Asp Phe Ala Lys Pro Tyr  
 115 120 125

Met Lys Val Ala Leu Gly Val Val Ser Lys Asp Gly Val Ile Lys Asn  
 130 135 140

Ile Glu Glu Leu Lys Asp Lys Glu Leu Ile Val Asn Lys Gly Thr Thr  
 145 150 155 160

Ala Asp Phe Tyr Phe Thr Lys Asn Tyr Pro Asn Ile Lys Leu Leu Lys  
 165 170 175

Phe Glu Gln Asn Thr Glu Thr Phe Leu Ala Leu Leu Asn Asn Lys Ala  
 180 185 190



Thr Ala Leu Ala His Asp Asn Thr Leu Leu Leu Ala Trp Thr Lys Gln  
195 200 205

His Pro Glu Phe Lys Leu Gly Ile Thr Ser Leu Gly Asp Lys Asp Val  
210 215 220

Ile Ala Pro Ala Ile Lys Lys Gly Asn Pro Lys Leu Leu Glu Trp Leu  
225 230 235 240

Asn Asn Glu Ile Asp Ser Leu Ile Ser Ser Asp Phe Leu Lys Glu Ala  
245 250 255

Tyr Gln Glu Thr Leu Ala Pro Val Tyr Gly Asp Glu Ile Lys Pro Glu  
260 265 270

Glu Ile Ile Phe Glu  
275

<210> 81  
<211> 1296  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(1296)

<400> 81  
gtg gcg tta gct gaa gac gat ggc ttt tat atg gga gtg ggc tat caa 48  
Val Ala Leu Ala Glu Asp Asp Gly Phe Tyr Met Gly Val Gly Tyr Gln  
1 5 10 15  
atc ggc ggc gcg caa caa aat atc gat aac aaa ggc agc acc cta agg 96  
Ile Gly Gly Ala Gln Gln Asn Ile Asp Asn Lys Gly Ser Thr Leu Arg  
20 25 30  
aat aat gtc att aat aat ttc cgc caa gtg ggc gtg ggt atg gca ggg 144  
Asn Asn Val Ile Asn Asn Phe Arg Gln Val Gly Val Gly Met Ala Gly  
35 40 45  
ggt aat ggg ctt tta gcc tta gcg aca aac acg acc atg gac gct ctt 192  
Gly Asn Gly Leu Leu Ala Leu Ala Thr Asn Thr Thr Met Asp Ala Leu  
50 55 60  
tta ggg ata ggc aac caa att gtc aat act aat aca act gtt agc aac 240  
Leu Gly Ile Gly Asn Gln Ile Val Asn Thr Asn Thr Thr Val Ser Asn  
65 70 75 80

aac aac gca gaa tta acc cag ttt aaa aaa ata ctc cct caa att gag	288
Asn Asn Ala Glu Leu Thr Gln Phe Lys Lys Ile Leu Pro Gln Ile Glu	
85 90 95	
caa cgc ttt gaa acg aat aaa aac gct tat agc gtt caa gcc ttg caa	336
Gln Arg Phe Glu Thr Asn Lys Asn Ala Tyr Ser Val Gln Ala Leu Gln	
100 105 110	
gtg tat ttg agt aat gtg ctt tat aac ttg gtt aat aat agt aat aat	384
Val Tyr Leu Ser Asn Val Leu Tyr Asn Leu Val Asn Asn Ser Asn Asn	
115 120 125	
ggc agt aat aat gga gtc gtt cct gaa tat gta gga att ata aaa gtt	432
Gly Ser Asn Asn Gly Val Val Pro Glu Tyr Val Gly Ile Ile Lys Val	
130 135 140	
ctc tat ggt tct caa aat gaa ttc agt ctc tta gcc acg gag agt gtg	480
Leu Tyr Gly Ser Gln Asn Glu Phe Ser Leu Leu Ala Thr Glu Ser Val	
145 150 155 160	
gtg ctt tta aac gcg ctt aca agg gtg aat ctg gat agt aat tcg gtg	528
Val Leu Leu Asn Ala Leu Thr Arg Val Asn Leu Asp Ser Asn Ser Val	
165 170 175	
ttt tta aaa ggg cta tta gcc caa atg cag ctt ttt aat gac act tct	576
Phe Leu Lys Gly Leu Leu Ala Gln Met Gln Leu Phe Asn Asp Thr Ser	
180 185 190	
tca gca aag cta ggc cag atc gca gaa aac ttg aag aac ggt ggt gca	624
Ser Ala Lys Leu Gly Gln Ile Ala Glu Asn Leu Lys Asn Gly Gly Ala	
195 200 205	
gga tca atg ctc caa aag gat gtg aaa acc atc tcg gat cga atc gct	672
Gly Ser Met Leu Gln Lys Asp Val Lys Thr Ile Ser Asp Arg Ile Ala	
210 215 220	
act tac caa gag aat cta aaa cag cta gga ggg atg cta aag aat tac	720
Thr Tyr Gln Glu Asn Leu Lys Gln Leu Gly Gly Met Leu Lys Asn Tyr	
225 230 235 240	
gat gaa ccc tac ttg ccc caa ttt ggg cca ggc aca agc tct cag cat	768
Asp Glu Pro Tyr Leu Pro Gln Phe Gly Pro Gly Thr Ser Ser Gln His	
245 250 255	
ggg gtt att aat ggc ttt ggc att caa gtg ggc tat aag caa ttt ttt	816
Gly Val Ile Asn Gly Phe Gly Ile Gln Val Gly Tyr Lys Gln Phe Phe	
260 265 270	
ggg aac aag cgg aat ata ggc tta cga tat tac gct ttc ttt gat tat	864
Gly Asn Lys Arg Asn Ile Gly Leu Arg Tyr Tyr Ala Phe Phe Asp Tyr	
275 280 285	
ggc ttt acg caa ttg ggc agt ctt agc agc gcc gtt aaa gcg aat atc	912

Gly	Phe	Thr	Gln	Leu	Gly	Ser	Leu	Ser	Ser	Ala	Val	Lys	Ala	Asn	Ile	
290						295					300					
ttt	act	tat	ggc	gct	ggc	acg	gac	ttt	tta	tgg	aat	atc	ttt	aga	agg	960
Phe	Thr	Tyr	Gly	Ala	Gly	Thr	Asp	Phe	Leu	Trp	Asn	Ile	Phe	Arg	Arg	
305					310					315					320	
gtt	ttt	agc	gat	cag	tcc	ttg	aat	gtg	ggg	gtg	ttt	ggg	ggc	att	caa	1008
Val	Phe	Ser	Asp	Gln	Ser	Leu	Asn	Val	Gly	Val	Phe	Gly	Gly	Ile	Gln	
				325					330					335		
ata	gcg	ggt	aac	act	tgg	gat	agc	tct	tta	aga	ggt	caa	att	gaa	aac	1056
Ile	Ala	Gly	Asn	Thr	Trp	Asp	Ser	Ser	Leu	Arg	Gly	Gln	Ile	Glu	Asn	
			340				345						350			
tcg	ttt	aaa	gaa	tac	ccc	act	ccc	acg	aat	ttc	caa	ttt	ttg	ttt	aat	1104
Ser	Phe	Lys	Glu	Tyr	Pro	Thr	Pro	Thr	Asn	Phe	Gln	Phe	Leu	Phe	Asn	
		355					360					365				
ttg	ggt	tta	agg	gct	cat	ttt	gcc	agc	acc	atg	cac	cgc	cgg	ttt	ttg	1152
Leu	Gly	Leu	Arg	Ala	His	Phe	Ala	Ser	Thr	Met	His	Arg	Arg	Phe	Leu	
	370					375					380					
agc	gcg	tct	caa	agc	att	cag	cat	ggg	atg	gaa	ttt	ggc	gtg	aaa	atc	1200
Ser	Ala	Ser	Gln	Ser	Ile	Gln	His	Gly	Met	Glu	Phe	Gly	Val	Lys	Ile	
385					390					395					400	
ccg	gct	atc	aat	caa	agg	tat	ttg	agg	gcc	aat	ggg	gct	gat	gtg	gat	1248
Pro	Ala	Ile	Asn	Gln	Arg	Tyr	Leu	Arg	Ala	Asn	Gly	Ala	Asp	Val	Asp	
				405					410					415		
tac	agg	cgt	ttg	tat	gcg	ttc	tat	atc	aat	tac	acg	ata	ggt	ttt	taa	1296
Tyr	Arg	Arg	Leu	Tyr	Ala	Phe	Tyr	Ile	Asn	Tyr	Thr	Ile	Gly	Phe		
			420					425					430			

<210> 82  
 <211> 431  
 <212> PRT  
 <213> Helicobacter pylori

<400> 82

Val	Ala	Leu	Ala	Glu	Asp	Asp	Gly	Phe	Tyr	Met	Gly	Val	Gly	Tyr	Gln
1				5					10					15	

Ile	Gly	Gly	Ala	Gln	Gln	Asn	Ile	Asp	Asn	Lys	Gly	Ser	Thr	Leu	Arg
			20					25					30		

Asn	Asn	Val	Ile	Asn	Asn	Phe	Arg	Gln	Val	Gly	Val	Gly	Met	Ala	Gly
		35					40					45			

Gly	Asn	Gly	Leu	Leu	Ala	Leu	Ala	Thr	Asn	Thr	Thr	Met	Asp	Ala	Leu	50	55	60
Leu	Gly	Ile	Gly	Asn	Gln	Ile	Val	Asn	Thr	Asn	Thr	Thr	Val	Ser	Asn	65	70	75
Asn	Asn	Ala	Glu	Leu	Thr	Gln	Phe	Lys	Lys	Ile	Leu	Pro	Gln	Ile	Glu	85	90	95
Gln	Arg	Phe	Glu	Thr	Asn	Lys	Asn	Ala	Tyr	Ser	Val	Gln	Ala	Leu	Gln	100	105	110
Val	Tyr	Leu	Ser	Asn	Val	Leu	Tyr	Asn	Leu	Val	Asn	Asn	Ser	Asn	Asn	115	120	125
Gly	Ser	Asn	Asn	Gly	Val	Val	Pro	Glu	Tyr	Val	Gly	Ile	Ile	Lys	Val	130	135	140
Leu	Tyr	Gly	Ser	Gln	Asn	Glu	Phe	Ser	Leu	Leu	Ala	Thr	Glu	Ser	Val	145	150	155
Val	Leu	Leu	Asn	Ala	Leu	Thr	Arg	Val	Asn	Leu	Asp	Ser	Asn	Ser	Val	165	170	175
Phe	Leu	Lys	Gly	Leu	Leu	Ala	Gln	Met	Gln	Leu	Phe	Asn	Asp	Thr	Ser	180	185	190
Ser	Ala	Lys	Leu	Gly	Gln	Ile	Ala	Glu	Asn	Leu	Lys	Asn	Gly	Gly	Ala	195	200	205
Gly	Ser	Met	Leu	Gln	Lys	Asp	Val	Lys	Thr	Ile	Ser	Asp	Arg	Ile	Ala	210	215	220
Thr	Tyr	Gln	Glu	Asn	Leu	Lys	Gln	Leu	Gly	Gly	Met	Leu	Lys	Asn	Tyr	225	230	235
Asp	Glu	Pro	Tyr	Leu	Pro	Gln	Phe	Gly	Pro	Gly	Thr	Ser	Ser	Gln	His	245	250	255
Gly	Val	Ile	Asn	Gly	Phe	Gly	Ile	Gln	Val	Gly	Tyr	Lys	Gln	Phe	Phe	260	265	270

Gly Asn Lys Arg Asn Ile Gly Leu Arg Tyr Tyr Ala Phe Phe Asp Tyr  
 275 280 285

Gly Phe Thr Gln Leu Gly Ser Leu Ser Ser Ala Val Lys Ala Asn Ile  
 290 295 300

Phe Thr Tyr Gly Ala Gly Thr Asp Phe Leu Trp Asn Ile Phe Arg Arg  
 305 310 315 320

Val Phe Ser Asp Gln Ser Leu Asn Val Gly Val Phe Gly Gly Ile Gln  
 325 330 335

Ile Ala Gly Asn Thr Trp Asp Ser Ser Leu Arg Gly Gln Ile Glu Asn  
 340 345 350

Ser Phe Lys Glu Tyr Pro Thr Pro Thr Asn Phe Gln Phe Leu Phe Asn  
 355 360 365

Leu Gly Leu Arg Ala His Phe Ala Ser Thr Met His Arg Arg Phe Leu  
 370 375 380

Ser Ala Ser Gln Ser Ile Gln His Gly Met Glu Phe Gly Val Lys Ile  
 385 390 395 400

Pro Ala Ile Asn Gln Arg Tyr Leu Arg Ala Asn Gly Ala Asp Val Asp  
 405 410 415

Tyr Arg Arg Leu Tyr Ala Phe Tyr Ile Asn Tyr Thr Ile Gly Phe  
 420 425 430

<210> 83  
 <211> 1197  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1197)

<400> 83  
 atg gaa tca gta aaa aca gga aaa aca aat aag gtt ggc aag aat aca

Met	Glu	Ser	Val	Lys	Thr	Gly	Lys	Thr	Asn	Lys	Val	Gly	Lys	Asn	Thr	
1				5					10					15		
gag atg gct aat aca aag gca aat aaa gag act cat ttt aaa caa gtg																96
Glu	Met	Ala	Asn	Thr	Lys	Ala	Asn	Lys	Glu	Thr	His	Phe	Lys	Gln	Val	
			20					25					30			
agc gcc att aca aat ata atc aga tca gtt ggt ggg ttt ttt aca aaa																144
Ser	Ala	Ile	Thr	Asn	Ile	Ile	Arg	Ser	Val	Gly	Gly	Phe	Phe	Thr	Lys	
		35					40					45				
att gca aag aga gtt aga gga ctt gta aaa aaa cac ccc aag aaa agc																192
Ile	Ala	Lys	Arg	Val	Arg	Gly	Leu	Val	Lys	Lys	His	Pro	Lys	Lys	Ser	
	50					55					60					
agt gcg gca tta gta gta ttg acc cat att gcg tgc aag aaa gcg aaa																240
Ser	Ala	Ala	Leu	Val	Val	Leu	Thr	His	Ile	Ala	Cys	Lys	Lys	Ala	Lys	
65					70					75					80	
gaa tta gac gat aaa gtc caa gat aaa tcc aaa caa gct gaa aaa gaa																288
Glu	Leu	Asp	Asp	Lys	Val	Gln	Asp	Lys	Ser	Lys	Gln	Ala	Glu	Lys	Glu	
				85					90					95		
aat caa atc aat tgg tgg aaa tat tca gga tta aca ata gcg gca agt																336
Asn	Gln	Ile	Asn	Trp	Trp	Lys	Tyr	Ser	Gly	Leu	Thr	Ile	Ala	Ala	Ser	
			100					105					110			
tta tta tta gcc gct tgt agc gct ggt gat act gat aaa cag ata gaa																384
Leu	Leu	Leu	Ala	Ala	Cys	Ser	Ala	Gly	Asp	Thr	Asp	Lys	Gln	Ile	Glu	
		115					120					125				
cta gaa caa gaa aaa aag gaa gct gaa aac gct agg gat aga gcg aac																432
Leu	Glu	Gln	Glu	Lys	Lys	Glu	Ala	Glu	Asn	Ala	Arg	Asp	Arg	Ala	Asn	
	130					135					140					
aag agt ggg ata gaa cta gaa caa gaa aga cag aaa aca aac aag agt																480
Lys	Ser	Gly	Ile	Glu	Leu	Glu	Gln	Glu	Arg	Gln	Lys	Thr	Asn	Lys	Ser	
145					150					155					160	
ggg ata gaa ctc gct aat agt caa ata aaa gca gaa caa gaa aga caa																528
Gly	Ile	Glu	Leu	Ala	Asn	Ser	Gln	Ile	Lys	Ala	Glu	Gln	Glu	Arg	Gln	
			165						170					175		
aag aca gaa caa gaa aaa caa aaa gca aat aag agt gcg ata gag tta																576
Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys	Ala	Asn	Lys	Ser	Ala	Ile	Glu	Leu	
			180					185					190			
gaa cag caa aaa caa aag acc att aat aca caa aga gat ttg att aaa																624
Glu	Gln	Gln	Lys	Gln	Lys	Thr	Ile	Asn	Thr	Gln	Arg	Asp	Leu	Ile	Lys	
		195				200						205				
gaa cag aaa gat ttc att aaa gaa aca gaa caa aat tgc caa gaa aat																672
Glu	Gln	Lys	Asp	Phe	Ile	Lys	Glu	Thr	Glu	Gln	Asn	Cys	Gln	Glu	Asn	
	210					215					220					

cat	aat	caa	ttc	ttt	att	aaa	aaa	tta	gga	att	aag	ggt	ggc	att	gct	720
His	Asn	Gln	Phe	Phe	Ile	Lys	Lys	Leu	Gly	Ile	Lys	Gly	Gly	Ile	Ala	
225					230					235					240	
ata	gaa	gta	gaa	gct	gaa	tgc	aaa	acc	cct	aaa	cct	gca	aaa	acc	aat	768
Ile	Glu	Val	Glu	Ala	Glu	Cys	Lys	Thr	Pro	Lys	Pro	Ala	Lys	Thr	Asn	
				245					250					255		
caa	acc	cct	atc	cag	cca	aaa	cac	ctc	cca	aac	tct	aaa	caa	cct	cat	816
Gln	Thr	Pro	Ile	Gln	Pro	Lys	His	Leu	Pro	Asn	Ser	Lys	Gln	Pro	His	
			260					265					270			
tct	caa	aga	gga	tca	aaa	gcg	caa	gag	ttt	atc	gct	tat	ttg	caa	aaa	864
Ser	Gln	Arg	Gly	Ser	Lys	Ala	Gln	Glu	Phe	Ile	Ala	Tyr	Leu	Gln	Lys	
		275				280						285				
gag	cta	gaa	ttt	ctg	ccc	tat	tcg	caa	aaa	gct	atc	gct	aaa	caa	gtg	912
Glu	Leu	Glu	Phe	Leu	Pro	Tyr	Ser	Gln	Lys	Ala	Ile	Ala	Lys	Gln	Val	
	290					295					300					
aat	ttc	tat	aaa	cca	agt	tct	atc	gct	tat	tta	gaa	cta	gat	cct	aga	960
Asn	Phe	Tyr	Lys	Pro	Ser	Ser	Ile	Ala	Tyr	Leu	Glu	Leu	Asp	Pro	Arg	
305					310					315					320	
gat	ttt	aag	gtt	aca	gaa	gaa	tgg	caa	aaa	gaa	aat	cta	aaa	ata	cgc	1008
Asp	Phe	Lys	Val	Thr	Glu	Glu	Trp	Gln	Lys	Glu	Asn	Leu	Lys	Ile	Arg	
				325					330					335		
tct	aaa	gct	caa	gct	aaa	atg	ctt	gaa	atg	agg	gat	tta	aaa	cca	gac	1056
Ser	Lys	Ala	Gln	Ala	Lys	Met	Leu	Glu	Met	Arg	Asp	Leu	Lys	Pro	Asp	
			340					345					350			
cca	caa	gcc	cac	ctt	cca	acc	tct	caa	agc	ctt	ttg	ttc	gtt	caa	aaa	1104
Pro	Gln	Ala	His	Leu	Pro	Thr	Ser	Gln	Ser	Leu	Leu	Phe	Val	Gln	Lys	
		355					360					365				
ata	ttt	gct	gat	gtt	aat	aaa	gaa	ata	gaa	gca	gtt	gct	aat	act	gaa	1152
Ile	Phe	Ala	Asp	Val	Asn	Lys	Glu	Ile	Glu	Ala	Val	Ala	Asn	Thr	Glu	
	370					375					380					
aag	aaa	gca	gaa	aaa	gcg	ggt	tat	ggt	tat	agt	aaa	agg	atg	tag		1197
Lys	Lys	Ala	Glu	Lys	Ala	Gly	Tyr	Gly	Tyr	Ser	Lys	Arg	Met			
385					390					395						

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Helicobacter pylori

<400> 84

Met	Glu	Ser	Val	Lys	Thr	Gly	Lys	Thr	Asn	Lys	Val	Gly	Lys	Asn	Thr
1				5					10					15	

Glu	Met	Ala	Asn	Thr	Lys	Ala	Asn	Lys	Glu	Thr	His	Phe	Lys	Gln	Val
			20					25					30		
Ser	Ala	Ile	Thr	Asn	Ile	Ile	Arg	Ser	Val	Gly	Gly	Phe	Phe	Thr	Lys
		35					40					45			
Ile	Ala	Lys	Arg	Val	Arg	Gly	Leu	Val	Lys	Lys	His	Pro	Lys	Lys	Ser
	50					55					60				
Ser	Ala	Ala	Leu	Val	Val	Leu	Thr	His	Ile	Ala	Cys	Lys	Lys	Ala	Lys
65					70					75					80
Glu	Leu	Asp	Asp	Lys	Val	Gln	Asp	Lys	Ser	Lys	Gln	Ala	Glu	Lys	Glu
				85					90					95	
Asn	Gln	Ile	Asn	Trp	Trp	Lys	Tyr	Ser	Gly	Leu	Thr	Ile	Ala	Ala	Ser
			100					105					110		
Leu	Leu	Leu	Ala	Ala	Cys	Ser	Ala	Gly	Asp	Thr	Asp	Lys	Gln	Ile	Glu
		115					120					125			
Leu	Glu	Gln	Glu	Lys	Lys	Glu	Ala	Glu	Asn	Ala	Arg	Asp	Arg	Ala	Asn
	130					135					140				
Lys	Ser	Gly	Ile	Glu	Leu	Glu	Gln	Glu	Arg	Gln	Lys	Thr	Asn	Lys	Ser
145					150					155					160
Gly	Ile	Glu	Leu	Ala	Asn	Ser	Gln	Ile	Lys	Ala	Glu	Gln	Glu	Arg	Gln
				165					170					175	
Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys	Ala	Asn	Lys	Ser	Ala	Ile	Glu	Leu
			180					185					190		
Glu	Gln	Gln	Lys	Gln	Lys	Thr	Ile	Asn	Thr	Gln	Arg	Asp	Leu	Ile	Lys
		195					200					205			
Glu	Gln	Lys	Asp	Phe	Ile	Lys	Glu	Thr	Glu	Gln	Asn	Cys	Gln	Glu	Asn
	210					215					220				
His	Asn	Gln	Phe	Phe	Ile	Lys	Lys	Leu	Gly	Ile	Lys	Gly	Gly	Ile	Ala



225		230		235		240
Ile Glu Val Glu	Ala Glu Cys Lys Thr	Pro Lys Pro Ala Lys Thr	Asn			
	245	250	255			
Gln Thr Pro Ile	Gln Pro Lys His Leu	Pro Asn Ser Lys Gln	Pro His			
	260	265	270			
Ser Gln Arg Gly	Ser Lys Ala Gln Glu Phe Ile	Ala Tyr Leu Gln Lys				
	275	280	285			
Glu Leu Glu Phe	Leu Pro Tyr Ser Gln Lys	Ala Ile Ala Lys Gln	Val			
	290	295	300			
Asn Phe Tyr Lys	Pro Ser Ser Ile Ala Tyr	Leu Glu Leu Asp	Pro Arg			
305	310	315	320			
Asp Phe Lys Val	Thr Glu Glu Trp Gln	Lys Glu Asn Leu Lys	Ile Arg			
	325	330	335			
Ser Lys Ala Gln	Ala Lys Met Leu Glu Met	Arg Asp Leu Lys	Pro Asp			
	340	345	350			
Pro Gln Ala His	Leu Pro Thr Ser Gln Ser	Leu Leu Phe Val	Gln Lys			
	355	360	365			
Ile Phe Ala Asp	Val Asn Lys Glu Ile Glu	Ala Val Ala Asn	Thr Glu			
	370	375	380			
Lys Lys Ala Glu	Lys Ala Gly Tyr Gly Tyr	Ser Lys Arg Met				
385	390	395				

<210> 85  
 <211> 1131  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1131)

<400> 85  
 atg aat ttt ttt aaa atc ctt tta atg gaa tta aga gcc att gtt tct

Met	Asn	Phe	Phe	Lys	Ile	Leu	Leu	Met	Glu	Leu	Arg	Ala	Ile	Val	Ser	
1				5					10					15		
cat	aaa	ggc	gtt	tta	tta	atc	ctt	ata	ggc	gct	cct	tta	atc	tat	ggc	96
His	Lys	Gly	Val	Leu	Leu	Ile	Leu	Ile	Gly	Ala	Pro	Leu	Ile	Tyr	Gly	
			20					25					30			
tta	tta	tac	cct	ttg	cct	tat	tta	aga	gac	atc	gta	acg	cag	caa	aaa	144
Leu	Leu	Tyr	Pro	Leu	Pro	Tyr	Leu	Arg	Asp	Ile	Val	Thr	Gln	Gln	Lys	
		35					40				45					
atc	gcc	ctt	gta	gat	gaa	gac	aat	tcc	ttc	ctt	tct	agg	caa	tta	gcc	192
Ile	Ala	Leu	Val	Asp	Glu	Asp	Asn	Ser	Phe	Leu	Ser	Arg	Gln	Leu	Ala	
	50					55					60					
ttc	atg	gcg	caa	agc	tcc	aac	gag	tta	gaa	atc	gct	ttt	ttt	agc	ccc	240
Phe	Met	Ala	Gln	Ser	Ser	Asn	Glu	Leu	Glu	Ile	Ala	Phe	Phe	Ser	Pro	
65					70					75					80	
tct	atg	ctg	gaa	gcc	aaa	aag	ctt	tta	aaa	gaa	gaa	aaa	att	tat	ggg	288
Ser	Met	Leu	Glu	Ala	Lys	Lys	Leu	Leu	Lys	Glu	Glu	Lys	Ile	Tyr	Gly	
				85					90					95		
atc	ttg	cac	att	ccc	tct	cat	ttt	gaa	gcc	aat	atc	cat	aaa	caa	gtg	336
Ile	Leu	His	Ile	Pro	Ser	His	Phe	Glu	Ala	Asn	Ile	His	Lys	Gln	Val	
			100					105					110			
cct	gta	acg	ata	gat	ttt	tat	gcg	aat	tcc	aat	tac	ttt	ttg	att	tat	384
Pro	Val	Thr	Ile	Asp	Phe	Tyr	Ala	Asn	Ser	Asn	Tyr	Phe	Leu	Ile	Tyr	
		115					120					125				
ggt	gcg	tta	gcg	aat	gcg	gtg	gtg	gag	agc	atc	aac	gct	tta	aat	gat	432
Gly	Ala	Leu	Ala	Asn	Ala	Val	Val	Glu	Ser	Ile	Asn	Ala	Leu	Asn	Asp	
	130					135					140					
gag	ata	agg	ttc	aaa	cgc	aat	gcc	caa	ata	gaa	gaa	gct	gaa	tta	ggg	480
Glu	Ile	Arg	Phe	Lys	Arg	Asn	Ala	Gln	Ile	Glu	Glu	Ala	Glu	Leu	Gly	
145					150					155					160	
aca	gac	ggg	att	aaa	atc	agg	cct	atc	gct	tta	tat	aac	cct	agt	gag	528
Thr	Asp	Gly	Ile	Lys	Ile	Arg	Pro	Ile	Ala	Leu	Tyr	Asn	Pro	Ser	Glu	
				165					170					175		
ggg	tat	ttg	aat	tac	gcg	ctc	tct	agc	gtg	ttt	att	ttc	att	ttg	cac	576
Gly	Tyr	Leu	Asn	Tyr	Ala	Leu	Ser	Ser	Val	Phe	Ile	Phe	Ile	Leu	His	
			180					185					190			
cag	gtg	atg	ctc	att	gca	agc	agc	atg	ttt	act	agc	tcc	agg	cgt	ttg	624
Gln	Val	Met	Leu	Ile	Ala	Ser	Ser	Met	Phe	Thr	Ser	Ser	Arg	Arg	Leu	
		195					200					205				
gaa	tta	gcc	ctt	tta	gac	aga	aag	caa	atc	gct	tta	agg	ctg	tgc	aca	672
Glu	Leu	Ala	Leu	Leu	Asp	Arg	Lys	Gln	Ile	Ala	Leu	Arg	Leu	Cys	Thr	
	210					215					220					

aga	ctt	ttg	gtg	ttc	atg	ggg	gcg	ttt	agc	ggt	ttt	att	tta	tgg	tat	720
Arg	Leu	Leu	Val	Phe	Met	Gly	Ala	Phe	Ser	Val	Phe	Ile	Leu	Trp	Tyr	
225					230					235					240	
ttt	ggg	gcg	ctg	ttt	tct	ttt	tat	ggg	atc	gaa	cgg	cat	ggg	agc	gct	768
Phe	Gly	Ala	Leu	Phe	Ser	Phe	Tyr	Gly	Ile	Glu	Arg	His	Gly	Ser	Ala	
				245					250					255		
tta	atg	gtg	ttt	ttg	aat	agt	ttg	att	ttc	atg	ctt	gca	acc	ttg	agt	816
Leu	Met	Val	Phe	Leu	Asn	Ser	Leu	Ile	Phe	Met	Leu	Ala	Thr	Leu	Ser	
			260					265					270			
ttg	ggg	tcg	ttt	tta	ggc	gca	tgg	att	aaa	aat	gaa	gcc	cac	acc	act	864
Leu	Gly	Ser	Phe	Leu	Gly	Ala	Trp	Ile	Lys	Asn	Glu	Ala	His	Thr	Thr	
		275					280					285				
caa	atc	ggt	tta	att	tct	tct	ttg	ccc	ttg	att	ttt	atg	atg	ggt	ttt	912
Gln	Ile	Val	Leu	Ile	Ser	Ser	Leu	Pro	Leu	Ile	Phe	Met	Met	Gly	Phe	
	290					295					300					
gtg	tgg	cct	ttt	gaa	tcc	ttg	ccc	tct	tat	tta	cag	ggt	ttt	ggt	caa	960
Val	Trp	Pro	Phe	Glu	Ser	Leu	Pro	Ser	Tyr	Leu	Gln	Val	Phe	Val	Gln	
305					310					315					320	
ata	gtg	cca	gct	tat	cat	ggg	atc	agt	ttg	cta	ggg	cga	ttg	aat	caa	1008
Ile	Val	Pro	Ala	Tyr	His	Gly	Ile	Ser	Leu	Leu	Gly	Arg	Leu	Asn	Gln	
				325					330					335		
atg	cat	gcg	gaa	ttt	ata	gat	ggt	tcc	ttc	cat	ttt	tat	gcg	ctt	att	1056
Met	His	Ala	Glu	Phe	Ile	Asp	Val	Ser	Phe	His	Phe	Tyr	Ala	Leu	Ile	
			340					345					350			
gcg	att	ttt	att	gcg	agt	ttt	ata	ggg	agt	gtc	ttt	aaa	ctc	agc	tct	1104
Ala	Ile	Phe	Ile	Ala	Ser	Phe	Ile	Gly	Ser	Val	Phe	Lys	Leu	Ser	Ser	
		355					360					365				
tta	aag	aaa	gct	tgt	gaa	aac	gct	taa								1131
Leu	Lys	Lys	Ala	Cys	Glu	Asn	Ala									
	370					375										

<210> 86  
 <211> 376  
 <212> PRT  
 <213> Helicobacter pylori

<400> 86

Met	Asn	Phe	Phe	Lys	Ile	Leu	Leu	Met	Glu	Leu	Arg	Ala	Ile	Val	Ser
1				5					10					15	
His	Lys	Gly	Val	Leu	Leu	Ile	Leu	Ile	Gly	Ala	Pro	Leu	Ile	Tyr	Gly
			20					25					30		

Leu Leu Tyr Pro Leu Pro Tyr Leu Arg Asp Ile Val Thr Gln Gln Lys  
 35 40 45

Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu Ala  
 50 55 60

Phe Met Ala Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser Pro  
 65 70 75 80

Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr Gly  
 85 90 95

Ile Leu His Ile Pro Ser His Phe Glu Ala Asn Ile His Lys Gln Val  
 100 105 110

Pro Val Thr Ile Asp Phe Tyr Ala Asn Ser Asn Tyr Phe Leu Ile Tyr  
 115 120 125

Gly Ala Leu Ala Asn Ala Val Val Glu Ser Ile Asn Ala Leu Asn Asp  
 130 135 140

Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu Leu Gly  
 145 150 155 160

Thr Asp Gly Ile Lys Ile Arg Pro Ile Ala Leu Tyr Asn Pro Ser Glu  
 165 170 175

Gly Tyr Leu Asn Tyr Ala Leu Ser Ser Val Phe Ile Phe Ile Leu His  
 180 185 190

Gln Val Met Leu Ile Ala Ser Ser Met Phe Thr Ser Ser Arg Arg Leu  
 195 200 205

Glu Leu Ala Leu Leu Asp Arg Lys Gln Ile Ala Leu Arg Leu Cys Thr  
 210 215 220

Arg Leu Leu Val Phe Met Gly Ala Phe Ser Val Phe Ile Leu Trp Tyr  
 225 230 235 240

Phe Gly Ala Leu Phe Ser Phe Tyr Gly Ile Glu Arg His Gly Ser Ala

				245					250					255		
Leu	Met	Val	Phe 260	Leu	Asn	Ser	Leu	Ile 265	Phe	Met	Leu	Ala	Thr 270	Leu	Ser	
Leu	Gly	Ser 275	Phe	Leu	Gly	Ala,	Trp 280	Ile	Lys	Asn	Glu	Ala 285	His	Thr	Thr	
Gln	Ile 290	Val	Leu	Ile	Ser	Ser 295	Leu	Pro	Leu	Ile	Phe 300	Met	Met	Gly	Phe	
Val 305	Trp	Pro	Phe	Glu	Ser 310	Leu	Pro	Ser	Tyr	Leu 315	Gln	Val	Phe	Val	Gln 320	
Ile	Val	Pro	Ala	Tyr 325	His	Gly	Ile	Ser	Leu 330	Leu	Gly	Arg	Leu	Asn 335	Gln	
Met	His	Ala	Glu 340	Phe	Ile	Asp	Val	Ser 345	Phe	His	Phe	Tyr	Ala 350	Leu	Ile	
Ala	Ile	Phe 355	Ile	Ala	Ser	Phe	Ile 360	Gly	Ser	Val	Phe	Lys 365	Leu	Ser	Ser	
Leu	Lys 370	Lys	Ala	Cys	Glu	Asn 375	Ala									

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<212> DNA
<213> Helicobacter pylori
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<221> CDS
<222> (1) .. (516)
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1				5					10					15		
ttg	tgc	gct	act	gga	ttg	gat	att	tca	caa	aca	gat	att	ata	gag	cgt	96
Leu	Cys	Ala	Thr	Gly	Leu	Asp	Ile	Ser	Gln	Thr	Asp	Ile	Ile	Glu	Arg	
			20					25					30			
tct	tta	aat	ttc	ctt	tta	ttt	gtg	ggg	att	ttg	tgg	tat	ttt	tcg	gct	144

Ser	Leu	Asn	Phe	Leu	Leu	Phe	Val	Gly	Ile	Leu	Trp	Tyr	Phe	Ser	Ala	
		35					40					45				
aaa	aaa	ctg	cgt	tca	ttt	tta	cgc	tcc	aaa	agt	ctt	gaa	atc	tcc	aaa	192
Lys	Lys	Leu	Arg	Ser	Phe	Leu	Arg	Ser	Lys	Ser	Leu	Glu	Ile	Ser	Lys	
	50					55					60					
cgc	tta	gaa	gag	att	caa	gcc	caa	ctc	aaa	gtg	agt	aaa	gaa	aat	aag	240
Arg	Leu	Glu	Glu	Ile	Gln	Ala	Gln	Leu	Lys	Val	Ser	Lys	Glu	Asn	Lys	
65					70					75					80	
aaa	aaa	ctc	tta	aaa	gaa	tta	gag	caa	gcc	aaa	gaa	aaa	gcg	gaa	ttg	288
Lys	Lys	Leu	Leu	Lys	Glu	Leu	Glu	Gln	Ala	Lys	Glu	Lys	Ala	Glu	Leu	
				85					90					95		
att	gtt	tct	gat	gcg	aat	aaa	gaa	gct	tac	atg	atc	acg	caa	aaa	tac	336
Ile	Val	Ser	Asp	Ala	Asn	Lys	Glu	Ala	Tyr	Met	Ile	Thr	Gln	Lys	Tyr	
			100					105					110			
gaa	ttg	caa	acc	aaa	atg	gat	gtg	gaa	aat	ttg	atc	aaa	aat	tct	aag	384
Glu	Leu	Gln	Thr	Lys	Met	Asp	Val	Glu	Asn	Leu	Ile	Lys	Asn	Ser	Lys	
		115					120					125				
gcg	ttg	atg	gat	tta	gaa	gtt	aaa	aag	atc	aaa	aga	gag	ctg	gtt	gaa	432
Ala	Leu	Met	Asp	Leu	Glu	Val	Lys	Lys	Ile	Lys	Arg	Glu	Leu	Val	Glu	
	130					135					140					
agc	gtt	ttt	aaa	gat	cta	aga	gag	agc	aaa	aaa	gtc	tct	ttc	aat	gcg	480
Ser	Val	Phe	Lys	Asp	Leu	Arg	Glu	Ser	Lys	Lys	Val	Ser	Phe	Asn	Ala	
145					150					155					160	
caa	gat	tgc	gtg	aat	att	ttg	aaa	caa	agg	ctt	taa					516
Gln	Asp	Cys	Val	Asn	Ile	Leu	Lys	Gln	Arg	Leu						
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 <211> 171  
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 <213> Helicobacter pylori

<400> 88

Met	Phe	Val	Val	Lys	Met	Val	Leu	Gly	Phe	Leu	Ile	Leu	Leu	Ser	Pro	
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Leu	Cys	Ala	Thr	Gly	Leu	Asp	Ile	Ser	Gln	Thr	Asp	Ile	Ile	Glu	Arg	
			20					25					30			
Ser	Leu	Asn	Phe	Leu	Leu	Phe	Val	Gly	Ile	Leu	Trp	Tyr	Phe	Ser	Ala	
		35					40					45				

Lys Lys Leu Arg Ser Phe Leu Arg Ser Lys Ser Leu Glu Ile Ser Lys  
50 55 60

Arg Leu Glu Glu Ile Gln Ala Gln Leu Lys Val Ser Lys Glu Asn Lys  
65 70 75 80

Lys Lys Leu Leu Lys Glu Leu Glu Gln Ala Lys Glu Lys Ala Glu Leu  
85 90 95

Ile Val Ser Asp Ala Asn Lys Glu Ala Tyr Met Ile Thr Gln Lys Tyr  
100 105 110

Glu Leu Gln Thr Lys Met Asp Val Glu Asn Leu Ile Lys Asn Ser Lys  
115 120 125

Ala Leu Met Asp Leu Glu Val Lys Lys Ile Lys Arg Glu Leu Val Glu  
130 135 140

Ser Val Phe Lys Asp Leu Arg Glu Ser Lys Lys Val Ser Phe Asn Ala  
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Gln Asp Cys Val Asn Ile Leu Lys Gln Arg Leu  
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ggg gct tta ttg tta ggg cta atc gtg ctt ttt tat ttg gct tat cgc 96  
Gly Ala Leu Leu Leu Gly Leu Ile Val Leu Phe Tyr Leu Ala Tyr Arg  
20 25 30  
cct aag gct gaa gtg ttg caa gga ttt ttg gaa gcc aga gaa tac agc 144

Pro	Lys	Ala	Glu	Val	Leu	Gln	Gly	Phe	Leu	Glu	Ala	Arg	Glu	Tyr	Ser		
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gtg	agt	tcc	aaa	gtc	cct	ggc	cgc	att	gaa	aag	gtg	ttt	gtt	aaa	aaa	192	
Val	Ser	Ser	Lys	Val	Pro	Gly	Arg	Ile	Glu	Lys	Val	Phe	Val	Lys	Lys		
	50					55					60						
ggc	gat	cgc	att	aaa	aag	ggc	gat	ttg	gtt	ttt	agc	att	tct	agc	cct	240	
Gly	Asp	Arg	Ile	Lys	Lys	Gly	Asp	Leu	Val	Phe	Ser	Ile	Ser	Ser	Pro		
65					70					75					80		
gaa	tta	gaa	gcc	aag	ctc	gct	caa	gct	gaa	gcc	ggg	cat	aaa	gcc	gct	288	
Glu	Leu	Glu	Ala	Lys	Leu	Ala	Gln	Ala	Glu	Ala	Gly	His	Lys	Ala	Ala		
				85					90					95			
aaa	gcg	ctt	agc	gat	gaa	gtc	aaa	aga	ggc	tca	aga	gac	gaa	acg	atc	336	
Lys	Ala	Leu	Ser	Asp	Glu	Val	Lys	Arg	Gly	Ser	Arg	Asp	Glu	Thr	Ile		
			100					105					110				
aat	tct	gca	aga	gac	gtt	tgg	caa	gcg	gcc	aaa	tct	caa	gcc	act	tta	384	
Asn	Ser	Ala	Arg	Asp	Val	Trp	Gln	Ala	Ala	Lys	Ser	Gln	Ala	Thr	Leu		
		115					120					125					
gcc	aaa	gag	act	tat	aag	cgc	gtt	caa	gat	ttg	tat	gat	aat	ggc	gtg	432	
Ala	Lys	Glu	Thr	Tyr	Lys	Arg	Val	Gln	Asp	Leu	Tyr	Asp	Asn	Gly	Val		
	130					135					140						
gcg	agc	ttg	caa	aag	cgc	gat	gaa	gcc	tat	gcg	gct	tat	gaa	agc	act	480	
Ala	Ser	Leu	Gln	Lys	Arg	Asp	Glu	Ala	Tyr	Ala	Ala	Tyr	Glu	Ser	Thr		
145					150					155					160		
aaa	tac	aac	gag	agc	gcg	gct	tac	caa	aag	tat	aaa	atg	gct	tta	ggg	528	
Lys	Tyr	Asn	Glu	Ser	Ala	Ala	Tyr	Gln	Lys	Tyr	Lys	Met	Ala	Leu	Gly		
				165					170					175			
ggg	gcg	agc	tct	gaa	agt	aag	att	gcc	gct	aag	gct	aaa	gag	agc	gcg	576	
Gly	Ala	Ser	Ser	Glu	Ser	Lys	Ile	Ala	Ala	Lys	Ala	Lys	Glu	Ser	Ala		
			180					185					190				
gct	tta	ggg	caa	gtg	aat	gaa	gtg	gag	tct	tat	tta	aaa	gat	gtc	aaa	624	
Ala	Leu	Gly	Gln	Val	Asn	Glu	Val	Glu	Ser	Tyr	Leu	Lys	Asp	Val	Lys		
		195					200					205					
gcg	aca	gcc	cca	att	gat	ggg	gaa	gtg	agt	aat	gtg	ctt	tta	agc	ggc	672	
Ala	Thr	Ala	Pro	Ile	Asp	Gly	Glu	Val	Ser	Asn	Val	Leu	Leu	Ser	Gly		
	210					215					220						
ggc	gag	ctt	agc	cct	aag	ggc	ttt	cct	gtg	gtg	ctc	atg	att	gat	tta	720	
Gly	Glu	Leu	Ser	Pro	Lys	Gly	Phe	Pro	Val	Val	Leu	Met	Ile	Asp	Leu		
225					230					235					240		
aag	gat	agt	tgg	tta	aaa	atc	agc	gtg	cct	gaa	aag	tat	ttg	aac	gat	768	
Lys	Asp	Ser	Trp	Leu	Lys	Ile	Ser	Val	Pro	Glu	Lys	Tyr	Leu	Asn	Asp		



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ttt aaa gtg ggt aag gaa ttt gaa ggt tat atc ccg gcg ttg aaa aga				816
Phe Lys Val Gly Lys Glu Phe Glu Gly Tyr Ile Pro Ala Leu Lys Arg				
	260	265	270	
agc gcg aaa ttc agg gtc aaa tat ttg agc gtg atg ggg gat ttt gcg				864
Ser Ala Lys Phe Arg Val Lys Tyr Leu Ser Val Met Gly Asp Phe Ala				
	275	280	285	
act tgg aaa gcg acg aat aat tcc aac act tac gac atg aaa agc tat				912
Thr Trp Lys Ala Thr Asn Asn Ser Asn Thr Tyr Asp Met Lys Ser Tyr				
	290	295	300	
gaa gtg gag gcc ata ccc tta gaa gag ttg gaa aat ttt agg gta ggg				960
Glu Val Glu Ala Ile Pro Leu Glu Glu Leu Glu Asn Phe Arg Val Gly				
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atg agc gtg tta gtt acc att aaa cct taa				990
Met Ser Val Leu Val Thr Ile Lys Pro				
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 <213> Helicobacter pylori

<400> 90

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Pro Lys Ala Glu Val Leu Gln Gly Phe Leu Glu Ala Arg Glu Tyr Ser				
35 40 45				
Val Ser Ser Lys Val Pro Gly Arg Ile Glu Lys Val Phe Val Lys Lys				
50 55 60				
Gly Asp Arg Ile Lys Lys Gly Asp Leu Val Phe Ser Ile Ser Ser Pro				
65 70 75 80				
Glu Leu Glu Ala Lys Leu Ala Gln Ala Glu Ala Gly His Lys Ala Ala				
85 90 95				

Lys Ala Leu Ser Asp Glu Val Lys Arg Gly Ser Arg Asp Glu Thr Ile  
 100 105 110

Asn Ser Ala Arg Asp Val Trp Gln Ala Ala Lys Ser Gln Ala Thr Leu  
 115 120 125

Ala Lys Glu Thr Tyr Lys Arg Val Gln Asp Leu Tyr Asp Asn Gly Val  
 130 135 140

Ala Ser Leu Gln Lys Arg Asp Glu Ala Tyr Ala Ala Tyr Glu Ser Thr  
 145 150 155 160

Lys Tyr Asn Glu Ser Ala Ala Tyr Gln Lys Tyr Lys Met Ala Leu Gly  
 165 170 175

Gly Ala Ser Ser Glu Ser Lys Ile Ala Ala Lys Ala Lys Glu Ser Ala  
 180 185 190

Ala Leu Gly Gln Val Asn Glu Val Glu Ser Tyr Leu Lys Asp Val Lys  
 195 200 205

Ala Thr Ala Pro Ile Asp Gly Glu Val Ser Asn Val Leu Leu Ser Gly  
 210 215 220

Gly Glu Leu Ser Pro Lys Gly Phe Pro Val Val Leu Met Ile Asp Leu  
 225 230 235 240

Lys Asp Ser Trp Leu Lys Ile Ser Val Pro Glu Lys Tyr Leu Asn Asp  
 245 250 255

Phe Lys Val Gly Lys Glu Phe Glu Gly Tyr Ile Pro Ala Leu Lys Arg  
 260 265 270

Ser Ala Lys Phe Arg Val Lys Tyr Leu Ser Val Met Gly Asp Phe Ala  
 275 280 285

Thr Trp Lys Ala Thr Asn Asn Ser Asn Thr Tyr Asp Met Lys Ser Tyr  
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Glu Val Glu Ala Ile Pro Leu Glu Glu Leu Glu Asn Phe Arg Val Gly  
 305 310 315 320

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Met	Val	Phe	Asp	Arg	Thr	Ile	Ser	Val	Arg	Glu	Lys	Lys	Ala	Ala	Lys		
				5					10					15			
acg	ctt	ggg	att	att	ggg	atc	gtc	ttt	ttt	att	ttg	ttt	ggc	atc	gtg	96	
Thr	Leu	Gly	Ile	Ile	Gly	Ile	Val	Phe	Phe	Ile	Leu	Phe	Gly	Ile	Val		
				20					25					30			
ata	agc	ggg	gtg	gct	ttt	caa	aaa	gag	tgg	gtg	caa	caa	ttg	gat	tta	144	
Ile	Ser	Gly	Val	Ala	Phe	Gln	Lys	Glu	Trp	Val	Gln	Gln	Leu	Asp	Leu		
				35					40					45			
ttt	ttt	ata	gac	ttg	atc	cgc	aac	cct	gcc	ccc	att	caa	aaa	agc	gcg	192	
Phe	Phe	Ile	Asp	Leu	Ile	Arg	Asn	Pro	Ala	Pro	Ile	Gln	Lys	Ser	Ala		
		50					55					60					
tgg	ctt	tct	ttc	gtg	ttt	ttt	agc	act	tgg	ttt	gca	caa	agc	aag	ctc	240	
Trp	Leu	Ser	Phe	Val	Phe	Phe	Ser	Thr	Trp	Phe	Ala	Gln	Ser	Lys	Leu		
		65					70					75					80
acc	act	cct	ata	gcc	tta	ctc	att	ggc	ttg	tgg	ttt	ggg	ttt	caa	aaa	288	
Thr	Thr	Pro	Ile	Ala	Leu	Leu	Ile	Gly	Leu	Trp	Phe	Gly	Phe	Gln	Lys		
				85					90					95			
cgc	atc	gct	ttg	ggg	gtg	tgg	ttt	ttc	ttt	agc	atc	tta	tta	ggc	gaa	336	
Arg	Ile	Ala	Leu	Gly	Val	Trp	Phe	Phe	Phe	Ser	Ile	Leu	Leu	Gly	Glu		
			100					105					110				
ttc	acc	tta	aaa	tcc	ctt	aag	ctt	tta	gtg	gcg	cgc	cca	cgg	cct	gta	384	
Phe	Thr	Leu	Lys	Ser	Leu	Lys	Leu	Leu	Val	Ala	Arg	Pro	Arg	Pro	Val		
			115					120					125				
acc	aat	ggc	gaa	ttg	gtt	ttc	gcg	cat	ggc	ttt	agt	ttc	cct	agc	ggg	432	
Thr	Asn	Gly	Glu	Leu	Val	Phe	Ala	His	Gly	Phe	Ser	Phe	Pro	Ser	Gly		
		130					135					140					
cat	gct	ttg	gct	tca	gcg	ctt	ttt	tac	ggc	tct	ttg	gcg	ttg	ttg	tta	480	
His	Ala	Leu	Ala	Ser	Ala	Leu	Phe	Tyr	Gly	Ser	Leu	Ala	Leu	Leu	Leu		

145	150	155	160	
tgc tat tct aac gcc aac aat cgc att aaa acg att att gct gtg gtt				528
Cys Tyr Ser Asn Ala Asn Asn Arg Ile Lys Thr Ile Ile Ala Val Val	165	170	175	
ttg ctt ttt tgg att ttt tta atg gcg tat gat agg gtt tat tta ggg				576
Leu Leu Phe Trp Ile Phe Leu Met Ala Tyr Asp Arg Val Tyr Leu Gly	180	185	190	
gtg cat tac cct agc gat gtt tta gga ggg ttt tta tta ggg att gct				624
Val His Tyr Pro Ser Asp Val Leu Gly Gly Phe Leu Leu Gly Ile Ala	195	200	205	
tggtcg tgc tgc tct tta gcg ctt tat tta ggg ttt ttg aaa cgc cct				672
Trp Ser Cys Cys Ser Leu Ala Leu Tyr Leu Gly Phe Leu Lys Arg Pro	210	215	220	
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Tyr Asn Gln				
225				

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 <213> Helicobacter pylori

<400> 92

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20	25	30		
Ile Ser Gly Val Ala Phe Gln Lys Glu Trp Val Gln Gln Leu Asp Leu				
35	40	45		
Phe Phe Ile Asp Leu Ile Arg Asn Pro Ala Pro Ile Gln Lys Ser Ala				
50	55	60		
Trp Leu Ser Phe Val Phe Phe Ser Thr Trp Phe Ala Gln Ser Lys Leu				
65	70	75	80	
Thr Thr Pro Ile Ala Leu Leu Ile Gly Leu Trp Phe Gly Phe Gln Lys				
85	90	95		

Arg Ile Ala Leu Gly Val Trp Phe Phe Phe Ser Ile Leu Leu Gly Glu  
100 105 110

Thr Asn Gly Glu Leu Val Phe Ala His Gly Phe Ser Phe Pro Ser Gly  
130 135 140

His Ala Leu Ala Ser Ala Leu Phe Tyr Gly Ser Leu Ala Leu Leu Leu  
145 150 155 160

Cys Tyr Ser Asn Ala Asn Asn Arg Ile Lys Thr Ile Ile Ala Val Val  
165 170 175

Leu Leu Phe Trp Ile Phe Leu Met Ala Tyr Asp Arg Val Tyr Leu Gly  
180 185 190

Val His Tyr Pro Ser Asp Val Leu Gly Gly Phe Leu Leu Gly Ile Ala  
195 200 205

Trp Ser Cys Cys Ser Leu Ala Leu Tyr Leu Gly Phe Leu Lys Arg Pro  
210 215 220

Tyr Asn Gln  
225

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aat gcg cta cta gct atg gat ggt aat ggc gtg ttt ata ggg gcg ggt      96
Asn Ala Leu Leu Ala Met Asp Gly Asn Gly Val Phe Ile Gly Ala Gly
          20          25          30

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		35					40					45				
caa	gcc	act	agc	gct	act	atc	aag	ggg	ttt	gat	gcg	ctt	tta	ggg	tat	192
Gln	Ala	Thr	Ser	Ala	Thr	Ile	Lys	Gly	Phe	Asp	Ala	Leu	Leu	Gly	Tyr	
	50					55					60					
cag	ttt	ttc	ttt	ggg	aaa	tac	ttt	ggc	tta	cgc	ctt	tat	ggg	ttt	ttt	240
Gln	Phe	Phe	Phe	Gly	Lys	Tyr	Phe	Gly	Leu	Arg	Leu	Tyr	Gly	Phe	Phe	
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gac	tac	gcc	cat	gcc	aat	tct	att	agg	ctt	aaa	aac	cct	aat	tat	aac	288
Asp	Tyr	Ala	His	Ala	Asn	Ser	Ile	Arg	Leu	Lys	Asn	Pro	Asn	Tyr	Asn	
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aac	gaa	gtg	gtg	caa	ttg	gcg	ggt	caa	gtt	ctt	ggg	aaa	caa	gaa	atc	336
Asn	Glu	Val	Val	Gln	Leu	Ala	Gly	Gln	Val	Leu	Gly	Lys	Gln	Glu	Ile	
			100					105					110			
aat	cgt	tta	acg	agc	ctt	gct	gat	ccc	aaa	acc	ttt	gag	cca	aac	atg	384
Asn	Arg	Leu	Thr	Ser	Leu	Ala	Asp	Pro	Lys	Thr	Phe	Glu	Pro	Asn	Met	
		115					120					125				
ctc	act	tat	ggg	ggg	gct	atg	gat	gtg	atg	gtt	aat	gtc	att	aat	aat	432
Leu	Thr	Tyr	Gly	Gly	Ala	Met	Asp	Val	Met	Val	Asn	Val	Ile	Asn	Asn	
		130				135					140					
ggc	atc	atg	agt	ttg	ggg	gct	ttt	ggt	ggg	gtg	caa	tta	gcc	ggc	aat	480
Gly	Ile	Met	Ser	Leu	Gly	Ala	Phe	Gly	Gly	Val	Gln	Leu	Ala	Gly	Asn	
145					150					155					160	
tca	tgg	ctt	atg	gcg	acg	ccg	agc	ttt	gag	ggc	att	tta	gtg	gag	caa	528
Ser	Trp	Leu	Met	Ala	Thr	Pro	Ser	Phe	Glu	Gly	Ile	Leu	Val	Glu	Gln	
				165					170					175		
gct	ttg	gtg	agc	aag	aaa	gcc	act	tct	ttc	caa	ttt	tta	ttc	aat	gtg	576
Ala	Leu	Val	Ser	Lys	Lys	Ala	Thr	Ser	Phe	Gln	Phe	Leu	Phe	Asn	Val	
			180					185					190			
ggg	gct	cgc	tta	agg	atc	tta	aag	cat	tct	agc	att	gaa	gcg	ggc	gtg	624
Gly	Ala	Arg	Leu	Arg	Ile	Leu	Lys	His	Ser	Ser	Ile	Glu	Ala	Gly	Val	
		195					200					205				
aag	ttc	ccc	atg	tta	aag	aaa	aac	ccc	tat	atc	act	gca	aaa	aac	ttg	672
Lys	Phe	Pro	Met	Leu	Lys	Lys	Asn	Pro	Tyr	Ile	Thr	Ala	Lys	Asn	Leu	
	210					215					220					
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Asp	Ile	Gly	Phe	Arg	Arg	Val	Tyr	Ser	Trp	Tyr	Val	Asn	Tyr	Val	Phe	
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act	ttc	tag														729
Thr	Phe															

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 <212> PRT  
 <213> Helicobacter pylori

<400> 94

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 20 25 30

Tyr Leu Gln Gly Gln Ala Gln Met His Ala Asp Ile Asn Ser Gln Lys  
 35 40 45

Gln Ala Thr Ser Ala Thr Ile Lys Gly Phe Asp Ala Leu Leu Gly Tyr  
 50 55 60

Gln Phe Phe Phe Gly Lys Tyr Phe Gly Leu Arg Leu Tyr Gly Phe Phe  
 65 70 75 80

Asp Tyr Ala His Ala Asn Ser Ile Arg Leu Lys Asn Pro Asn Tyr Asn  
 85 90 95

Asn Glu Val Val Gln Leu Ala Gly Gln Val Leu Gly Lys Gln Glu Ile  
 100 105 110

Asn Arg Leu Thr Ser Leu Ala Asp Pro Lys Thr Phe Glu Pro Asn Met  
 115 120 125

Leu Thr Tyr Gly Gly Ala Met Asp Val Met Val Asn Val Ile Asn Asn  
 130 135 140

Gly Ile Met Ser Leu Gly Ala Phe Gly Gly Val Gln Leu Ala Gly Asn  
 145 150 155 160

Ser Trp Leu Met Ala Thr Pro Ser Phe Glu Gly Ile Leu Val Glu Gln  
 165 170 175

Ala Leu Val Ser Lys Lys Ala Thr Ser Phe Gln Phe Leu Phe Asn Val  
180 185 190

Gly Ala Arg Leu Arg Ile Leu Lys His Ser Ser Ile Glu Ala Gly Val  
195 200 205

Lys Phe Pro Met Leu Lys Lys Asn Pro Tyr Ile Thr Ala Lys Asn Leu  
210 215 220

Asp Ile Gly Phe Arg Arg Val Tyr Ser Trp Tyr Val Asn Tyr Val Phe  
225 230 235 240

Thr Phe

<210> 95  
<211> 975  
<212> DNA  
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<220>  
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<222> (1)..(975)

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1 5 10 15  
gac cct gtg gat cat tct aac agg aat ttt ttc ttt tct ctc att ctg 96  
Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Phe Ser Leu Ile Leu  
20 25 30  
tct gta ttg tta cac tgg ttg att tat ttt tta ttt gaa cac aga gaa 144  
Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu His Arg Glu  
35 40 45  
gat ttt ttt cct tca aaa ccc aag ctt gtt aaa tta aat cct gaa aat 192  
Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn Pro Glu Asn  
50 55 60  
tta ttg gtt tta aaa aga ggc cat tcg caa gat ccc agt aaa aac acc 240  
Leu Leu Val Leu Lys Arg Gly His Ser Gln Asp Pro Ser Lys Asn Thr  
65 70 75 80  
cag ggc gct cct aaa ccc acg ctg gct ggc ccc caa aaa cct cca acg 288  
Gln Gly Ala Pro Lys Pro Thr Leu Ala Gly Pro Gln Lys Pro Pro Thr  
85 90 95



cct	ccc	aca	ccc	cca	act	ccg	cca	acc	ccg	cca	acc	ccg	cca	aaa	cct	336
Pro	Pro	Thr	Pro	Pro	Thr	Pro	Pro	Thr	Pro	Pro	Thr	Pro	Pro	Lys	Pro	
			100					105						110		
ata	gaa	aag	cct	aag	cct	gag	cct	aaa	cca	aaa	ccc	aaa	cct	gaa	ccc	384
Ile	Glu	Lys	Pro	Lys	Pro	Glu	Pro	Lys	Pro	Lys	Pro	Lys	Pro	Glu	Pro	
		115					120					125				
aaa	aag	ccc	aat	cat	aaa	cac	aag	gct	ctt	aaa	aaa	gtg	gaa	aaa	gtg	432
Lys	Lys	Pro	Asn	His	Lys	His	Lys	Ala	Leu	Lys	Lys	Val	Glu	Lys	Val	
		130				135						140				
gaa	gag	aaa	aaa	gta	gta	gag	gag	aaa	aaa	gaa	gag	aaa	aaa	atc	gta	480
Glu	Glu	Lys	Lys	Val	Val	Glu	Glu	Lys	Lys	Glu	Glu	Lys	Lys	Ile	Val	
145					150					155					160	
gag	cag	aaa	gta	gaa	caa	aaa	gta	gag	cag	aaa	aaa	ata	gaa	gag	aaa	528
Glu	Gln	Lys	Val	Glu	Gln	Lys	Val	Glu	Gln	Lys	Lys	Ile	Glu	Glu	Lys	
			165						170						175	
aaa	cct	gtc	aaa	aaa	gaa	ttt	gac	cct	aac	cag	ctt	tct	ttc	ttg	cct	576
Lys	Pro	Val	Lys	Lys	Glu	Phe	Asp	Pro	Asn	Gln	Leu	Ser	Phe	Leu	Pro	
			180					185					190			
aaa	gaa	gtt	gcg	cca	ccc	aga	caa	gaa	aat	aat	aaa	ggc	ttg	gat	aac	624
Lys	Glu	Val	Ala	Pro	Pro	Arg	Gln	Glu	Asn	Asn	Lys	Gly	Leu	Asp	Asn	
		195					200					205				
caa	acc	aga	agg	gat	att	gat	gaa	ttg	tat	ggc	gaa	gaa	ttt	ggg	gat	672
Gln	Thr	Arg	Arg	Asp	Ile	Asp	Glu	Leu	Tyr	Gly	Glu	Glu	Phe	Gly	Asp	
	210					215					220					
tta	ggc	aca	gcc	gaa	aaa	gat	ttc	atc	agg	aat	aat	tta	agg	gat	att	720
Leu	Gly	Thr	Ala	Glu	Lys	Asp	Phe	Ile	Arg	Asn	Asn	Leu	Arg	Asp	Ile	
225					230					235					240	
ggg	cgc	atc	acg	caa	aaa	tat	tta	gaa	tac	cct	caa	gta	gcg	gct	tat	768
Gly	Arg	Ile	Thr	Gln	Lys	Tyr	Leu	Glu	Tyr	Pro	Gln	Val	Ala	Ala	Tyr	
			245					250						255		
tta	ggg	cag	gac	ggg	acg	aat	gcg	gta	gag	ttt	tac	ttg	cac	cct	aat	816
Leu	Gly	Gln	Asp	Gly	Thr	Asn	Ala	Val	Glu	Phe	Tyr	Leu	His	Pro	Asn	
			260					265					270			
ggc	gat	att	acc	gat	ctt	aaa	atc	atc	att	ggc	tct	gaa	tac	aaa	atg	864
Gly	Asp	Ile	Thr	Asp	Leu	Lys	Ile	Ile	Ile	Gly	Ser	Glu	Tyr	Lys	Met	
		275					280					285				
ctt	gat	gac	aac	acc	tta	aag	acc	att	cag	atc	gct	tat	aag	gat	tac	912
Leu	Asp	Asp	Asn	Thr	Leu	Lys	Thr	Ile	Gln	Ile	Ala	Tyr	Lys	Asp	Tyr	
	290					295					300					
cca	cgc	ccc	aaa	act	aaa	acc	ctc	att	cgc	atc	aga	gtg	cgt	tat	tac	960
Pro	Arg	Pro	Lys	Thr	Lys	Thr	Leu	Ile	Arg	Ile	Arg	Val	Arg	Tyr	Tyr	
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 Leu Gly Gly Asn

975

<210> 96  
 <211> 324  
 <212> PRT  
 <213> Helicobacter pylori

<400> 96

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Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Phe Ser Leu Ile Leu  
 20 25 30

Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu His Arg Glu  
 35 40 45

Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn Pro Glu Asn  
 50 55 60

Leu Leu Val Leu Lys Arg Gly His Ser Gln Asp Pro Ser Lys Asn Thr  
 65 70 75 80

Gln Gly Ala Pro Lys Pro Thr Leu Ala Gly Pro Gln Lys Pro Pro Thr  
 85 90 95

Pro Pro Thr Pro Pro Thr Pro Pro Thr Pro Pro Thr Pro Pro Lys Pro  
 100 105 110

Ile Glu Lys Pro Lys Pro Glu Pro Lys Pro Lys Pro Lys Pro Glu Pro  
 115 120 125

Lys Lys Pro Asn His Lys His Lys Ala Leu Lys Lys Val Glu Lys Val  
 130 135 140

Glu Glu Lys Lys Val Val Glu Glu Lys Lys Glu Glu Lys Lys Ile Val  
 145 150 155 160

Glu Gln Lys Val Glu Gln Lys Val Glu Gln Lys Lys Ile Glu Glu Lys  
 165 170 175

Lys Pro Val Lys Lys Glu Phe Asp Pro Asn Gln Leu Ser Phe Leu Pro  
180 185 190

Lys Glu Val Ala Pro Pro Arg Gln Glu Asn Asn Lys Gly Leu Asp Asn  
195 200 205

Gln Thr Arg Arg Asp Ile Asp Glu Leu Tyr Gly Glu Glu Phe Gly Asp  
210 215 220

Leu Gly Thr Ala Glu Lys Asp Phe Ile Arg Asn Asn Leu Arg Asp Ile  
225 230 235 240

Gly Arg Ile Thr Gln Lys Tyr Leu Glu Tyr Pro Gln Val Ala Ala Tyr  
245 250 255

Leu Gly Gln Asp Gly Thr Asn Ala Val Glu Phe Tyr Leu His Pro Asn  
260 265 270

Gly Asp Ile Thr Asp Leu Lys Ile Ile Ile Gly Ser Glu Tyr Lys Met  
275 280 285

Leu Asp Asp Asn Thr Leu Lys Thr Ile Gln Ile Ala Tyr Lys Asp Tyr  
290 295 300

Pro Arg Pro Lys Thr Lys Thr Leu Ile Arg Ile Arg Val Arg Tyr Tyr  
305 310 315 320

Leu Gly Gly Asn

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<211> 1290  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(1290)

<400> 97  
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gtt tca act ttt tgt gcg ata agc ttg aac gct aaa agc tat ctg ttt	Val Ser Thr Phe Cys Ala Ile Ser Leu Asn Ala Lys Ser Tyr Leu Phe																96
	20				25				30								
tcc cct ttg ccc cca gca cac cag caa atc att aag aca gag cct tgc	Ser Pro Leu Pro Pro Ala His Gln Gln Ile Ile Lys Thr Glu Pro Cys																144
	35				40				45								
tct ttg gaa tgc ttg aaa gac ttg atg ctg caa aat caa atc ttt tct	Ser Leu Glu Cys Leu Lys Asp Leu Met Leu Gln Asn Gln Ile Phe Ser																192
	50				55				60								
ttt gtg tct caa tac gat aac aac aac caa gat gag agc ctt aaa act	Phe Val Ser Gln Tyr Asp Asn Asn Asn Gln Asp Glu Ser Leu Lys Thr																240
	65				70				75				80				
tat tat cat gac ata ctc aat aaa ctc aac ccc gta ttc atc gct tct	Tyr Tyr His Asp Ile Leu Asn Lys Leu Asn Pro Val Phe Ile Ala Ser																288
	85				90								95				
caa act cca gct aaa gaa agc tat gag cct aag att gaa tta gcg gtt	Gln Thr Pro Ala Lys Glu Ser Tyr Glu Pro Lys Ile Glu Leu Ala Val																336
	100				105				110								
tta ctg cct aaa aag gtg gtg ggg cgt tat gcg att tcg gtg atg aac	Leu Leu Pro Lys Lys Val Val Gly Arg Tyr Ala Ile Ser Val Met Asn																384
	115				120				125								
acc ctt tta gcg tat ttg aac acc aga aac aac gat ttc aat atc caa	Thr Leu Leu Ala Tyr Leu Asn Thr Arg Asn Asn Asp Phe Asn Ile Gln																432
	130				135				140								
gtc ttt gac agc gat gaa gaa agc cct gaa aaa tta gag caa acc tat	Val Phe Asp Ser Asp Glu Glu Ser Pro Glu Lys Leu Glu Gln Thr Tyr																480
	145				150				155				160				
aaa gaa att gaa aaa gaa aaa ttc cct ttt gtg ata gcc tta ttg act	Lys Glu Ile Glu Lys Glu Lys Phe Pro Phe Val Ile Ala Leu Leu Thr																528
	165				170				175								
aaa gag ggc gtg gaa aat ttg ctc caa aac acc acc att agc acc cct	Lys Glu Gly Val Glu Asn Leu Leu Gln Asn Thr Thr Ile Ser Thr Pro																576
	180				185				190								
act tat gtg cct acg gtg aat aga gcg caa ttg gaa aat caa act gaa	Thr Tyr Val Pro Thr Val Asn Arg Ala Gln Leu Glu Asn Gln Thr Glu																624
	195				200				205								
cgt tct ttg agc gag cgc ttg tat ttt ggg ggg att gat tat aaa gag	Arg Ser Leu Ser Glu Arg Leu Tyr Phe Gly Gly Ile Asp Tyr Lys Glu																672
	210				215				220								
caa tta agc atg ctc acg gct ttc att aac cct aat tcg ccc gtg att																	720

Gln	Leu	Ser	Met	Leu	Thr	Ala	Phe	Ile	Asn	Pro	Asn	Ser	Pro	Val	Ile		
225					230					235					240		
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Glu	Tyr	Asp	Asp	Asp	Gly	Leu	Ile	Gly	Glu	Arg	Leu	Arg	Gln	Ile	Thr		
				245					250					255			
gag	tct	tta	agc	att	gaa	gtc	aaa	cac	caa	gaa	aat	att	tct	tac	aag		816
Glu	Ser	Leu	Ser	Ile	Glu	Val	Lys	His	Gln	Glu	Asn	Ile	Ser	Tyr	Lys		
			260					265					270				
caa	gcc	acg	agt	ttt	tct	aaa	aat	ttt	aga	aaa	aac	gat	gcg	ttt	ttt		864
Gln	Ala	Thr	Ser	Phe	Ser	Lys	Asn	Phe	Arg	Lys	Asn	Asp	Ala	Phe	Phe		
		275					280					285					
aaa	aat	tct	att	ttg	att	tta	aac	acc	cct	acc	act	aaa	agc	ggc	ctt		912
Lys	Asn	Ser	Ile	Leu	Ile	Leu	Asn	Thr	Pro	Thr	Thr	Lys	Ser	Gly	Leu		
	290					295					300						
att	ctt	tct	caa	ata	ggg	ctt	tta	gaa	tac	aag	cct	ctt	aaa	atc	ctt		960
Ile	Leu	Ser	Gln	Ile	Gly	Leu	Leu	Glu	Tyr	Lys	Pro	Leu	Lys	Ile	Leu		
305					310					315					320		
tcc	aca	caa	atc	aat	ttc	aac	ccc	tct	cta	ctc	tta	ctc	acc	caa	cct		1008
Ser	Thr	Gln	Ile	Asn	Phe	Asn	Pro	Ser	Leu	Leu	Leu	Leu	Thr	Gln	Pro		
				325					330					335			
aaa	gac	aga	aag	gat	tta	ttc	att	gtc	aat	gcc	ttg	caa	aat	agc	gat		1056
Lys	Asp	Arg	Lys	Asp	Leu	Phe	Ile	Val	Asn	Ala	Leu	Gln	Asn	Ser	Asp		
			340					345					350				
gaa	acg	ctt	ata	gaa	tac	gcc	tcc	tta	ttg	gag	agc	gat	tta	agg	cat		1104
Glu	Thr	Leu	Ile	Glu	Tyr	Ala	Ser	Leu	Leu	Glu	Ser	Asp	Leu	Arg	His		
		355					360					365					
gat	tgg	gtg	aat	tat	tcc	agc	gca	atc	ggg	cta	gag	gtg	ttt	tta	aac		1152
Asp	Trp	Val	Asn	Tyr	Ser	Ser	Ala	Ile	Gly	Leu	Glu	Val	Phe	Leu	Asn		
	370					375					380						
acg	cta	gat	ccg	cat	ttt	aaa	aaa	tct	ttt	caa	gag	aat	tta	gaa	gac		1200
Thr	Leu	Asp	Pro	His	Phe	Lys	Lys	Ser	Phe	Gln	Glu	Asn	Leu	Glu	Asp		
385					390					395					400		
aat	cag	gtc	cgt	tac	cac	aat	caa	att	tat	cag	gct	tta	ggg	tat	tct		1248
Asn	Gln	Val	Arg	Tyr	His	Asn	Gln	Ile	Tyr	Gln	Ala	Leu	Gly	Tyr	Ser		
				405					410					415			
ttt	gag	cca	ata	aaa	aat	gaa	agc	gga	aca	aaa	aaa	gaa	taa				1290
Phe	Glu	Pro	Ile	Lys	Asn	Glu	Ser	Gly	Thr	Lys	Lys	Glu					
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<213> Helicobacter pylori

<400> 98

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Val Ser Thr Phe Cys Ala Ile Ser Leu Asn Ala Lys Ser Tyr Leu Phe  
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Ser Pro Leu Pro Pro Ala His Gln Gln Ile Ile Lys Thr Glu Pro Cys  
35 40 45

Ser Leu Glu Cys Leu Lys Asp Leu Met Leu Gln Asn Gln Ile Phe Ser  
50 55 60

Phe Val Ser Gln Tyr Asp Asn Asn Asn Gln Asp Glu Ser Leu Lys Thr  
65 70 75 80

Tyr Tyr His Asp Ile Leu Asn Lys Leu Asn Pro Val Phe Ile Ala Ser  
85 90 95

Gln Thr Pro Ala Lys Glu Ser Tyr Glu Pro Lys Ile Glu Leu Ala Val  
100 105 110

Leu Leu Pro Lys Lys Val Val Gly Arg Tyr Ala Ile Ser Val Met Asn  
115 120 125

Thr Leu Leu Ala Tyr Leu Asn Thr Arg Asn Asn Asp Phe Asn Ile Gln  
130 135 140

Val Phe Asp Ser Asp Glu Glu Ser Pro Glu Lys Leu Glu Gln Thr Tyr  
145 150 155 160

Lys Glu Ile Glu Lys Glu Lys Phe Pro Phe Val Ile Ala Leu Leu Thr  
165 170 175

Lys Glu Gly Val Glu Asn Leu Leu Gln Asn Thr Thr Ile Ser Thr Pro  
180 185 190

Thr Tyr Val Pro Thr Val Asn Arg Ala Gln Leu Glu Asn Gln Thr Glu  
195 200 205

Arg Ser Leu Ser Glu Arg Leu Tyr Phe Gly Gly Ile Asp Tyr Lys Glu  
 210 215 220

Gln Leu Ser Met Leu Thr Ala Phe Ile Asn Pro Asn Ser Pro Val Ile  
 225 230 235 240

Glu Tyr Asp Asp Asp Gly Leu Ile Gly Glu Arg Leu Arg Gln Ile Thr  
 245 250 255

Glu Ser Leu Ser Ile Glu Val Lys His Gln Glu Asn Ile Ser Tyr Lys  
 260 265 270

Gln Ala Thr Ser Phe Ser Lys Asn Phe Arg Lys Asn Asp Ala Phe Phe  
 275 280 285

Lys Asn Ser Ile Leu Ile Leu Asn Thr Pro Thr Thr Lys Ser Gly Leu  
 290 295 300

Ile Leu Ser Gln Ile Gly Leu Leu Glu Tyr Lys Pro Leu Lys Ile Leu  
 305 310 315 320

Ser Thr Gln Ile Asn Phe Asn Pro Ser Leu Leu Leu Leu Thr Gln Pro  
 325 330 335

Lys Asp Arg Lys Asp Leu Phe Ile Val Asn Ala Leu Gln Asn Ser Asp  
 340 345 350

Glu Thr Leu Ile Glu Tyr Ala Ser Leu Leu Glu Ser Asp Leu Arg His  
 355 360 365

Asp Trp Val Asn Tyr Ser Ser Ala Ile Gly Leu Glu Val Phe Leu Asn  
 370 375 380

Thr Leu Asp Pro His Phe Lys Lys Ser Phe Gln Glu Asn Leu Glu Asp  
 385 390 395 400

Asn Gln Val Arg Tyr His Asn Gln Ile Tyr Gln Ala Leu Gly Tyr Ser  
 405 410 415

Phe Glu Pro Ile Lys Asn Glu Ser Gly Thr Lys Lys Glu

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 <211> 1644  
 <212> DNA  
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<220>  
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 <222> (1)..(1644)

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 tct ttc ttg ttt atc gct ctt tat agc tat ttt ttc caa aaa cca aac 96  
 Ser Phe Leu Phe Ile Ala Leu Tyr Ser Tyr Phe Phe Gln Lys Pro Asn  
 20 25 30  
 aaa aca aca acc caa acc aca aag caa gaa aca acc aac aac cat aca 144  
 Lys Thr Thr Thr Gln Thr Thr Lys Gln Glu Thr Thr Asn Asn His Thr  
 35 40 45  
 gca aca agt cct aac gcg ccc aac gcc caa cat ttt agc acc act caa 192  
 Ala Thr Ser Pro Asn Ala Pro Asn Ala Gln His Phe Ser Thr Thr Gln  
 50 55 60  
 aca acc ccc caa gag aat ttg cta agc acg att tct ttt gag cat gcc 240  
 Thr Thr Pro Gln Glu Asn Leu Leu Ser Thr Ile Ser Phe Glu His Ala  
 65 70 75 80  
 agg att gaa att gat tct tta ggg cgc atc aaa cag gtt tat ctc aag 288  
 Arg Ile Glu Ile Asp Ser Leu Gly Arg Ile Lys Gln Val Tyr Leu Lys  
 85 90 95  
 gat aaa aag tat cta acc cct aaa caa aag ggc ttt tta gag cat gtg 336  
 Asp Lys Lys Tyr Leu Thr Pro Lys Gln Lys Gly Phe Leu Glu His Val  
 100 105 110  
 ggc cat ctt ttt agc tcc aaa gaa aac gcg caa ccc ccc cta aaa gag 384  
 Gly His Leu Phe Ser Ser Lys Glu Asn Ala Gln Pro Pro Leu Lys Glu  
 115 120 125  
 ctc ccc ctt tta gca gcc gat aaa ctc aag cct tta gaa gtg cgt ttt 432  
 Leu Pro Leu Leu Ala Ala Asp Lys Leu Lys Pro Leu Glu Val Arg Phe  
 130 135 140  
 tta gac cct acg ctc aat aac aaa gcg ttc aac acc cct tat agc gct 480  
 Leu Asp Pro Thr Leu Asn Asn Lys Ala Phe Asn Thr Pro Tyr Ser Ala  
 145 150 155 160  
 tca aaa acc act ctt ggg cct aac gaa cag ctt gtt tta acc caa gat 528



Ser	Lys	Thr	Thr	Leu	Gly	Pro	Asn	Glu	Gln	Leu	Val	Leu	Thr	Gln	Asp	
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Leu	Gly	Thr	Leu	Ser	Ile	Ile	Lys	Thr	Leu	Thr	Phe	Tyr	Asp	Asp	Leu	
			180					185					190			
cat	tat	gat	tta	aaa	atc	gca	ttc	aaa	tcg	ccc	aat	aac	ctt	atc	cct	624
His	Tyr	Asp	Leu	Lys	Ile	Ala	Phe	Lys	Ser	Pro	Asn	Asn	Leu	Ile	Pro	
		195				200						205				
agc	tat	gtg	atc	acc	aat	ggg	tac	agg	ccg	gtg	gct	gat	ttg	gac	agc	672
Ser	Tyr	Val	Ile	Thr	Asn	Gly	Tyr	Arg	Pro	Val	Ala	Asp	Leu	Asp	Ser	
	210					215					220					
tac	acc	ttt	tca	ggc	gtg	ctt	tta	gaa	aat	agc	gac	aaa	aaa	att	gaa	720
Tyr	Thr	Phe	Ser	Gly	Val	Leu	Leu	Glu	Asn	Ser	Asp	Lys	Lys	Ile	Glu	
225				230						235					240	
aaa	att	gaa	gat	aaa	gac	gct	aaa	gaa	atc	aaa	cgc	ttt	tct	aac	acc	768
Lys	Ile	Glu	Asp	Lys	Asp	Ala	Lys	Glu	Ile	Lys	Arg	Phe	Ser	Asn	Thr	
				245					250					255		
ctc	ttt	tta	tcc	agc	gtg	gat	agg	tat	ttc	acc	acc	ttg	ctt	ttc	act	816
Leu	Phe	Leu	Ser	Ser	Val	Asp	Arg	Tyr	Phe	Thr	Thr	Leu	Leu	Phe	Thr	
			260					265					270			
aaa	gat	cct	caa	ggg	ttt	gaa	gcc	tta	att	gat	tca	gaa	atc	ggc	act	864
Lys	Asp	Pro	Gln	Gly	Phe	Glu	Ala	Leu	Ile	Asp	Ser	Glu	Ile	Gly	Thr	
		275					280					285				
aaa	aac	ccc	tta	ggg	ttc	att	tcc	ctt	aaa	aat	gaa	gcg	aat	ttg	cat	912
Lys	Asn	Pro	Leu	Gly	Phe	Ile	Ser	Leu	Lys	Asn	Glu	Ala	Asn	Leu	His	
	290					295					300					
ggc	tat	att	ggc	cct	aag	gat	tac	cgc	tct	ttg	aaa	gcg	att	tca	ccc	960
Gly	Tyr	Ile	Gly	Pro	Lys	Asp	Tyr	Arg	Ser	Leu	Lys	Ala	Ile	Ser	Pro	
305					310					315					320	
atg	ctc	acc	gat	gtg	ata	gag	tat	ggc	tta	atc	act	ttc	ttt	gca	aaa	1008
Met	Leu	Thr	Asp	Val	Ile	Glu	Tyr	Gly	Leu	Ile	Thr	Phe	Phe	Ala	Lys	
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Gly	Val	Phe	Val	Leu	Leu	Asp	Tyr	Leu	Tyr	Gln	Phe	Val	Gly	Asn	Trp	
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Gly	Trp	Ala	Ile	Ile	Leu	Leu	Thr	Ile	Ile	Val	Arg	Ile	Ile	Leu	Tyr	
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cct	tta	agc	tat	aag	ggc	atg	gtg	agc	atg	caa	aag	ctc	aaa	gaa	tta	1152
Pro	Leu	Ser	Tyr	Lys	Gly	Met	Val	Ser	Met	Gln	Lys	Leu	Lys	Glu	Leu	
	370					375					380					

gcc cct aaa atg aaa gaa ctc caa gaa aaa tac aag ggc gaa ccc caa	1200
Ala Pro Lys Met Lys Glu Leu Gln Glu Lys Tyr Lys Gly Glu Pro Gln	
385 390 395 400	
aaa ttg caa gcc cac atg atg cag ctt tac aaa aaa cat ggg gct aac	1248
Lys Leu Gln Ala His Met Met Gln Leu Tyr Lys Lys His Gly Ala Asn	
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cca cta ggg ggt tgt ctg ccc tta atc tta caa atc ccg gtg ttt ttt	1296
Pro Leu Gly Gly Cys Leu Pro Leu Ile Leu Gln Ile Pro Val Phe Phe	
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gcc att tat aga gtg ctt tat aac gct gtg gaa ttg aaa agc tca gag	1344
Ala Ile Tyr Arg Val Leu Tyr Asn Ala Val Glu Leu Lys Ser Ser Glu	
435 440 445	
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Trp Ile Leu Trp Ile His Asp Leu Ser Ile Met Asp Pro Tyr Phe Ile	
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Leu Pro Leu Leu Met Gly Ala Ser Met Tyr Trp His Gln Ser Val Thr	
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Pro Asn Thr Met Thr Asp Pro Met Gln Ala Lys Ile Phe Lys Leu Leu	
485 490 495	
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Pro Leu Leu Phe Thr Ile Phe Leu Ile Thr Phe Pro Ala Gly Leu Val	
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Leu Tyr Trp Thr Thr Asn Asn Ile Leu Ser Val Leu Gln Gln Leu Ile	
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Ala Thr Ser Pro Asn Ala Pro Asn Ala Gln His Phe Ser Thr Thr Gln  
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Thr Thr Pro Gln Glu Asn Leu Leu Ser Thr Ile Ser Phe Glu His Ala  
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Asp Lys Lys Tyr Leu Thr Pro Lys Gln Lys Gly Phe Leu Glu His Val  
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Gly His Leu Phe Ser Ser Lys Glu Asn Ala Gln Pro Pro Leu Lys Glu  
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Ser Lys Thr Thr Leu Gly Pro Asn Glu Gln Leu Val Leu Thr Gln Asp  
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Leu Gly Thr Leu Ser Ile Ile Lys Thr Leu Thr Phe Tyr Asp Asp Leu  
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His Tyr Asp Leu Lys Ile Ala Phe Lys Ser Pro Asn Asn Leu Ile Pro  
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Ser Tyr Val Ile Thr Asn Gly Tyr Arg Pro Val Ala Asp Leu Asp Ser  
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Tyr Thr Phe Ser Gly Val Leu Leu Glu Asn Ser Asp Lys Lys Ile Glu  
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Lys Ile Glu Asp Lys Asp Ala Lys Glu Ile Lys Arg Phe Ser Asn Thr  
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Leu Phe Leu Ser Ser Val Asp Arg Tyr Phe Thr Thr Leu Leu Phe Thr  
260 265 270

Lys Asp Pro Gln Gly Phe Glu Ala Leu Ile Asp Ser Glu Ile Gly Thr  
275 280 285

Lys Asn Pro Leu Gly Phe Ile Ser Leu Lys Asn Glu Ala Asn Leu His  
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Gly Tyr Ile Gly Pro Lys Asp Tyr Arg Ser Leu Lys Ala Ile Ser Pro  
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Met Leu Thr Asp Val Ile Glu Tyr Gly Leu Ile Thr Phe Phe Ala Lys  
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Gly Val Phe Val Leu Leu Asp Tyr Leu Tyr Gln Phe Val Gly Asn Trp  
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Gly Trp Ala Ile Ile Leu Leu Thr Ile Ile Val Arg Ile Ile Leu Tyr  
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Pro Leu Ser Tyr Lys Gly Met Val Ser Met Gln Lys Leu Lys Glu Leu  
370 375 380

Ala Pro Lys Met Lys Glu Leu Gln Glu Lys Tyr Lys Gly Glu Pro Gln  
385 390 395 400

Lys Leu Gln Ala His Met Met Gln Leu Tyr Lys Lys His Gly Ala Asn  
405 410 415

Pro Leu Gly Gly Cys Leu Pro Leu Ile Leu Gln Ile Pro Val Phe Phe  
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Ala Ile Tyr Arg Val Leu Tyr Asn Ala Val Glu Leu Lys Ser Ser Glu  
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Trp Ile Leu Trp Ile His Asp Leu Ser Ile Met Asp Pro Tyr Phe Ile  
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Leu Pro Leu Leu Met Gly Ala Ser Met Tyr Trp His Gln Ser Val Thr  
465 470 475 480

Pro Asn Thr Met Thr Asp Pro Met Gln Ala Lys Ile Phe Lys Leu Leu  
485 490 495

Pro Leu Leu Phe Thr Ile Phe Leu Ile Thr Phe Pro Ala Gly Leu Val  
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Leu Tyr Trp Thr Thr Asn Asn Ile Leu Ser Val Leu Gln Gln Leu Ile  
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Val Ile Val Gly Ala Ile Leu Ile Leu Phe Phe Gly Thr Tyr Ser Phe  
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Ile Asn Thr Pro Val Asp Ala Phe Pro Asp Ile Ser Pro Thr Gln Val  
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Lys Ile Ile Leu Lys Leu Pro Gly Ser Ser Pro Glu Glu Met Glu Asn  
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Asn Ile Val Arg Pro Leu Glu Leu Glu Leu Leu Gly Leu Lys Gly Gln	
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Lys Ser Leu Arg Ser Val Ser Lys Tyr Ser Ile Ser Asp Ile Thr Ile	
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Asp Phe Asp Asp Ser Val Asp Ile Tyr Leu Ala Arg Asn Ile Val Asn	
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Glu Arg Leu Ser Ser Val Met Lys Asp Leu Pro Val Gly Val Glu Gly	
115 120 125	
ggc atg gcg ccc att gtt acg ccg cta tca gat atc ttt atg ttc act	432
Gly Met Ala Pro Ile Val Thr Pro Leu Ser Asp Ile Phe Met Phe Thr	
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Ile Asp Gly Asn Ile Thr Glu Ile Glu Lys Arg Gln Leu Leu Asp Phe	
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Val Ile Arg Pro Gln Leu Arg Met Ile Ser Gly Val Ala Asp Val Asn	
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Ser Ile Gly Gly Phe Ser Arg Ala Phe Val Ile Val Pro Asp Phe Asn	
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gac atg gca agg ctt ggg gtg agt att tct gat tta gaa tcg gct gtg	624
Asp Met Ala Arg Leu Gly Val Ser Ile Ser Asp Leu Glu Ser Ala Val	
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Arg Val Asn Leu Arg Asn Ser Gly Ala Gly Arg Val Asp Arg Asp Gly	
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Glu Thr Phe Leu Val Lys Ile Gln Thr Ala Ser Leu Ser Leu Glu Asp	
225 230 235 240	
att ggc aaa atc acc gtt tcc act aat tta ggg cat ttg cac att aag	768
Ile Gly Lys Ile Thr Val Ser Thr Asn Leu Gly His Leu His Ile Lys	
245 250 255	
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Asp Phe Ala Lys Val Ile Ser Gln Ser Arg Thr Arg Leu Gly Phe Val	
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Thr	Lys	Asp	Gly	Val	Gly	Glu	Thr	Thr	Glu	Gly	Leu	Val	Leu	Ser	Leu	
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Lys	Asp	Ala	Asn	Thr	Lys	Glu	Ile	Ile	Thr	Gln	Val	Tyr	Gln	Lys	Leu	
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Tyr	Asp	Arg	Ser	Glu	Phe	Thr	Gln	Lys	Ala	Ile	Ala	Thr	Val	Ser	Lys	
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Thr	Leu	Ile	Glu	Ala	Val	Val	Leu	Ile	Ile	Ile	Thr	Leu	Phe	Leu	Phe	
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Leu	Gly	Asn	Leu	Arg	Ala	Ser	Val	Ala	Val	Gly	Val	Ile	Leu	Pro	Leu	
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Ser	Leu	Ser	Val	Ala	Phe	Ile	Phe	Ile	Lys	Phe	Ser	Asp	Leu	Thr	Leu	
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Asp	Ser	Ala	Val	Val	Val	Val	Glu	Asn	Ala	Phe	Glu	Lys	Leu	Ser	Ala	
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Asn	Thr	Lys	Thr	Thr	Lys	Leu	His	Ala	Ile	Tyr	Arg	Ser	Cys	Lys	Glu	
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Ile	Ala	Val	Ser	Val	Val	Ser	Gly	Val	Val	Ile	Ile	Ile	Val	Phe	Phe	
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Val	Pro	Ile	Leu	Thr	Leu	Gln	Gly	Leu	Glu	Gly	Lys	Met	Phe	Arg	Pro	
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Leu	Ala	Gln	Ser	Ile	Val	Tyr	Ala	Leu	Leu	Gly	Thr	Leu	Val	Leu	Ser	
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Ile	Thr	Ile	Ile	Pro	Val	Val	Ser	Ser	Leu	Val	Leu	Lys	Ala	Thr	Pro	
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His	Ser	Glu	Thr	Phe	Leu	Thr	Arg	Phe	Leu	Asn	Arg	Ile	Tyr	Ala	Pro	
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Leu	Leu	Glu	Phe	Phe	Val	His	Asn	Pro	Lys	Lys	Val	Ile	Leu	Gly	Ala	
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Phe	Val	Phe	Leu	Ile	Ala	Ser	Leu	Ser	Leu	Phe	Pro	Phe	Val	Gly	Lys	
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Asn	Phe	Met	Pro	Val	Leu	Asp	Glu	Gly	Asp	Val	Val	Leu	Ser	Val	Glu	
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Thr	Thr	Pro	Ser	Ile	Ser	Leu	Asp	Gln	Ser	Arg	Asp	Leu	Met	Leu	Asn	
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Ile	Glu	Ser	Ala	Ile	Lys	Lys	His	Val	Lys	Glu	Val	Lys	Ser	Ile	Val	
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gcg	cgc	aca	ggg	agc	gat	gaa	ttg	ggg	ctg	gat	tta	gga	ggt	ttg	aat	1824
Ala	Arg	Thr	Gly	Ser	Asp	Glu	Leu	Gly	Leu	Asp	Leu	Gly	Gly	Leu	Asn	
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Gln	Thr	Asp	Thr	Phe	Ile	Ser	Phe	Ile	Pro	Lys	Lys	Glu	Trp	Ser	Val	
	610					615					620					
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Lys	Thr	Lys	Asp	Glu	Leu	Leu	Glu	Lys	Ile	Met	Asp	Ser	Leu	Lys	Asp	
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Ser	Glu	Met	Leu	Thr	Gly	Val	Arg	Gly	Asp	Leu	Ala	Val	Lys	Ile	Phe	
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Ala	Leu	Lys	Gly	Ile	Lys	Gly	Ser	Ser	Glu	Val	Leu	Thr	Thr	Leu	Asn	
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Glu	Gly	Val	Asn	Tyr	Leu	Tyr	Val	Thr	Pro	Asn	Lys	Glu	Ser	Met	Ala	
705					710					715					720	
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Asp	Val	Gly	Ile	Thr	Ser	Asp	Glu	Phe	Ser	Lys	Phe	Leu	Lys	Ser	Ala	
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Leu	Glu	Gly	Leu	Val	Val	Asp	Val	Ile	Pro	Thr	Gly	Ile	Ser	Arg	Thr	
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Pro	Val	Met	Ile	Arg	Gln	Glu	Ser	Asp	Phe	Ala	Ser	Ser	Ile	Thr	Lys	
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Ile	Lys	Ser	Leu	Ala	Leu	Thr	Ser	Lys	Tyr	Gly	Val	Leu	Val	Pro	Ile	
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Thr	Ser	Ile	Ala	Lys	Ile	Glu	Glu	Val	Asp	Gly	Pro	Val	Ser	Val	Val	
785					790					795					800	
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Arg	Glu	Asn	Ser	Met	Arg	Met	Ser	Val	Val	Arg	Ser	Asn	Val	Val	Gly	
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Arg	Asp	Leu	Lys	Ser	Phe	Val	Glu	Glu	Ala	Lys	Lys	Val	Ile	Ala	Gln	
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Glu	Asn	Gln	Gln	Arg	Ala	Asn	Lys	Arg	Leu	Ser	Thr	Val	Ile	Pro	Leu	
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Ser	Ile	Leu	Ala	Ile	Phe	Phe	Ile	Leu	Phe	Phe	Thr	Phe	Lys	Ser	Ile	
865					870					875					880	
cct	tta	gcc	ttg	ctc	att	ctt	ttg	aat	atc	cct	ttt	gcg	gtt	acc	gga	2688
Pro	Leu	Ala	Leu	Leu	Ile	Leu	Leu	Asn	Ile	Pro	Phe	Ala	Val	Thr	Gly	
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Ile Asn Thr Pro Val Asp Ala Phe Pro Asp Ile Ser Pro Thr Gln Val  
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Lys Ile Ile Leu Lys Leu Pro Gly Ser Ser Pro Glu Glu Met Glu Asn  
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Asn Ile Val Arg Pro Leu Glu Leu Glu Leu Leu Gly Leu Lys Gly Gln  
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Lys Ser Leu Arg Ser Val Ser Lys Tyr Ser Ile Ser Asp Ile Thr Ile  
 85 90 95

Asp Phe Asp Asp Ser Val Asp Ile Tyr Leu Ala Arg Asn Ile Val Asn  
 100 105 110

Glu Arg Leu Ser Ser Val Met Lys Asp Leu Pro Val Gly Val Glu Gly  
 115 120 125

Gly Met Ala Pro Ile Val Thr Pro Leu Ser Asp Ile Phe Met Phe Thr  
 130 135 140

Ile Asp Gly Asn Ile Thr Glu Ile Glu Lys Arg Gln Leu Leu Asp Phe  
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Val Ile Arg Pro Gln Leu Arg Met Ile Ser Gly Val Ala Asp Val Asn  
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Ser Ile Gly Gly Phe Ser Arg Ala Phe Val Ile Val Pro Asp Phe Asn  
 180 185 190

Asp Met Ala Arg Leu Gly Val Ser Ile Ser Asp Leu Glu Ser Ala Val  
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Arg Val Asn Leu Arg Asn Ser Gly Ala Gly Arg Val Asp Arg Asp Gly  
 210 215 220

Glu Thr Phe Leu Val Lys Ile Gln Thr Ala Ser Leu Ser Leu Glu Asp  
 225 230 235 240

Ile Gly Lys Ile Thr Val Ser Thr Asn Leu Gly His Leu His Ile Lys  
 245 250 255

Asp Phe Ala Lys Val Ile Ser Gln Ser Arg Thr Arg Leu Gly Phe Val  
 260 265 270

Thr Lys Asp Gly Val Gly Glu Thr Thr Glu Gly Leu Val Leu Ser Leu  
 275 280 285

Lys Asp Ala Asn Thr Lys Glu Ile Ile Thr Gln Val Tyr Gln Lys Leu

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Glu 305	Glu	Leu	Lys	Pro	Phe 310	Leu	Pro	Asn	Gly	Val 315	Ser	Ile	Asn	Val	Phe 320
Tyr	Asp	Arg	Ser	Glu 325	Phe	Thr	Gln	Lys	Ala 330	Ile	Ala	Thr	Val	Ser 335	Lys
Thr	Leu	Ile	Glu 340	Ala	Val	Val	Leu	Ile 345	Ile	Ile	Thr	Leu	Phe 350	Leu	Phe
Leu	Gly	Asn 355	Leu	Arg	Ala	Ser	Val 360	Ala	Val	Gly	Val	Ile 365	Leu	Pro	Leu
Ser 370	Leu	Ser	Val	Ala	Phe	Ile 375	Phe	Ile	Lys	Phe	Ser 380	Asp	Leu	Thr	Leu
Asn 385	Leu	Met	Ser	Leu	Gly 390	Gly	Leu	Val	Ile	Ala 395	Ile	Gly	Met	Leu	Ile 400
Asp	Ser	Ala	Val	Val 405	Val	Val	Glu	Asn	Ala 410	Phe	Glu	Lys	Leu	Ser 415	Ala
Asn	Thr	Lys	Thr 420	Thr	Lys	Leu	His	Ala 425	Ile	Tyr	Arg	Ser	Cys 430	Lys	Glu
Ile	Ala	Val 435	Ser	Val	Val	Ser	Gly 440	Val	Val	Ile	Ile	Ile 445	Val	Phe	Phe
Val 450	Pro	Ile	Leu	Thr	Leu	Gln 455	Gly	Leu	Glu	Gly	Lys 460	Met	Phe	Arg	Pro
Leu 465	Ala	Gln	Ser	Ile	Val 470	Tyr	Ala	Leu	Leu	Gly 475	Thr	Leu	Val	Leu	Ser 480
Ile	Thr	Ile	Ile 485	Pro	Val	Val	Ser	Ser	Leu 490	Val	Leu	Lys	Ala	Thr 495	Pro
His	Ser	Glu	Thr 500	Phe	Leu	Thr	Arg	Phe 505	Leu	Asn	Arg	Ile	Tyr 510	Ala	Pro

Leu Leu Glu Phe Phe Val His Asn Pro Lys Lys Val Ile Leu Gly Ala  
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Phe Val Phe Leu Ile Ala Ser Leu Ser Leu Phe Pro Phe Val Gly Lys  
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Asn Phe Met Pro Val Leu Asp Glu Gly Asp Val Val Leu Ser Val Glu  
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Thr Thr Pro Ser Ile Ser Leu Asp Gln Ser Arg Asp Leu Met Leu Asn  
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Ile Glu Ser Ala Ile Lys Lys His Val Lys Glu Val Lys Ser Ile Val  
 580 585 590

Ala Arg Thr Gly Ser Asp Glu Leu Gly Leu Asp Leu Gly Gly Leu Asn  
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Gln Thr Asp Thr Phe Ile Ser Phe Ile Pro Lys Lys Glu Trp Ser Val  
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Lys Thr Lys Asp Glu Leu Leu Glu Lys Ile Met Asp Ser Leu Lys Asp  
 625 630 635 640

Phe Lys Gly Ile Asn Phe Ser Phe Thr Gln Pro Ile Glu Met Arg Ile  
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Ser Glu Met Leu Thr Gly Val Arg Gly Asp Leu Ala Val Lys Ile Phe  
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Gly Asp Gly Ile Ser Glu Leu Asn Glu Leu Ser Phe Gln Ile Ala Gln  
 675 680 685

Ala Leu Lys Gly Ile Lys Gly Ser Ser Glu Val Leu Thr Thr Leu Asn  
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Glu Gly Val Asn Tyr Leu Tyr Val Thr Pro Asn Lys Glu Ser Met Ala  
 705 710 715 720

Asp Val Gly Ile Thr Ser Asp Glu Phe Ser Lys Phe Leu Lys Ser Ala  
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Leu	Glu	Gly	Leu	Val	Val	Asp	Val	Ile	Pro	Thr	Gly	Ile	Ser	Arg	Thr	740	745	750
Pro	Val	Met	Ile	Arg	Gln	Glu	Ser	Asp	Phe	Ala	Ser	Ser	Ile	Thr	Lys	755	760	765
Ile	Lys	Ser	Leu	Ala	Leu	Thr	Ser	Lys	Tyr	Gly	Val	Leu	Val	Pro	Ile	770	775	780
Thr	Ser	Ile	Ala	Lys	Ile	Glu	Glu	Val	Asp	Gly	Pro	Val	Ser	Val	Val	785	790	795
Arg	Glu	Asn	Ser	Met	Arg	Met	Ser	Val	Val	Arg	Ser	Asn	Val	Val	Gly	805	810	815
Arg	Asp	Leu	Lys	Ser	Phe	Val	Glu	Glu	Ala	Lys	Lys	Val	Ile	Ala	Gln	820	825	830
Asn	Ile	Lys	Leu	Pro	Pro	Ser	Tyr	Tyr	Ile	Thr	Tyr	Gly	Gly	Gln	Phe	835	840	845
Glu	Asn	Gln	Gln	Arg	Ala	Asn	Lys	Arg	Leu	Ser	Thr	Val	Ile	Pro	Leu	850	855	860
Ser	Ile	Leu	Ala	Ile	Phe	Phe	Ile	Leu	Phe	Phe	Thr	Phe	Lys	Ser	Ile	865	870	875
Pro	Leu	Ala	Leu	Leu	Ile	Leu	Leu	Asn	Ile	Pro	Phe	Ala	Val	Thr	Gly	885	890	895
Gly	Leu	Ile	Ala	Leu	Phe	Ala	Val	Gly	Glu	Tyr	Ile	Ser	Val	Pro	Ala	900	905	910
Ser	Val	Gly	Phe	Ile	Ala	Leu	Phe	Gly	Ile	Ala	Val	Leu	Asn	Gly	Val	915	920	925
Val	Met	Ile	Gly	Tyr	Phe	Lys	Glu	Leu	Leu	Leu	Gln	Gly	Lys	Ser	Val	930	935	940
Glu	Glu	Cys	Val	Leu	Leu	Gly	Ala	Lys	Arg	Arg	Leu	Arg	Pro	Val	Leu	945	950	955

Met Thr Ala Cys Ile Ala Gly Leu Gly Leu Leu Pro Leu Leu Phe Ser  
965 970 975

His Ser Val Gly Ser Glu Val Gln Lys Pro Leu Ala Ile Val Val Leu  
980 985 990

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1 5 10 15  
ttg att gtg atc gtg tgc gtg agc att tta ggg gtg tcc tta aac agc 96  
Leu Ile Val Ile Val Cys Val Ser Ile Leu Gly Val Ser Leu Asn Ser  
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agg gtg aaa gag att tta aaa gaa agc gct ctg cat tct atg caa gat 144  
Arg Val Lys Glu Ile Leu Lys Glu Ser Ala Leu His Ser Met Gln Asp  
35 40 45  
agt ttg cat ttt aag gtt aat gaa gtg caa ggg gtt tta gaa aac act 192  
Ser Leu His Phe Lys Val Asn Glu Val Gln Gly Val Leu Glu Asn Thr  
50 55 60  
tat acg agc atg ggc att gtt aaa gaa atg ctc cct aaa gac acc aaa 240  
Tyr Thr Ser Met Gly Ile Val Lys Glu Met Leu Pro Lys Asp Thr Lys  
65 70 75 80  
aga gaa atc aaa atc ggc ttg tta aaa aac ttc att tta gcc aat tcg 288  
Arg Glu Ile Lys Ile Gly Leu Leu Lys Asn Phe Ile Leu Ala Asn Ser  
85 90 95  
cat gtc gct ggg gtg agc atg ttt ttt aaa ggc aga gaa gat tta aga 336  
His Val Ala Gly Val Ser Met Phe Phe Lys Gly Arg Glu Asp Leu Arg

100						105						110						
tta	acg	ctt	tta	agg	gat	aac	aat	acg	att	aag	cta	gtg	gaa	aat	ccg			384
Leu	Thr	Leu	Leu	Arg	Asp	Asn	Asn	Thr	Ile	Lys	Leu	Val	Glu	Asn	Pro			
		115					120					125						
tca	tta	gag	aat	agc	cct	tta	gcg	caa	aaa	gcg	atg	aaa	aat	aaa	gaa			432
Ser	Leu	Glu	Asn	Ser	Pro	Leu	Ala	Gln	Lys	Ala	Met	Lys	Asn	Lys	Glu			
		130				135					140							
att	tct	aaa	agt	ttg	ggt	tat	tat	agg	aaa	atg	cct	aat	ggg	gcg	gaa			480
Ile	Ser	Lys	Ser	Leu	Gly	Tyr	Tyr	Arg	Lys	Met	Pro	Asn	Gly	Ala	Glu			
145					150					155					160			
gtt	tat	ggg	gtg	gat	att	ctt	tta	cct	tta	ttg	aat	gag	aac	gct	caa			528
Val	Tyr	Gly	Val	Asp	Ile	Leu	Leu	Pro	Leu	Leu	Asn	Glu	Asn	Ala	Gln			
				165					170					175				
gag	gtt	gta	ggg	gct	ttg	atg	att	ttt	att	tcc	att	gac	agc	ttc	agc			576
Glu	Val	Val	Gly	Ala	Leu	Met	Ile	Phe	Ile	Ser	Ile	Asp	Ser	Phe	Ser			
			180					185					190					
aat	gaa	atc	act	aaa	aac	agg	agc	gat	tta	ttt	tta	att	ggc	act	aaa			624
Asn	Glu	Ile	Thr	Lys	Asn	Arg	Ser	Asp	Leu	Phe	Leu	Ile	Gly	Thr	Lys			
		195					200					205						
ggt	aaa	gtg	ctt	ttg	agc	gcg	aat	aag	agt	ttg	caa	gac	aaa	cct	atc			672
Gly	Lys	Val	Leu	Leu	Ser	Ala	Asn	Lys	Ser	Leu	Gln	Asp	Lys	Pro	Ile			
	210					215					220							
gca	gaa	att	tat	aag	agc	gtg	cct	aaa	gcc	acc	aac	gaa	gtg	atg	gct			720
Ala	Glu	Ile	Tyr	Lys	Ser	Val	Pro	Lys	Ala	Thr	Asn	Glu	Val	Met	Ala			
225					230					235					240			
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Ile	Leu	Glu	Asn	Gly	Ser	Lys	Ala	Thr	Leu	Glu	Tyr	Leu	Asp	Pro	Phe			
			245					250						255				
agc	cat	aag	gaa	aat	ttt	tta	gcc	gtt	gaa	acc	ttt	aaa	atg	cta	ggc			816
Ser	His	Lys	Glu	Asn	Phe	Leu	Ala	Val	Glu	Thr	Phe	Lys	Met	Leu	Gly			
		260						265					270					
aaa	aca	gaa	agt	aaa	gac	aat	ctt	aat	tgg	atg	atc	gct	tta	atc	att			864
Lys	Thr	Glu	Ser	Lys	Asp	Asn	Leu	Asn	Trp	Met	Ile	Ala	Leu	Ile	Ile			
		275					280					285						
gaa	aaa	gac	aag	gtc	tat	gag	caa	gta	ggc	tcg	gtg	cgt	ttt	gtg	gtg			912
Glu	Lys	Asp	Lys	Val	Tyr	Glu	Gln	Val	Gly	Ser	Val	Arg	Phe	Val	Val			
	290					295				300								
atc	ata	gcg	agc	gca	atc	atg	gtg	tta	gcc	ttg	att	ata	gcg	atc	act			960
Ile	Ile	Ala	Ser	Ala	Ile	Met	Val	Leu	Ala	Leu	Ile	Ile	Ala	Ile	Thr			
305					310					315					320			
ctc	tta	atg	cga	gcg	atc	gtg	agc	agt	cgt	ttg	gaa	gcc	gtt	tct	agc			1008



Leu	Leu	Met	Arg	Ala	Ile	Val	Ser	Ser	Arg	Leu	Glu	Ala	Val	Ser	Ser	
				325					330					335		
acc	ttg	tct	cat	ttc	ttt	aaa	tta	ttg	aac	aat	caa	gcc	aat	tct	agc	1056
Thr	Leu	Ser	His	Phe	Phe	Lys	Leu	Leu	Asn	Asn	Gln	Ala	Asn	Ser	Ser	
			340					345					350			
ggt	att	aaa	ttg	att	gaa	gcg	aaa	tcc	aat	gac	gag	tta	ggc	cgc	atg	1104
Gly	Ile	Lys	Leu	Ile	Glu	Ala	Lys	Ser	Asn	Asp	Glu	Leu	Gly	Arg	Met	
		355					360					365				
caa	aca	gcg	atc	aat	aaa	aat	atc	ttg	caa	acc	caa	aaa	atc	atg	caa	1152
Gln	Thr	Ala	Ile	Asn	Lys	Asn	Ile	Leu	Gln	Thr	Gln	Lys	Ile	Met	Gln	
	370					375					380					
gaa	gac	agg	caa	gcc	gtc	caa	gac	acc	att	aaa	gtg	gtt	tca	gat	gtg	1200
Glu	Asp	Arg	Gln	Ala	Val	Gln	Asp	Thr	Ile	Lys	Val	Val	Ser	Asp	Val	
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aaa	gca	ggg	aat	ttt	gcg	gtg	cgc	atc	acg	gct	gag	ccc	gca	agc	cct	1248
Lys	Ala	Gly	Asn	Phe	Ala	Val	Arg	Ile	Thr	Ala	Glu	Pro	Ala	Ser	Pro	
				405					410					415		
gat	ttg	aaa	gaa	ttg	agg	gac	gcg	cta	aat	ggg	atc	atg	gat	tat	ttg	1296
Asp	Leu	Lys	Glu	Leu	Arg	Asp	Ala	Leu	Asn	Gly	Ile	Met	Asp	Tyr	Leu	
			420					425					430			
caa	gaa	agc	gta	ggg	act	cac	atg	cca	agc	att	ttc	aaa	atc	ttt	gaa	1344
Gln	Glu	Ser	Val	Gly	Thr	His	Met	Pro	Ser	Ile	Phe	Lys	Ile	Phe	Glu	
		435					440					445				
agc	tat	tct	ggt	ttg	gat	ttt	aga	ggc	cgg	atc	caa	aac	gct	tcg	ggt	1392
Ser	Tyr	Ser	Gly	Leu	Asp	Phe	Arg	Gly	Arg	Ile	Gln	Asn	Ala	Ser	Gly	
	450					455					460					
agg	gtg	gaa	ctg	gtt	act	aac	gct	tta	ggg	caa	gaa	atc	caa	aaa	atg	1440
Arg	Val	Glu	Leu	Val	Thr	Asn	Ala	Leu	Gly	Gln	Glu	Ile	Gln	Lys	Met	
465					470				475						480	
cta	gaa	act	tcg	tct	aat	ttt	gcc	aaa	gat	tta	gcg	aac	gat	agc	gcg	1488
Leu	Glu	Thr	Ser	Ser	Asn	Phe	Ala	Lys	Asp	Leu	Ala	Asn	Asp	Ser	Ala	
				485					490					495		
aat	tta	aaa	gag	tgc	gtg	caa	aat	tta	gaa	aaa	gct	tca	aac	tcc	caa	1536
Asn	Leu	Lys	Glu	Cys	Val	Gln	Asn	Leu	Glu	Lys	Ala	Ser	Asn	Ser	Gln	
			500					505					510			
cac	aaa	agc	ttg	atg	gaa	act	tcc	aaa	acg	ata	gaa	aat	atc	acc	act	1584
His	Lys	Ser	Leu	Met	Glu	Thr	Ser	Lys	Thr	Ile	Glu	Asn	Ile	Thr	Thr	
		515					520					525				
tcc	att	caa	ggc	gtg	agc	tct	caa	agt	gaa	gcc	atg	att	gaa	caa	ggg	1632
Ser	Ile	Gln	Gly	Val	Ser	Ser	Gln	Ser	Glu	Ala	Met	Ile	Glu	Gln	Gly	
	530					535					540					

caa gac att aaa agc att gta gaa atc att aga gat att gct gat caa	1680
Gln Asp Ile Lys Ser Ile Val Glu Ile Ile Arg Asp Ile Ala Asp Gln	
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acc aat ctt tta gcc tta aac gcc gct att gaa gcc gca agg gcc ggc	1728
Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala Arg Ala Gly	
565 570 575	
gag cat ggc aga ggc ttt gcg gtg gtg gct gat gag gta aga aag ctc	1776
Glu His Gly Arg Gly Phe Ala Val Val Ala Asp Glu Val Arg Lys Leu	
580 585 590	
gct gaa agg acg caa aaa tcg ctc agc gag att gaa gcc aat atc aat	1824
Ala Glu Arg Thr Gln Lys Ser Leu Ser Glu Ile Glu Ala Asn Ile Asn	
595 600 605	
att tta gtg caa agc att tca gac acg agc gaa agc att aaa aac cag	1872
Ile Leu Val Gln Ser Ile Ser Asp Thr Ser Glu Ser Ile Lys Asn Gln	
610 615 620	
gtt aaa gaa gtg gaa gaa atc aac gct tct att gaa gcc tta aga tcg	1920
Val Lys Glu Val Glu Glu Ile Asn Ala Ser Ile Glu Ala Leu Arg Ser	
625 630 635 640	
gtt act gag ggc aat cta aaa atc gct agc gat tct tta gaa atc agt	1968
Val Thr Glu Gly Asn Leu Lys Ile Ala Ser Asp Ser Leu Glu Ile Ser	
645 650 655	
caa gaa att gac aaa gtt tct aac gat att tta gaa gat gtg aat aaa	2016
Gln Glu Ile Asp Lys Val Ser Asn Asp Ile Leu Glu Asp Val Asn Lys	
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Lys Gln Phe	
675	

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Arg Val Lys Glu Ile Leu Lys Glu Ser Ala Leu His Ser Met Gln Asp
35 40 45

Ser	Leu	His	Phe	Lys	Val	Asn	Glu	Val	Gln	Gly	Val	Leu	Glu	Asn	Thr	50	55	60
Tyr	Thr	Ser	Met	Gly	Ile	Val	Lys	Glu	Met	Leu	Pro	Lys	Asp	Thr	Lys	65	70	75
Arg	Glu	Ile	Lys	Ile	Gly	Leu	Leu	Lys	Asn	Phe	Ile	Leu	Ala	Asn	Ser	85	90	95
His	Val	Ala	Gly	Val	Ser	Met	Phe	Phe	Lys	Gly	Arg	Glu	Asp	Leu	Arg	100	105	110
Leu	Thr	Leu	Leu	Arg	Asp	Asn	Asn	Thr	Ile	Lys	Leu	Val	Glu	Asn	Pro	115	120	125
Ser	Leu	Glu	Asn	Ser	Pro	Leu	Ala	Gln	Lys	Ala	Met	Lys	Asn	Lys	Glu	130	135	140
Ile	Ser	Lys	Ser	Leu	Gly	Tyr	Tyr	Arg	Lys	Met	Pro	Asn	Gly	Ala	Glu	145	150	155
Val	Tyr	Gly	Val	Asp	Ile	Leu	Leu	Pro	Leu	Leu	Asn	Glu	Asn	Ala	Gln	165	170	175
Glu	Val	Val	Gly	Ala	Leu	Met	Ile	Phe	Ile	Ser	Ile	Asp	Ser	Phe	Ser	180	185	190
Asn	Glu	Ile	Thr	Lys	Asn	Arg	Ser	Asp	Leu	Phe	Leu	Ile	Gly	Thr	Lys	195	200	205
Gly	Lys	Val	Leu	Leu	Ser	Ala	Asn	Lys	Ser	Leu	Gln	Asp	Lys	Pro	Ile	210	215	220
Ala	Glu	Ile	Tyr	Lys	Ser	Val	Pro	Lys	Ala	Thr	Asn	Glu	Val	Met	Ala	225	230	235
Ile	Leu	Glu	Asn	Gly	Ser	Lys	Ala	Thr	Leu	Glu	Tyr	Leu	Asp	Pro	Phe	245	250	255
Ser	His	Lys	Glu	Asn	Phe	Leu	Ala	Val	Glu	Thr	Phe	Lys	Met	Leu	Gly	260	265	270

Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile Ala Leu Ile Ile  
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Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val Arg Phe Val Val  
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Ile Ile Ala Ser Ala Ile Met Val Leu Ala Leu Ile Ile Ala Ile Thr  
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Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln Ala Asn Ser Ser  
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Gly Ile Lys Leu Ile Glu Ala Lys Ser Asn Asp Glu Leu Gly Arg Met  
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Gln Thr Ala Ile Asn Lys Asn Ile Leu Gln Thr Gln Lys Ile Met Gln  
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Glu Asp Arg Gln Ala Val Gln Asp Thr Ile Lys Val Val Ser Asp Val  
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Lys Ala Gly Asn Phe Ala Val Arg Ile Thr Ala Glu Pro Ala Ser Pro  
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Asp Leu Lys Glu Leu Arg Asp Ala Leu Asn Gly Ile Met Asp Tyr Leu  
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Gln Glu Ser Val Gly Thr His Met Pro Ser Ile Phe Lys Ile Phe Glu  
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Ser Tyr Ser Gly Leu Asp Phe Arg Gly Arg Ile Gln Asn Ala Ser Gly  
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Arg Val Glu Leu Val Thr Asn Ala Leu Gly Gln Glu Ile Gln Lys Met  
 465 470 475 480

Leu Glu Thr Ser Ser Asn Phe Ala Lys Asp Leu Ala Asn Asp Ser Ala

485

490

495

Asn Leu Lys Glu Cys Val Gln Asn Leu Glu Lys Ala Ser Asn Ser Gln  
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His Lys Ser Leu Met Glu Thr Ser Lys Thr Ile Glu Asn Ile Thr Thr  
 515 520 525

Ser Ile Gln Gly Val Ser Ser Gln Ser Glu Ala Met Ile Glu Gln Gly  
 530 535 540

Gln Asp Ile Lys Ser Ile Val Glu Ile Ile Arg Asp Ile Ala Asp Gln  
 545 550 555 560

Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala Arg Ala Gly  
 565 570 575

Glu His Gly Arg Gly Phe Ala Val Val Ala Asp Glu Val Arg Lys Leu  
 580 585 590

Ala Glu Arg Thr Gln Lys Ser Leu Ser Glu Ile Glu Ala Asn Ile Asn  
 595 600 605

Ile Leu Val Gln Ser Ile Ser Asp Thr Ser Glu Ser Ile Lys Asn Gln  
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Val Lys Glu Val Glu Glu Ile Asn Ala Ser Ile Glu Ala Leu Arg Ser  
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Val Thr Glu Gly Asn Leu Lys Ile Ala Ser Asp Ser Leu Glu Ile Ser  
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Lys Gln Phe  
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Leu	Ser	Ala	Asp	Ser	Ala	Gln	Ala	Asn	Lys	Ala	Ile	Ser	Asn	Ala	Asp	
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Leu	Ile	Lys	Glu	Ile	Arg	Asp	Leu	Lys	Lys	Ile	Ile	Ser	Ala	Gln	Asn	
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act	gag	att	aac	aac	tta	aga	aaa	gtg	caa	gaa	gtg	ttg	tct	ggg	caa	192
Thr	Glu	Ile	Asn	Asn	Leu	Arg	Lys	Val	Gln	Glu	Val	Leu	Ser	Gly	Gln	
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Leu	Gly	Asp	Met	Arg	Lys	Asp	Ile	Leu	Ser	Thr	Arg	Asp	Tyr	Cys	Ile	
65					70					75					80	

agc	tta	agg	cct	tat	atc	tat	aat	tgg	cgc	tag						273
Ser	Leu	Arg	Pro	Tyr	Ile	Tyr	Asn	Trp	Arg							
				85					90							

<210> 106

<211> 90

<212> PRT

<213> Helicobacter pylori

<400> 106

Val	Ala	Val	Lys	Lys	Ile	Val	Val	Ser	Trp	Cys	Val	Ala	Leu	Ala	Phe
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Leu	Ser	Ala	Asp	Ser	Ala	Gln	Ala	Asn	Lys	Ala	Ile	Ser	Asn	Ala	Asp
			20					25					30		

Leu	Ile	Lys	Glu	Ile	Arg	Asp	Leu	Lys	Lys	Ile	Ile	Ser	Ala	Gln	Asn
		35					40					45			

Thr	Glu	Ile	Asn	Asn	Leu	Arg	Lys	Val	Gln	Glu	Val	Leu	Ser	Gly	Gln
	50					55					60				

Leu Gly Asp Met Arg Lys Asp Ile Leu Ser Thr Arg Asp Tyr Cys Ile  
65 70 75 80

Ser Leu Arg Pro Tyr Ile Tyr Asn Trp Arg  
85 90

<210> 107  
<211> 759  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(759)

<400> 107  
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Met Leu Gly Lys Lys Asn Glu Glu Val Leu Ile Asp Glu Asn Leu Val  
1 5 10 15  
ggg ggt gtg ata gcc ctt gat aga ttg gca aaa ctc aat aag gcc aat 96  
Gly Gly Val Ile Ala Leu Asp Arg Leu Ala Lys Leu Asn Lys Ala Asn  
20 25 30  
agg act ttc aaa agg gct ttt tat ctc tct atg gca ctc aat gtc gcc 144  
Arg Thr Phe Lys Arg Ala Phe Tyr Leu Ser Met Ala Leu Asn Val Ala  
35 40 45  
gct gta acg agt att gtg atg atg atg cct ttg aag aaa acg gat ata 192  
Ala Val Thr Ser Ile Val Met Met Met Pro Leu Lys Lys Thr Asp Ile  
50 55 60  
ttt gtt tat ggc att gat cga tac aca gga gaa ttt aaa att gtc aaa 240  
Phe Val Tyr Gly Ile Asp Arg Tyr Thr Gly Glu Phe Lys Ile Val Lys  
65 70 75 80  
cgc tcc gat gct agg caa atc gtc aat tct gaa gcc gtt gtg gat agt 288  
Arg Ser Asp Ala Arg Gln Ile Val Asn Ser Glu Ala Val Val Asp Ser  
85 90 95  
gca act tca aaa ttt gta tca ttg ctg ttt ggt tat agc aaa aat tct 336  
Ala Thr Ser Lys Phe Val Ser Leu Leu Phe Gly Tyr Ser Lys Asn Ser  
100 105 110  
ttg agg gat cgc aag gat caa cta atg cag tat tgc gat gtg agt ttc 384  
Leu Arg Asp Arg Lys Asp Gln Leu Met Gln Tyr Cys Asp Val Ser Phe  
115 120 125  
caa acc caa gca atg aga atg ttc aat gaa aat atc aga caa ttc gta 432  
Gln Thr Gln Ala Met Arg Met Phe Asn Glu Asn Ile Arg Gln Phe Val  
130 135 140

gat	aaa	gtc	cga	gca	gaa	gct	atc	att	agc	tct	aac	ata	caa	aga	gaa	480
Asp	Lys	Val	Arg	Ala	Glu	Ala	Ile	Ile	Ser	Ser	Asn	Ile	Gln	Arg	Glu	
145					150					155					160	

aaa	gtc	aaa	aat	agt	ccc	tta	acg	aga	tta	aca	ttt	ttc	att	acc	atc	528
Lys	Val	Lys	Asn	Ser	Pro	Leu	Thr	Arg	Leu	Thr	Phe	Phe	Ile	Thr	Ile	
				165					170					175		

aaa	atc	aca	cct	gat	aca	atg	gaa	aat	tat	gaa	tat	atc	act	aaa	aaa	576
Lys	Ile	Thr	Pro	Asp	Thr	Met	Glu	Asn	Tyr	Glu	Tyr	Ile	Thr	Lys	Lys	
			180					185					190			

caa	gta	act	att	tat	tat	gat	ttt	gct	aga	ggg	aac	tct	tct	caa	gaa	624
Gln	Val	Thr	Ile	Tyr	Tyr	Asp	Phe	Ala	Arg	Gly	Asn	Ser	Ser	Gln	Glu	
		195					200					205				

aat	ctt	atc	atc	aat	cct	ttt	ggc	ttc	aaa	gtg	ttt	gac	att	caa	atc	672
Asn	Leu	Ile	Ile	Asn	Pro	Phe	Gly	Phe	Lys	Val	Phe	Asp	Ile	Gln	Ile	
	210					215					220					

aca	gat	tta	caa	aac	gaa	cag	acg	gta	agc	gaa	att	ttg	aga	aag	atc	720
Thr	Asp	Leu	Gln	Asn	Glu	Gln	Thr	Val	Ser	Glu	Ile	Leu	Arg	Lys	Ile	
225					230					235					240	

aga	gaa	gtg	gaa	tca	aaa	aat	aag	gca	tta	aat	aaa	taa				759
Arg	Glu	Val	Glu	Ser	Lys	Asn	Lys	Ala	Leu	Asn	Lys					
				245					250							

<210> 108  
 <211> 252  
 <212> PRT  
 <213> Helicobacter pylori

<400> 108

Met	Leu	Gly	Lys	Lys	Asn	Glu	Glu	Val	Leu	Ile	Asp	Glu	Asn	Leu	Val
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Gly	Gly	Val	Ile	Ala	Leu	Asp	Arg	Leu	Ala	Lys	Leu	Asn	Lys	Ala	Asn
			20					25					30		

Arg	Thr	Phe	Lys	Arg	Ala	Phe	Tyr	Leu	Ser	Met	Ala	Leu	Asn	Val	Ala
		35					40					45			

Ala	Val	Thr	Ser	Ile	Val	Met	Met	Met	Pro	Leu	Lys	Lys	Thr	Asp	Ile
	50					55					60				

Phe	Val	Tyr	Gly	Ile	Asp	Arg	Tyr	Thr	Gly	Glu	Phe	Lys	Ile	Val	Lys
65					70					75					80



Arg Ser Asp Ala Arg Gln Ile Val Asn Ser Glu Ala Val Val Asp Ser  
85 90 95

Ala Thr Ser Lys Phe Val Ser Leu Leu Phe Gly Tyr Ser Lys Asn Ser  
100 105 110

Leu Arg Asp Arg Lys Asp Gln Leu Met Gln Tyr Cys Asp Val Ser Phe  
115 120 125

Gln Thr Gln Ala Met Arg Met Phe Asn Glu Asn Ile Arg Gln Phe Val  
130 135 140

Asp Lys Val Arg Ala Glu Ala Ile Ile Ser Ser Asn Ile Gln Arg Glu  
145 150 155 160

Lys Val Lys Asn Ser Pro Leu Thr Arg Leu Thr Phe Phe Ile Thr Ile  
165 170 175

Lys Ile Thr Pro Asp Thr Met Glu Asn Tyr Glu Tyr Ile Thr Lys Lys  
180 185 190

Gln Val Thr Ile Tyr Tyr Asp Phe Ala Arg Gly Asn Ser Ser Gln Glu  
195 200 205

Asn Leu Ile Ile Asn Pro Phe Gly Phe Lys Val Phe Asp Ile Gln Ile  
210 215 220

Thr Asp Leu Gln Asn Glu Gln Thr Val Ser Glu Ile Leu Arg Lys Ile  
225 230 235 240

Arg Glu Val Glu Ser Lys Asn Lys Ala Leu Asn Lys  
245 250

<210> 109  
<211> 1245  
<212> DNA  
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<220>  
<221> CDS  
<222> (1)..(1245)

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att Ile	tgt Cys	att Ile	ttt Phe 20	tat Tyr	ttg Leu	ctc Leu	ttt Phe	ttt Phe 25	acg Thr	act Thr	cct Pro	tac Tyr 30	att Ile	gta Val	ggc Gly	96
gat Asp	att Ile	ttg Leu 35	caa Gln	ttg Leu	aaa Lys	ttt Phe	atc Ile 40	cgc Arg	caa Gln	aag Lys	ctc Leu	tgc Cys 45	gaa Glu	aaa Lys	cct Pro	144
gtt Val	tta Leu 50	ctc Leu	cca Pro	caa Gln	aag Lys	gat Asp 55	tat Tyr	gaa Glu	gaa Glu	gcg Ala	gga Gly 60	aat Asn	tat Tyr	gcc Ala	att Ile	192
agg Arg 65	aaa Lys	atg Met	caa Gln	tta Leu	tcc Ser 70	att Ile	att Ile	tct Ser	caa Gln	att Ile 75	tta Leu	gac Asp	ggg Gly	ata Ile 80	atc Ile	240
ttt Phe	gct Ala	ggg Gly	tgg Trp	gtc Val 85	ttt Phe	ttt Phe	ggg Gly	ttg Leu	acg Thr 90	cat His	tta Leu	gaa Glu	gat Asp	ctc Leu 95	acg Thr	288
cat His	tat Tyr	tta Leu	aac Asn 100	ctt Leu	cct Pro	gaa Glu	acg Thr	cta Leu 105	ggg Gly	tac Tyr	ttg Leu	gtg Val	ttt Phe 110	gcc Ala	ttg Leu	336
ttg Leu	ttt Phe 115	tta Leu	gcg Ala	att Ile	caa Gln	agc Ser	gtt Val 120	tta Leu	gct Ala	tta Leu	ccc Pro	att Ile 125	agc Ser	tac Tyr	tac Tyr	384
acc Thr	acg Thr 130	atg Met	cat His	ttg Leu	gat Asp	aag Lys 135	gaa Glu	ttt Phe	ggc Gly	ttt Phe	tct Ser 140	aag Lys	gtg Val	agc Ser	ttg Leu	432
tcg Ser 145	ttg Leu	ttt Phe	ttt Phe	aag Lys 150	gat Asp	ttt Phe	ttc Phe	aaa Lys	ggg Gly	tta Leu 155	tcg Ser	ctc Leu	act Thr	tta Leu	agc Ser 160	480
gtg Val	ggg Gly	ttg Leu	ttg Leu	ttg Leu 165	att Ile	tac Tyr	act Thr	ctc Leu	att Ile 170	atg Met	atc Ile	att Ile	gaa Glu	cat His 175	gtg Val	528
gaa Glu	cat His	tgg Trp	gag Glu 180	att Ile	agc Ser	tcg Ser	ttt Phe	ttt Phe 185	gtc Val	gtg Val	ttt Phe	gtt Val	ttt Phe 190	atg Met	atc Ile	576
ttg Leu	gct Ala	aat Asn 195	ctt Leu	ttt Phe	tac Tyr	cct Pro	aaa Lys 200	atc Ile	gct Ala	cag Gln	ctt Leu	ttc Phe 205	aac Asn	caa Gln	ttc Phe	624
acc	ccc	ttg	aac	aat	agg	gat	tta	gag	agt	caa	att	gag	ggc	atg	atg	672

Thr	Pro	Leu	Asn	Asn	Arg	Asp	Leu	Glu	Ser	Gln	Ile	Glu	Gly	Met	Met	
	210					215					220					
gat	aag	gtg	ggt	ttt	aaa	tct	gaa	ggt	atc	ttt	gtg	atg	gac	gct	agc	720
Asp	Lys	Val	Gly	Phe	Lys	Ser	Glu	Gly	Ile	Phe	Val	Met	Asp	Ala	Ser	
225					230					235					240	
aag	agg	gac	ggg	cgt	ttg	aac	gcg	tat	ttt	gga	ggc	ttg	ggt	aaa	aac	768
Lys	Arg	Asp	Gly	Arg	Leu	Asn	Ala	Tyr	Phe	Gly	Gly	Leu	Gly	Lys	Asn	
				245					250					255		
aag	cgg	gtg	gtg	ttg	ttt	gac	act	ttg	atc	tct	aaa	ggt	ggg	aca	gaa	816
Lys	Arg	Val	Val	Leu	Phe	Asp	Thr	Leu	Ile	Ser	Lys	Val	Gly	Thr	Glu	
			260					265					270			
ggg	ctt	tta	gcc	att	tta	ggg	cat	gaa	tta	ggg	cat	ttt	aaa	aat	aag	864
Gly	Leu	Leu	Ala	Ile	Leu	Gly	His	Glu	Leu	Gly	His	Phe	Lys	Asn	Lys	
		275					280					285				
gat	ttg	ttg	aaa	agt	tta	ggg	att	atg	gga	ggc	tta	ctc	gct	ctt	gtt	912
Asp	Leu	Leu	Lys	Ser	Leu	Gly	Ile	Met	Gly	Gly	Leu	Leu	Ala	Leu	Val	
	290					295					300					
ttt	gct	ctg	atc	gct	cat	ttg	ccg	ccg	ttg	gtt	ttt	gaa	ggc	ttc	aat	960
Phe	Ala	Leu	Ile	Ala	His	Leu	Pro	Pro	Leu	Val	Phe	Glu	Gly	Phe	Asn	
305					310					315					320	
gtc	tca	caa	acg	cca	gcg	agt	ttg	att	gcg	att	tta	ctc	ttg	ttt	ttg	1008
Val	Ser	Gln	Thr	Pro	Ala	Ser	Leu	Ile	Ala	Ile	Leu	Leu	Leu	Phe	Leu	
				325					330					335		
ccg	gta	ttt	tct	ttt	tac	gct	atg	cct	ttg	atc	ggg	ttt	ttt	agc	cga	1056
Pro	Val	Phe	Ser	Phe	Tyr	Ala	Met	Pro	Leu	Ile	Gly	Phe	Phe	Ser	Arg	
			340					345					350			
aag	aat	gaa	tac	aat	gca	gac	aag	ttt	ggg	gcg	agt	tta	agc	tct	aaa	1104
Lys	Asn	Glu	Tyr	Asn	Ala	Asp	Lys	Phe	Gly	Ala	Ser	Leu	Ser	Ser	Lys	
		355					360					365				
gag	gtt	tta	gcc	aaa	gcg	tta	gtg	tct	att	gtg	agt	gag	aat	aaa	gcg	1152
Glu	Val	Leu	Ala	Lys	Ala	Leu	Val	Ser	Ile	Val	Ser	Glu	Asn	Lys	Ala	
	370					375				380						
ttc	ccc	tat	tcg	cac	cct	ttt	tat	gtt	ttc	ttg	cat	ttc	acg	cac	ccg	1200
Phe	Pro	Tyr	Ser	His	Pro	Phe	Tyr	Val	Phe	Leu	His	Phe	Thr	His	Pro	
385					390					395					400	
ccc	tta	tta	gag	cgc	ttg	aaa	gct	ttg	gat	tat	gaa	att	gaa	tga		1245
Pro	Leu	Leu	Glu	Arg	Leu	Lys	Ala	Leu	Asp	Tyr	Glu	Ile	Glu			
				405					410							
<210>	110															
<211>	414															
<212>	PRT															

<213> Helicobacter pylori

<400> 110

Met Glu Lys Gly Val Trp Asn Met Leu Asp Ile Trp Ile Asp Met Ile  
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Ile Cys Ile Phe Tyr Leu Leu Phe Phe Thr Thr Pro Tyr Ile Val Gly  
20 25 30

Asp Ile Leu Gln Leu Lys Phe Ile Arg Gln Lys Leu Cys Glu Lys Pro  
35 40 45

Val Leu Leu Pro Gln Lys Asp Tyr Glu Glu Ala Gly Asn Tyr Ala Ile  
50 55 60

Arg Lys Met Gln Leu Ser Ile Ile Ser Gln Ile Leu Asp Gly Ile Ile  
65 70 75 80

Phe Ala Gly Trp Val Phe Phe Gly Leu Thr His Leu Glu Asp Leu Thr  
85 90 95

His Tyr Leu Asn Leu Pro Glu Thr Leu Gly Tyr Leu Val Phe Ala Leu  
100 105 110

Leu Phe Leu Ala Ile Gln Ser Val Leu Ala Leu Pro Ile Ser Tyr Tyr  
115 120 125

Thr Thr Met His Leu Asp Lys Glu Phe Gly Phe Ser Lys Val Ser Leu  
130 135 140

Ser Leu Phe Phe Lys Asp Phe Phe Lys Gly Leu Ser Leu Thr Leu Ser  
145 150 155 160

Val Gly Leu Leu Leu Ile Tyr Thr Leu Ile Met Ile Ile Glu His Val  
165 170 175

Glu His Trp Glu Ile Ser Ser Phe Phe Val Val Phe Val Phe Met Ile  
180 185 190

Leu Ala Asn Leu Phe Tyr Pro Lys Ile Ala Gln Leu Phe Asn Gln Phe  
195 200 205

Thr Pro Leu Asn Asn Arg Asp Leu Glu Ser Gln Ile Glu Gly Met Met  
 210 215 220

Asp Lys Val Gly Phe Lys Ser Glu Gly Ile Phe Val Met Asp Ala Ser  
 225 230 235 240

Lys Arg Asp Gly Arg Leu Asn Ala Tyr Phe Gly Gly Leu Gly Lys Asn  
 245 250 255

Lys Arg Val Val Leu Phe Asp Thr Leu Ile Ser Lys Val Gly Thr Glu  
 260 265 270

Gly Leu Leu Ala Ile Leu Gly His Glu Leu Gly His Phe Lys Asn Lys  
 275 280 285

Asp Leu Leu Lys Ser Leu Gly Ile Met Gly Gly Leu Leu Ala Leu Val  
 290 295 300

Phe Ala Leu Ile Ala His Leu Pro Pro Leu Val Phe Glu Gly Phe Asn  
 305 310 315 320

Val Ser Gln Thr Pro Ala Ser Leu Ile Ala Ile Leu Leu Leu Phe Leu  
 325 330 335

Pro Val Phe Ser Phe Tyr Ala Met Pro Leu Ile Gly Phe Phe Ser Arg  
 340 345 350

Lys Asn Glu Tyr Asn Ala Asp Lys Phe Gly Ala Ser Leu Ser Ser Lys  
 355 360 365

Glu Val Leu Ala Lys Ala Leu Val Ser Ile Val Ser Glu Asn Lys Ala  
 370 375 380

Phe Pro Tyr Ser His Pro Phe Tyr Val Phe Leu His Phe Thr His Pro  
 385 390 395 400

Pro Leu Leu Glu Arg Leu Lys Ala Leu Asp Tyr Glu Ile Glu  
 405 410

<210> 111

<211> 1566  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> misc\_feature  
 <222> (1)..(1566)

<220>  
 <221> CDS  
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 1 5 10 15  
 aat att ttt aaa aac act gat aat gaa aat gaa aga cta aaa aaa ttc 96  
 Asn Ile Phe Lys Asn Thr Asp Asn Glu Asn Glu Arg Leu Lys Lys Phe  
 20 25 30  
 aac caa gaa gcg ttg gag gtg ttt caa aaa tta gag cgt gaa agt tta 144  
 Asn Gln Glu Ala Leu Glu Val Phe Gln Lys Leu Glu Arg Glu Ser Leu  
 35 40 45  
 aaa gag ctt gaa agc tta aaa aat aat gag gag tgg gaa aat ttt act 192  
 Lys Glu Leu Glu Ser Leu Lys Asn Asn Glu Glu Trp Glu Asn Phe Thr  
 50 55 60  
 atc gct ttt tat ggg gaa acc ggt gcg ggg aaa tca acc ttc att gaa 240  
 Ile Ala Phe Tyr Gly Glu Thr Gly Ala Gly Lys Ser Thr Phe Ile Glu  
 65 70 75 80  
 tgt ttg aga atg ttt ttt aaa gaa caa agt aaa gta gtt caa caa gaa 288  
 Cys Leu Arg Met Phe Phe Lys Glu Gln Ser Lys Val Val Gln Gln Glu  
 85 90 95  
 cga ttc aag cgg ctt tat tcc aat tac caa aac aac tat caa aat gat 336  
 Arg Phe Lys Arg Leu Tyr Ser Asn Tyr Gln Asn Asn Tyr Gln Asn Asp  
 100 105 110  
 gaa tgc aaa aag caa gct att tta aac gaa ctt cat tca ttg caa gat 384  
 Glu Cys Lys Lys Gln Ala Ile Leu Asn Glu Leu His Ser Leu Gln Asp  
 115 120 125  
 gga gcg atc ata ggc gat ggg agg agc gat ttc act tta aaa aca cga 432  
 Gly Ala Ile Ile Gly Asp Gly Arg Ser Asp Phe Thr Leu Lys Thr Arg  
 130 135 140  
 tct tat tct ttc caa tac aac cat caa aac ttt act ttg ctt gat gtt 480  
 Ser Tyr Ser Phe Gln Tyr Asn His Gln Asn Phe Thr Leu Leu Asp Val  
 145 150 155 160  
 cca ggg ata gaa ggc gac gaa aaa aaa gtg atc gat cag att tct aac 528

Pro	Gly	Ile	Glu	Gly	Asp	Glu	Lys	Lys	Val	Ile	Asp	Gln	Ile	Ser	Asn	
				165					170					175		
gca	acg	caa	aaa	gcc	cat	gct	att	ttt	tat	gtt	acc	aaa	acg	cct	aat	576
Ala	Thr	Gln	Lys	Ala	His	Ala	Ile	Phe	Tyr	Val	Thr	Lys	Thr	Pro	Asn	
			180					185					190			
cct	ccg	caa	aaa	gga	gaa	gag	aaa	aaa	gaa	ggg	acg	att	gaa	aaa	atc	624
Pro	Pro	Gln	Lys	Gly	Glu	Glu	Lys	Lys	Glu	Gly	Thr	Ile	Glu	Lys	Ile	
			195				200					205				
caa	aaa	caa	ctt	gat	tcg	caa	aca	gag	gta	tgg	acg	att	ttt	aac	aaa	672
Gln	Lys	Gln	Leu	Asp	Ser	Gln	Thr	Glu	Val	Trp	Thr	Ile	Phe	Asn	Lys	
	210					215					220					
ccg	att	aac	aac	cca	aga	gct	ttc	aaa	gat	ggg	ctt	att	gat	gga	agc	720
Pro	Ile	Asn	Asn	Pro	Arg	Ala	Phe	Lys	Asp	Gly	Leu	Ile	Asp	Gly	Ser	
225					230					235					240	
gaa	aaa	gaa	agc	tta	aaa	att	tta	aat	aaa	gaa	atg	aaa	aac	att	tta	768
Glu	Lys	Glu	Ser	Leu	Lys	Ile	Leu	Asn	Lys	Glu	Met	Lys	Asn	Ile	Leu	
				245					250					255		
ggc	aaa	cac	tac	aag	ggc	tat	aaa	gca	gtg	agc	gcc	caa	gtg	gct	ttt	816
Gly	Lys	His	Tyr	Lys	Gly	Tyr	Lys	Ala	Val	Ser	Ala	Gln	Val	Ala	Phe	
			260					265					270			
tat	ggt	ctt	tca	tcg	gct	ttg	atc	cca	ggg	act	gat	ttt	gat	aaa	aac	864
Tyr	Gly	Leu	Ser	Ser	Ala	Leu	Ile	Pro	Gly	Thr	Asp	Phe	Asp	Lys	Asn	
		275					280					285				
aaa	caa	aaa	ttt	tta	aaa	gat	ttt	aaa	gca	aga	gaa	tta	ttg	tat	caa	912
Lys	Gln	Lys	Phe	Leu	Lys	Asp	Phe	Lys	Ala	Arg	Glu	Leu	Leu	Tyr	Gln	
	290					295					300					
tcc	cat	ttc	caa	caa	tta	gga	gaa	ttt	ata	gcc	gaa	gag	ctt	att	aaa	960
Ser	His	Phe	Gln	Gln	Leu	Gly	Glu	Phe	Ile	Ala	Glu	Glu	Leu	Ile	Lys	
305					310					315					320	
aac	tcg	cgt	gcc	aaa	atc	att	caa	tca	aac	tgc	aat	aaa	gcc	tta	aaa	1008
Asn	Ser	Arg	Ala	Lys	Ile	Ile	Gln	Ser	Asn	Cys	Asn	Lys	Ala	Leu	Lys	
				325					330					335		
gtg	gta	gaa	caa	ttg	caa	aag	gcg	atc	gaa	att	acg	att	gaa	aaa	cgg	1056
Val	Val	Glu	Gln	Leu	Gln	Lys	Ala	Ile	Glu	Ile	Thr	Ile	Glu	Lys	Arg	
			340					345					350			
atc	gat	cca	atg	att	aaa	gaa	gca	caa	gaa	tac	caa	cac	gaa	gcc	cgc	1104
Ile	Asp	Pro	Met	Ile	Lys	Glu	Ala	Gln	Glu	Tyr	Gln	His	Glu	Ala	Arg	
		355					360					365				
tat	aat	ctg	gat	cgt	tct	aca	gat	aaa	ttt	ata	tta	aat	tta	acc	aat	1152
Tyr	Asn	Leu	Asp	Arg	Ser	Thr	Asp	Lys	Phe	Ile	Leu	Asn	Leu	Thr	Asn	
	370					375					380					

tca gcg ttc tac gaa atc gat caa ttc aaa tct gac ttg aga gaa aaa	1200
Ser Ala Phe Tyr Glu Ile Asp Gln Phe Lys Ser Asp Leu Arg Glu Lys	
385 390 395 400	

atg tat gcg cat att aac aaa aat att gaa gat gag gaa tgt aaa gaa	1248
Met Tyr Ala His Ile Asn Lys Asn Ile Glu Asp Glu Glu Cys Lys Glu	
405 410 415	

att ttt aaa aat gaa ctc att caa gga att gaa aca ttg cat gaa gac	1296
Ile Phe Lys Asn Glu Leu Ile Gln Gly Ile Glu Thr Leu His Glu Asp	
420 425 430	

ata aaa tgg cgg ttt aga gaa tgt gag aaa cga ttt gat gga gag ata	1344
Ile Lys Trp Arg Phe Arg Glu Cys Glu Lys Arg Phe Asp Gly Glu Ile	
435 440 445	

aaa gaa gct att aaa caa ctt gaa tac aga att aaa gat tct cta gca	1392
Lys Glu Ala Ile Lys Gln Leu Glu Tyr Arg Ile Lys Asp Ser Leu Ala	
450 455 460	

atg tta gag cgc atc agt att gat aga gac ttt aat ctt aat ttt gat	1440
Met Leu Glu Arg Ile Ser Ile Asp Arg Asp Phe Asn Leu Asn Phe Asp	
465 470 475 480	

act gat agc ggt att gat gga aca aaa tta gcc act tca ata gga ggt	1488
Thr Asp Ser Gly Ile Asp Gly Thr Lys Leu Ala Thr Ser Ile Gly Gly	
485 490 495	

ttg ggt ttg ctt ggg ata ttt aac gct tgg aat cct atg ggt tgg ctt	1536
Leu Gly Leu Leu Gly Ile Phe Asn Ala Trp Asn Pro Met Gly Trp Leu	
500 505 510	

gct ctg acc gca gga tta ttg cag gat tag	1566
Ala Leu Thr Ala Gly Leu Leu Gln Asp	
515 520	

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 <212> PRT  
 <213> Helicobacter pylori

<400> 112

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Asn Ile Phe Lys Asn Thr Asp Asn Glu Asn Glu Arg Leu Lys Lys Phe
20 25 30

Asn Gln Glu Ala Leu Glu Val Phe Gln Lys Leu Glu Arg Glu Ser Leu
35 40 45



Lys	Glu	Leu	Glu	Ser	Leu	Lys	Asn	Asn	Glu	Glu	Trp	Glu	Asn	Phe	Thr	50	55	60
Ile	Ala	Phe	Tyr	Gly	Glu	Thr	Gly	Ala	Gly	Lys	Ser	Thr	Phe	Ile	Glu	65	70	75
Cys	Leu	Arg	Met	Phe	Phe	Lys	Glu	Gln	Ser	Lys	Val	Val	Gln	Gln	Glu	85	90	95
Arg	Phe	Lys	Arg	Leu	Tyr	Ser	Asn	Tyr	Gln	Asn	Asn	Tyr	Gln	Asn	Asp	100	105	110
Glu	Cys	Lys	Lys	Gln	Ala	Ile	Leu	Asn	Glu	Leu	His	Ser	Leu	Gln	Asp	115	120	125
Gly	Ala	Ile	Ile	Gly	Asp	Gly	Arg	Ser	Asp	Phe	Thr	Leu	Lys	Thr	Arg	130	135	140
Ser	Tyr	Ser	Phe	Gln	Tyr	Asn	His	Gln	Asn	Phe	Thr	Leu	Leu	Asp	Val	145	150	155
Pro	Gly	Ile	Glu	Gly	Asp	Glu	Lys	Lys	Val	Ile	Asp	Gln	Ile	Ser	Asn	165	170	175
Ala	Thr	Gln	Lys	Ala	His	Ala	Ile	Phe	Tyr	Val	Thr	Lys	Thr	Pro	Asn	180	185	190
Pro	Pro	Gln	Lys	Gly	Glu	Glu	Lys	Lys	Glu	Gly	Thr	Ile	Glu	Lys	Ile	195	200	205
Gln	Lys	Gln	Leu	Asp	Ser	Gln	Thr	Glu	Val	Trp	Thr	Ile	Phe	Asn	Lys	210	215	220
Pro	Ile	Asn	Asn	Pro	Arg	Ala	Phe	Lys	Asp	Gly	Leu	Ile	Asp	Gly	Ser	225	230	235
Glu	Lys	Glu	Ser	Leu	Lys	Ile	Leu	Asn	Lys	Glu	Met	Lys	Asn	Ile	Leu	245	250	255
Gly	Lys	His	Tyr	Lys	Gly	Tyr	Lys	Ala	Val	Ser	Ala	Gln	Val	Ala	Phe			

260					265					270					
Tyr	Gly	Leu	Ser	Ser	Ala	Leu	Ile	Pro	Gly	Thr	Asp	Phe	Asp	Lys	Asn
		275					280					285			
Lys	Gln	Lys	Phe	Leu	Lys	Asp	Phe	Lys	Ala	Arg	Glu	Leu	Leu	Tyr	Gln
	290					295					300				
Ser	His	Phe	Gln	Gln	Leu	Gly	Glu	Phe	Ile	Ala	Glu	Glu	Leu	Ile	Lys
305					310					315					320
Asn	Ser	Arg	Ala	Lys	Ile	Ile	Gln	Ser	Asn	Cys	Asn	Lys	Ala	Leu	Lys
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Val	Val	Glu	Gln	Leu	Gln	Lys	Ala	Ile	Glu	Ile	Thr	Ile	Glu	Lys	Arg
			340					345					350		
Ile	Asp	Pro	Met	Ile	Lys	Glu	Ala	Gln	Glu	Tyr	Gln	His	Glu	Ala	Arg
		355					360					365			
Tyr	Asn	Leu	Asp	Arg	Ser	Thr	Asp	Lys	Phe	Ile	Leu	Asn	Leu	Thr	Asn
	370					375					380				
Ser	Ala	Phe	Tyr	Glu	Ile	Asp	Gln	Phe	Lys	Ser	Asp	Leu	Arg	Glu	Lys
385					390					395					400
Met	Tyr	Ala	His	Ile	Asn	Lys	Asn	Ile	Glu	Asp	Glu	Glu	Cys	Lys	Glu
				405					410					415	
Ile	Phe	Lys	Asn	Glu	Leu	Ile	Gln	Gly	Ile	Glu	Thr	Leu	His	Glu	Asp
			420					425					430		
Ile	Lys	Trp	Arg	Phe	Arg	Glu	Cys	Glu	Lys	Arg	Phe	Asp	Gly	Glu	Ile
		435					440					445			
Lys	Glu	Ala	Ile	Lys	Gln	Leu	Glu	Tyr	Arg	Ile	Lys	Asp	Ser	Leu	Ala
	450					455					460				
Met	Leu	Glu	Arg	Ile	Ser	Ile	Asp	Arg	Asp	Phe	Asn	Leu	Asn	Phe	Asp
465					470					475					480

Thr Asp Ser Gly Ile Asp Gly Thr Lys Leu Ala Thr Ser Ile Gly Gly  
485 490 495

Leu Gly Leu Leu Gly Ile Phe Asn Ala Trp Asn Pro Met Gly Trp Leu  
500 505 510

Ala Leu Thr Ala Gly Leu Leu Gln Asp  
515 520

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<211> 1782  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(1782)

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1 5 10 15  
atc agc gtg aat agg gcg ttg ttt gat tta aaa gat tcg caa tta aaa 96  
Ile Ser Val Asn Arg Ala Leu Phe Asp Leu Lys Asp Ser Gln Leu Lys  
20 25 30  
ggg gaa tta acg cca aaa ata gtg aat ttt ggg ggt tat aaa agc agc 144  
Gly Glu Leu Thr Pro Lys Ile Val Asn Phe Gly Gly Tyr Lys Ser Ser  
35 40 45  
act gaa gag tgg ggg gct acg gct tta aac tat atc aat gcg gct aat 192  
Thr Glu Glu Trp Gly Ala Thr Ala Leu Asn Tyr Ile Asn Ala Ala Asn  
50 55 60  
ggc gat gcg aaa aaa ttc agc act cta gtg gaa aaa atg cgt ttt aac 240  
Gly Asp Ala Lys Lys Phe Ser Thr Leu Val Glu Lys Met Arg Phe Asn  
65 70 75 80  
tcc ggt ata ttg ggg aat tta aga gtg cat gca cgt ttg agg caa gcc 288  
Ser Gly Ile Leu Gly Asn Leu Arg Val His Ala Arg Leu Arg Gln Ala  
85 90 95  
cta aaa ttg caa aag aat ttg aaa tat tgc ctt aaa atc atc gct agg 336  
Leu Lys Leu Gln Lys Asn Leu Lys Tyr Cys Leu Lys Ile Ile Ala Arg  
100 105 110  
gat tct ttt tat agc tac cgc acc ggt att tat atc ccc tta ggc att 384  
Asp Ser Phe Tyr Ser Tyr Arg Thr Gly Ile Tyr Ile Pro Leu Gly Ile  
115 120 125

tct tta aaa gat caa aaa acg gct caa aaa atg ctc gct gat ttg agc Ser Leu Lys Asp Gln Lys Thr Ala Gln Lys Met Leu Ala Asp Leu Ser 130 135 140	432
gtg gta ggg gcg tat ctt aaa aaa caa caa gag aat gaa aag gct caa Val Val Gly Ala Tyr Leu Lys Lys Gln Gln Glu Asn Glu Lys Ala Gln 145 150 155 160	480
agc cct tat tac aga aac aac aac tat tac aac tct tac tat agc cct Ser Pro Tyr Tyr Arg Asn Asn Asn Tyr Tyr Asn Ser Tyr Tyr Ser Pro 165 170 175	528
tat tac gga atg tat ggt atg tat ggc atg ggc atg tat gga atg tat Tyr Tyr Gly Met Tyr Gly Met Tyr Gly Met Gly Met Tyr Gly Met Tyr 180 185 190	576
ggc atg ggc atg tat gat ttt tat gac ttt tat gat ggc atg tat gga Gly Met Gly Met Tyr Asp Phe Tyr Asp Phe Tyr Asp Gly Met Tyr Gly 195 200 205	624
ttc tac cct aac atg ttt ttc atg atg caa gtt caa gat tac ttg atg Phe Tyr Pro Asn Met Phe Phe Met Met Gln Val Gln Asp Tyr Leu Met 210 215 220	672
tta gaa aat tac atg tat gcg ctc gat caa gaa gag att tta gat cat Leu Glu Asn Tyr Met Tyr Ala Leu Asp Gln Glu Glu Ile Leu Asp His 225 230 235 240	720
gac gct tct act gac caa ctt gat acg cct act gat gat gac aaa gac Asp Ala Ser Thr Asp Gln Leu Asp Thr Pro Thr Asp Asp Asp Lys Asp 245 250 255	768
gat aaa gac gat aaa tcc tta cag cag gca aat ctt atg aac ttt tat Asp Lys Asp Asp Lys Ser Leu Gln Gln Ala Asn Leu Met Asn Phe Tyr 260 265 270	816
cgt gat ccc aaa ttc agc aaa ggc att caa acc aac cgc ttg aat agc Arg Asp Pro Lys Phe Ser Lys Gly Ile Gln Thr Asn Arg Leu Asn Ser 275 280 285	864
gct tta gtc aat tta gac aac agt cgc atg ctc aaa gac aat tcg ctt Ala Leu Val Asn Leu Asp Asn Ser Arg Met Leu Lys Asp Asn Ser Leu 290 295 300	912
ttc cac act aaa gcc atg ccc act aaa agc gtg gat gcg ata act tct Phe His Thr Lys Ala Met Pro Thr Lys Ser Val Asp Ala Ile Thr Ser 305 310 315 320	960
caa gcc aaa gag ctt aac cat tta gtg ggg caa atc aaa gaa atg aag Gln Ala Lys Glu Leu Asn His Leu Val Gly Gln Ile Lys Glu Met Lys 325 330 335	1008
caa gac ggg gcg agt cct agt aag att gat tca gtt gtc aat aaa gct	1056

Gln	Asp	Gly	Ala	Ser	Pro	Ser	Lys	Ile	Asp	Ser	Val	Val	Asn	Lys	Ala	
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atg	gaa	gtg	agg	gac	aag	cta	gac	aat	aat	ctc	aac	caa	cta	gac	aat	1104
Met	Glu	Val	Arg	Asp	Lys	Leu	Asp	Asn	Asn	Leu	Asn	Gln	Leu	Asp	Asn	
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gac	tta	aaa	gat	caa	aaa	ggg	ctt	tca	agc	gag	caa	caa	gct	caa	gtg	1152
Asp	Leu	Lys	Asp	Gln	Lys	Gly	Leu	Ser	Ser	Glu	Gln	Gln	Ala	Gln	Val	
	370					375				380						
gat	aaa	gcc	cta	gac	agc	gtg	caa	caa	tta	agc	cat	agc	agc	gat	gtg	1200
Asp	Lys	Ala	Leu	Asp	Ser	Val	Gln	Gln	Leu	Ser	His	Ser	Ser	Asp	Val	
385					390					395					400	
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Val	Gly	Asn	Tyr	Leu	Asp	Gly	Ser	Leu	Lys	Ile	Asp	Gly	Asp	Asp	Arg	
				405					410					415		
gat	gat	ttg	aat	gat	gcg	atg	aat	aac	cct	atg	caa	caa	ccc	gtg	caa	1296
Asp	Asp	Leu	Asn	Asp	Ala	Met	Asn	Asn	Pro	Met	Gln	Gln	Pro	Val	Gln	
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caa	acg	cct	act	agc	aac	atg	gcc	gac	acc	cat	gca	aat	gac	agc	aag	1344
Gln	Thr	Pro	Thr	Ser	Asn	Met	Ala	Asp	Thr	His	Ala	Asn	Asp	Ser	Lys	
		435					440					445				
gat	caa	ggg	agt	aac	gcg	ctc	ata	aac	cct	aac	agc	gcc	act	aac	gcc	1392
Asp	Gln	Gly	Ser	Asn	Ala	Leu	Ile	Asn	Pro	Asn	Ser	Ala	Thr	Asn	Ala	
	450					455					460					
gac	gac	act	cac	act	gac	gat	act	cac	act	gac	act	aac	acc	aca	aac	1440
Asp	Asp	Thr	His	Thr	Asp	Asp	Thr	His	Thr	Asp	Thr	Asn	Thr	Thr	Asn	
465					470					475					480	
gat	gct	agc	acc	act	gac	acc	ccc	act	gac	gat	aaa	gat	gct	agc	ggc	1488
Asp	Ala	Ser	Thr	Thr	Asp	Thr	Pro	Thr	Asp	Asp	Lys	Asp	Ala	Ser	Gly	
				485					490					495		
ttg	aac	aat	acc	ggc	gat	atg	aat	aac	acg	gat	acc	ggc	aac	acg	gac	1536
Leu	Asn	Asn	Thr	Gly	Asp	Met	Asn	Asn	Thr	Asp	Thr	Gly	Asn	Thr	Asp	
			500					505					510			
acc	ggc	aat	acg	gat	acc	ggt	aac	act	gat	gat	atg	agc	aac	atg	aac	1584
Thr	Gly	Asn	Thr	Asp	Thr	Gly	Asn	Thr	Asp	Asp	Met	Ser	Asn	Met	Asn	
		515					520					525				
aac	ggc	aac	gat	gat	acg	ggt	aac	gct	aat	gac	gac	atg	agc	aac	ggc	1632
Asn	Gly	Asn	Asp	Asp	Thr	Gly	Asn	Ala	Asn	Asp	Asp	Met	Ser	Asn	Gly	
	530					535					540					
aac	gac	atg	ggc	gat	gat	ttg	aac	aac	gcg	aac	gat	atg	aac	gac	gac	1680
Asn	Asp	Met	Gly	Asp	Asp	Leu	Asn	Asn	Ala	Asn	Asp	Met	Asn	Asp	Asp	

545		550		555		560	
atg ggt aat ggc aac gat gac atg ggc gat atg ggg gat atg aac gac							1728
Met Gly Asn Gly Asn Asp Asp Met Gly Asp Met Gly Asp Met Asn Asp							
		565		570		575	
gat atg ggt ggc gat atg gga gac atg ggg gat atg ggc gat atg ggg							1776
Asp Met Gly Gly Asp Met Gly Asp Met Gly Asp Met Gly Asp Met Gly							
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aat tga							1782
Asn							

<210> 114  
 <211> 593  
 <212> PRT  
 <213> Helicobacter pylori

<400> 114

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Gly Glu Leu Thr Pro Lys Ile Val Asn Phe Gly Gly Tyr Lys Ser Ser
35 40 45

Thr Glu Glu Trp Gly Ala Thr Ala Leu Asn Tyr Ile Asn Ala Ala Asn
50 55 60

Gly Asp Ala Lys Lys Phe Ser Thr Leu Val Glu Lys Met Arg Phe Asn
65 70 75 80

Ser Gly Ile Leu Gly Asn Leu Arg Val His Ala Arg Leu Arg Gln Ala
85 90 95

Leu Lys Leu Gln Lys Asn Leu Lys Tyr Cys Leu Lys Ile Ile Ala Arg
100 105 110

Asp Ser Phe Tyr Ser Tyr Arg Thr Gly Ile Tyr Ile Pro Leu Gly Ile
115 120 125

Ser Leu Lys Asp Gln Lys Thr Ala Gln Lys Met Leu Ala Asp Leu Ser
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130	135	140														
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Ser	Pro	Tyr	Tyr	Arg 165	Asn	Asn	Asn	Tyr	Tyr 170	Asn	Ser	Tyr	Tyr	Ser 175	Pro	
Tyr	Tyr	Gly	Met 180	Tyr	Gly	Met	Tyr	Gly 185	Met	Gly	Met	Tyr	Gly 190	Met	Tyr	
Gly	Met	Gly 195	Met	Tyr	Asp	Phe	Tyr 200	Asp	Phe	Tyr	Asp	Gly 205	Met	Tyr	Gly	
Phe	Tyr 210	Pro	Asn	Met	Phe	Phe 215	Met	Met	Gln	Val	Gln 220	Asp	Tyr	Leu	Met	
Leu 225	Glu	Asn	Tyr	Met	Tyr 230	Ala	Leu	Asp	Gln	Glu 235	Glu	Ile	Leu	Asp	His 240	
Asp	Ala	Ser	Thr	Asp 245	Gln	Leu	Asp	Thr	Pro 250	Thr	Asp	Asp	Asp	Lys 255	Asp	
Asp	Lys	Asp	Asp 260	Lys	Ser	Leu	Gln	Gln 265	Ala	Asn	Leu	Met	Asn 270	Phe	Tyr	
Arg	Asp 275	Pro	Lys	Phe	Ser	Lys	Gly 280	Ile	Gln	Thr	Asn 285	Arg	Leu	Asn	Ser	
Ala 290	Leu	Val	Asn	Leu	Asp	Asn 295	Ser	Arg	Met	Leu	Lys 300	Asp	Asn	Ser	Leu	
Phe 305	His	Thr	Lys	Ala	Met 310	Pro	Thr	Lys	Ser	Val 315	Asp	Ala	Ile	Thr	Ser 320	
Gln	Ala	Lys	Glu	Leu 325	Asn	His	Leu	Val	Gly 330	Gln	Ile	Lys	Glu	Met 335	Lys	
Gln	Asp	Gly	Ala	Ser	Pro	Ser	Lys	Ile 345	Asp	Ser	Val	Val	Asn 350	Lys	Ala	

Met	Glu	Val	Arg	Asp	Lys	Leu	Asp	Asn	Asn	Leu	Asn	Gln	Leu	Asp	Asn			
		355					360					365						
Asp	Leu	Lys	Asp	Gln	Lys	Gly	Leu	Ser	Ser	Glu	Gln	Gln	Ala	Gln	Val			
	370					375					380							
Asp	Lys	Ala	Leu	Asp	Ser	Val	Gln	Gln	Leu	Ser	His	Ser	Ser	Asp	Val			
	385				390					395					400			
Val	Gly	Asn	Tyr	Leu	Asp	Gly	Ser	Leu	Lys	Ile	Asp	Gly	Asp	Asp	Arg			
				405					410					415				
Asp	Asp	Leu	Asn	Asp	Ala	Met	Asn	Asn	Pro	Met	Gln	Gln	Pro	Val	Gln			
			420					425					430					
Gln	Thr	Pro	Thr	Ser	Asn	Met	Ala	Asp	Thr	His	Ala	Asn	Asp	Ser	Lys			
		435					440					445						
Asp	Gln	Gly	Ser	Asn	Ala	Leu	Ile	Asn	Pro	Asn	Ser	Ala	Thr	Asn	Ala			
	450					455					460							
Asp	Asp	Thr	His	Thr	Asp	Asp	Thr	His	Thr	Asp	Thr	Asn	Thr	Thr	Asn			
	465				470					475					480			
Asp	Ala	Ser	Thr	Thr	Asp	Thr	Pro	Thr	Asp	Asp	Lys	Asp	Ala	Ser	Gly			
				485					490					495				
Leu	Asn	Asn	Thr	Gly	Asp	Met	Asn	Asn	Thr	Asp	Thr	Gly	Asn	Thr	Asp			
			500					505					510					
Thr	Gly	Asn	Thr	Asp	Thr	Gly	Asn	Thr	Asp	Asp	Met	Ser	Asn	Met	Asn			
		515					520					525						
Asn	Gly	Asn	Asp	Asp	Thr	Gly	Asn	Ala	Asn	Asp	Asp	Met	Ser	Asn	Gly			
	530					535					540							
Asn	Asp	Met	Gly	Asp	Asp	Leu	Asn	Asn	Ala	Asn	Asp	Met	Asn	Asp	Asp			
	545				550					555					560			
Met	Gly	Asn	Gly	Asn	Asp	Asp	Met	Gly	Asp	Met	Gly	Asp	Met	Asn	Asp			
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Asp Met Gly Gly Asp Met Gly Asp Met Gly Asp Met Gly Asp Met Gly  
580 585 590

Asn

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<211> 8709  
<212> DNA  
<213> Helicobacter pylori

<220>  
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<222> (1)..(8709)

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aat caa aaa aca atc tta aag cgt cct tta tgg ctt atg cct tta ctg 96  
Asn Gln Lys Thr Ile Leu Lys Arg Pro Leu Trp Leu Met Pro Leu Leu  
20 25 30  
att ggc ggg ttt gct agt ggg gtg tat gcg gat gga aca gac att ttg 144  
Ile Gly Gly Phe Ala Ser Gly Val Tyr Ala Asp Gly Thr Asp Ile Leu  
35 40 45  
ggg ctt agt tgg ggg gaa aaa agc caa aag gta tgc gtg cat cgt cca 192  
Gly Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro  
50 55 60  
tgg tat gct ata tgg agt tgc gat aaa tgg gag gaa aaa aca caa caa 240  
Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln  
65 70 75 80  
ttt aca gga aac caa ctc atc aca aaa act tgg gca ggg ggt aat gcg 288  
Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala  
85 90 95  
gct aac tac tac cac tct caa aac aac caa gac atc aca gcc aat tta 336  
Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu  
100 105 110  
aaa aat gat aac ggc act tat ttt tta agc ggt ctg tat aac tac acc 384  
Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr  
115 120 125  
gga ggg gaa tat aat ggg ggg aat tta gac att gaa tta ggc agt aac 432  
Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn

130	135	140	
gct act ttt aat cta ggt gcg agt agt ggg aat agc ttc act tct tgg Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp 145 150 155 160			480
tat cct aat ggg cat act gat gtt act ttt agc gct ggg act atc aat Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn 165 170 175			528
gtg aat aac agc gta gaa gtg ggc aat cgt gtg gga tcg gga gct ggc Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly 180 185 190			576
acg cac acc ggc aca gcc act tta aac ttg aac gct aat aag gtt act Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr 195 200 205			624
atc aat tcc aat atc agc gcg tat aaa act tcg caa gtg aat gta ggc Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly 210 215 220			672
aat gct aac agc gtt att acc att aat tcg gtt tct tta aat ggg gat Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Asp 225 230 235 240			720
act tgc agt tct tta gct agg gtg ggc gta ggg gct aat tgc tcc act Thr Cys Ser Ser Leu Ala Arg Val Gly Val Gly Ala Asn Cys Ser Thr 245 250 255			768
tct ggg cct agc tat tct ttt aaa ggg acg act aac gct act aac acg Ser Gly Pro Ser Tyr Ser Phe Lys Gly Thr Thr Asn Ala Thr Asn Thr 260 265 270			816
act ttt agc aat tca agc ggc agt ttc act ttt gaa gag aac gcc act Thr Phe Ser Asn Ser Ser Gly Ser Phe Thr Phe Glu Glu Asn Ala Thr 275 280 285			864
ttt agc ggg gcg aaa tta aat ggg ggg gca ttc act ttc aat aaa aag Phe Ser Gly Ala Lys Leu Asn Gly Gly Ala Phe Thr Phe Asn Lys Lys 290 295 300			912
ttt aac gct acc aat aat acc gct ttt aat agc ggt agt ttt act ttt Phe Asn Ala Thr Asn Asn Thr Ala Phe Asn Ser Gly Ser Phe Thr Phe 305 310 315 320			960
aaa ggc aca agc tct ttt aat ggt gcg aat ttt agt aac gct tcc tat Lys Gly Thr Ser Ser Phe Asn Gly Ala Asn Phe Ser Asn Ala Ser Tyr 325 330 335			1008
act ttt aat aat caa gcc act ttc caa aac agc tcc ttt aat ggg ggg Thr Phe Asn Asn Gln Ala Thr Phe Gln Asn Ser Ser Phe Asn Gly Gly 340 345 350			1056
act ttt act ttt aat gac cag acc aat caa agc acc cag cac ccc caa			1104

Thr	Phe	Thr	Phe	Asn	Asp	Gln	Thr	Asn	Gln	Ser	Thr	Gln	His	Pro	Gln	
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Ile	Gln	Asn	Ser	Ser	Phe	Ser	Gly	Ser	Ala	Thr	Thr	Leu	Lys	Gly	Phe	
	370					375					380					
gcg	act	ttt	gag	caa	gcc	ttt	aac	aat	tca	aac	cac	caa	cta	acg	ata	1200
Ala	Thr	Phe	Glu	Gln	Ala	Phe	Asn	Asn	Ser	Asn	His	Gln	Leu	Thr	Ile	
385					390					395					400	
caa	aac	gct	tcc	ttt	aat	aac	gct	act	ttc	aac	aat	acc	ggc	aaa	atc	1248
Gln	Asn	Ala	Ser	Phe	Asn	Asn	Ala	Thr	Phe	Asn	Asn	Thr	Gly	Lys	Ile	
				405					410					415		
act	ata	gaa	aaa	gat	gcg	agc	ttt	aat	aac	act	tcg	ttc	aac	act	cct	1296
Thr	Ile	Glu	Lys	Asp	Ala	Ser	Phe	Asn	Asn	Thr	Ser	Phe	Asn	Thr	Pro	
			420					425					430			
gtt	gat	aca	aac	aac	atg	act	att	agt	ggc	ggc	gtt	act	tta	agc	ggc	1344
Val	Asp	Thr	Asn	Asn	Met	Thr	Ile	Ser	Gly	Gly	Val	Thr	Leu	Ser	Gly	
		435					440					445				
aaa	aat	gac	ttg	aaa	aat	ggc	gca	acc	ctt	gat	ttt	ggg	agt	tct	aaa	1392
Lys	Asn	Asp	Leu	Lys	Asn	Gly	Ala	Thr	Leu	Asp	Phe	Gly	Ser	Ser	Lys	
	450					455					460					
atc	act	ctc	act	caa	ggg	acg	act	ttc	aac	ctc	aca	agt	tta	ggc	agt	1440
Ile	Thr	Leu	Thr	Gln	Gly	Thr	Thr	Phe	Asn	Leu	Thr	Ser	Leu	Gly	Ser	
465					470					475					480	
gag	aag	agc	gta	acg	att	tta	aat	tct	aga	ggc	ggg	atc	act	tac	aat	1488
Glu	Lys	Ser	Val	Thr	Ile	Leu	Asn	Ser	Arg	Gly	Gly	Ile	Thr	Tyr	Asn	
				485					490					495		
cat	ctt	tta	aac	cat	gcg	atc	aat	agc	ttg	aca	aac	gcc	cta	aaa	acg	1536
His	Leu	Leu	Asn	His	Ala	Ile	Asn	Ser	Leu	Thr	Asn	Ala	Leu	Lys	Thr	
			500					505					510			
aac	gaa	agc	tct	tca	aaa	ccg	caa	agt	ttc	gct	caa	ggc	ttg	tgg	gat	1584
Asn	Glu	Ser	Ser	Ser	Lys	Pro	Gln	Ser	Phe	Ala	Gln	Gly	Leu	Trp	Asp	
		515					520					525				
atg	atc	act	tac	aat	ggg	gtt	acc	ggg	cag	ctt	ttg	aat	gaa	aac	gct	1632
Met	Ile	Thr	Tyr	Asn	Gly	Val	Thr	Gly	Gln	Leu	Leu	Asn	Glu	Asn	Ala	
	530					535					540					
gca	aca	tct	aaa	ccc	act	gac	tct	tcg	ccc	tct	aaa	tcc	tct	aca	aac	1680
Ala	Thr	Ser	Lys	Pro	Thr	Asp	Ser	Ser	Pro	Ser	Lys	Ser	Ser	Thr	Asn	
545					550					555					560	
tct	acg	caa	gtc	tat	caa	gtg	ggc	tac	aaa	ata	ggg	gat	act	atc	tac	1728
Ser	Thr	Gln	Val	Tyr	Gln	Val	Gly	Tyr	Lys	Ile	Gly	Asp	Thr	Ile	Tyr	
				565					570					575		

aaa	ctg	caa	gaa	act	ttc	agc	cac	aat	tcc	att	att	att	cag	gct	tta	1776
Lys	Leu	Gln	Glu	Thr	Phe	Ser	His	Asn	Ser	Ile	Ile	Ile	Gln	Ala	Leu	
			580					585					590			
gag	agc	ggg	act	tac	acg	cca	ccc	cct	gtc	att	aac	ggc	tcc	aaa	ttt	1824
Glu	Ser	Gly	Thr	Tyr	Thr	Pro	Pro	Pro	Val	Ile	Asn	Gly	Ser	Lys	Phe	
		595					600					605				
gac	tta	tcc	gct	tca	aat	tat	atc	aat	gct	gac	atg	cct	tg	tat	aac	1872
Asp	Leu	Ser	Ala	Ser	Asn	Tyr	Ile	Asn	Ala	Asp	Met	Pro	Trp	Tyr	Asn	
	610					615					620					
cat	aaa	tat	tat	att	cct	aaa	tcc	caa	aat	ttt	aca	gag	agc	ggg	act	1920
His	Lys	Tyr	Tyr	Ile	Pro	Lys	Ser	Gln	Asn	Phe	Thr	Glu	Ser	Gly	Thr	
625					630					635					640	
tat	tac	ttg	ccg	agc	gtt	caa	ata	tgg	ggg	agc	tac	act	aac	tcg	ttt	1968
Tyr	Tyr	Leu	Pro	Ser	Val	Gln	Ile	Trp	Gly	Ser	Tyr	Thr	Asn	Ser	Phe	
				645					650					655		
aaa	caa	acc	ttt	agc	gca	agt	aat	agc	aat	ctg	gtg	att	ggg	tat	aac	2016
Lys	Gln	Thr	Phe	Ser	Ala	Ser	Asn	Ser	Asn	Leu	Val	Ile	Gly	Tyr	Asn	
			660					665					670			
gca	aca	tgg	act	gat	cac	aat	gtt	tct	tct	agc	gac	acg	gtg	gct	ttt	2064
Ala	Thr	Trp	Thr	Asp	His	Asn	Val	Ser	Ser	Ser	Asp	Thr	Val	Ala	Phe	
		675					680					685				
ggg	gac	act	tca	ggg	agc	gct	ctt	aat	ggg	cat	tgc	ggg	cct	tg	ccc	2112
Gly	Asp	Thr	Ser	Gly	Ser	Ala	Leu	Asn	Gly	His	Cys	Gly	Pro	Trp	Pro	
	690					695					700					
tat	tac	caa	tgc	aca	ggc	acg	act	aac	ggc	act	tat	agc	gct	tat	cat	2160
Tyr	Tyr	Gln	Cys	Thr	Gly	Thr	Thr	Asn	Gly	Thr	Tyr	Ser	Ala	Tyr	His	
705					710					715					720	
gtc	tat	atc	aca	gcg	aat	ctg	cgt	tct	ggc	aat	cgt	ata	ggc	acc	ggt	2208
Val	Tyr	Ile	Thr	Ala	Asn	Leu	Arg	Ser	Gly	Asn	Arg	Ile	Gly	Thr	Gly	
			725						730					735		
ggg	gca	gcc	aat	cta	atc	ttt	aat	ggg	gta	gat	agt	atc	aat	atc	gct	2256
Gly	Ala	Ala	Asn	Leu	Ile	Phe	Asn	Gly	Val	Asp	Ser	Ile	Asn	Ile	Ala	
			740					745					750			
aac	gct	acc	atc	acg	caa	cat	aac	gcc	ggg	gct	tat	tca	agc	tct	atg	2304
Asn	Ala	Thr	Ile	Thr	Gln	His	Asn	Ala	Gly	Ala	Tyr	Ser	Ser	Ser	Met	
		755					760					765				
act	ttt	tcc	acg	caa	aac	atg	gac	aat	tcg	cag	aat	ttg	aat	ggc	cta	2352
Thr	Phe	Ser	Thr	Gln	Asn	Met	Asp	Asn	Ser	Gln	Asn	Leu	Asn	Gly	Leu	
	770					775					780					
aat	tct	aac	ggc	aag	ctt	ttg	gtg	tat	ggc	aca	act	ttc	act	aac	caa	2400
Asn	Ser	Asn	Gly	Lys	Leu	Leu	Val	Tyr	Gly	Thr	Thr	Phe	Thr	Asn	Gln	
785					790					795					800	

gcc aaa gac ggg aaa ttc att ttc aat gca ggg caa gcg act ttt gaa	2448
Ala Lys Asp Gly Lys Phe Ile Phe Asn Ala Gly Gln Ala Thr Phe Glu	
805 810 815	
aac acc aac ttt aat gga ggg agt tac caa ttc agc ggc gat agc ttg	2496
Asn Thr Asn Phe Asn Gly Gly Ser Tyr Gln Phe Ser Gly Asp Ser Leu	
820 825 830	
aat ttt tca aat aac aac cag ttc aat agc ggt tcg ttt gag att ggc	2544
Asn Phe Ser Asn Asn Asn Gln Phe Asn Ser Gly Ser Phe Glu Ile Gly	
835 840 845	
gca aaa aat act att ttt aat aac gct aat ttt aac aac agc act tct	2592
Ala Lys Asn Thr Ile Phe Asn Asn Ala Asn Phe Asn Asn Ser Thr Ser	
850 855 860	
ttt aat ttc aat aat tct agc gcg acc act tcg ttt gtg ggg gat ttc	2640
Phe Asn Phe Asn Asn Ser Ser Ala Thr Thr Ser Phe Val Gly Asp Phe	
865 870 875 880	
act aac gct aat tca aat ttg caa atc gct ggg aac gct gtt ttt ggg	2688
Thr Asn Ala Asn Ser Asn Leu Gln Ile Ala Gly Asn Ala Val Phe Gly	
885 890 895	
aac tct act aat ggc tct caa aat acc gct aat ttt aat aat acc ggc	2736
Asn Ser Thr Asn Gly Ser Gln Asn Thr Ala Asn Phe Asn Asn Thr Gly	
900 905 910	
tct gtt aat att gca ggg aat gca acc ttt gat aac gtg gta ttt aac	2784
Ser Val Asn Ile Ala Gly Asn Ala Thr Phe Asp Asn Val Val Phe Asn	
915 920 925	
agc cct acg aac acg agc gtg aaa ggg aaa gtt act ctc aat aac atc	2832
Ser Pro Thr Asn Thr Ser Val Lys Gly Lys Val Thr Leu Asn Asn Ile	
930 935 940	
act tta aaa aac ttg aac gct cct ttg tct ttt ggc gat ggg acg att	2880
Thr Leu Lys Asn Leu Asn Ala Pro Leu Ser Phe Gly Asp Gly Thr Ile	
945 950 955 960	
gtt ttt agc gct cat tcg gtg att aat att ggt gaa gct atc aca aat	2928
Val Phe Ser Ala His Ser Val Ile Asn Ile Gly Glu Ala Ile Thr Asn	
965 970 975	
ggc aac cct atc acc ctt gta agc tct tct aaa gca att gaa tac aac	2976
Gly Asn Pro Ile Thr Leu Val Ser Ser Ser Lys Ala Ile Glu Tyr Asn	
980 985 990	
gac gct ttc agt aaa aat cta tgg cag ctc atc aac tac caa ggg cat	3024
Asp Ala Phe Ser Lys Asn Leu Trp Gln Leu Ile Asn Tyr Gln Gly His	
995 1000 1005	
ggg gct agc agt gaa aag ctc gtt tct agt gcg ggt aat ggc gtc	3069
Gly Ala Ser Ser Glu Lys Leu Val Ser Ser Ala Gly Asn Gly Val	

1010	1015	1020	
tat gat gtg gtg tat tct ttc aac aac caa acc tac aat ttc caa Tyr Asp Val Val Tyr Ser Phe Asn Asn Gln Thr Tyr Asn Phe Gln 1025 1030 1035			3114
gag gtt ttt tca ccc aac agc att tct atc cgg cgt ttg ggc gtt Glu Val Phe Ser Pro Asn Ser Ile Ser Ile Arg Arg Leu Gly Val 1040 1045 1050			3159
ggc atg gtg ttt gat tat gtg gat atg gaa aaa tcg gat cgt ttg Gly Met Val Phe Asp Tyr Val Asp Met Glu Lys Ser Asp Arg Leu 1055 1060 1065			3204
tat tat caa aac gct ctc ggt ttt atg acc tac atg cct aat agc Tyr Tyr Gln Asn Ala Leu Gly Phe Met Thr Tyr Met Pro Asn Ser 1070 1075 1080			3249
tat aac aat aat tta ggg aat tta aac aac acc att tac tat tac Tyr Asn Asn Asn Leu Gly Asn Leu Asn Asn Thr Ile Tyr Tyr Tyr 1085 1090 1095			3294
gac aac agc att gac ttt tat gcg agc ggg aaa act cta ttc act Asp Asn Ser Ile Asp Phe Tyr Ala Ser Gly Lys Thr Leu Phe Thr 1100 1105 1110			3339
aaa gcg gaa ttt tct caa acg ttc act ggg caa aac agc gcg atc Lys Ala Glu Phe Ser Gln Thr Phe Thr Gly Gln Asn Ser Ala Ile 1115 1120 1125			3384
gtt ttt ggg gct aaa aat ata tgg acg agc gta agc gat gcg ccg Val Phe Gly Ala Lys Asn Ile Trp Thr Ser Val Ser Asp Ala Pro 1130 1135 1140			3429
caa tct aat gtg atc att cgc ttt ggg gac aat aag gga gca ggg Gln Ser Asn Val Ile Ile Arg Phe Gly Asp Asn Lys Gly Ala Gly 1145 1150 1155			3474
agt aat gat gcg agt ggg cat tgc tgg aat ttg caa tgc ata ggc Ser Asn Asp Ala Ser Gly His Cys Trp Asn Leu Gln Cys Ile Gly 1160 1165 1170			3519
ttt atc aca ggg cat tat gaa gcg caa aag att tac atc acc ggc Phe Ile Thr Gly His Tyr Glu Ala Gln Lys Ile Tyr Ile Thr Gly 1175 1180 1185			3564
agt att gaa agc ggg aac cgc att tct agc ggt ggg ggc gcg agc Ser Ile Glu Ser Gly Asn Arg Ile Ser Ser Gly Gly Gly Ala Ser 1190 1195 1200			3609
ctt aat ttt aac ggg ctt caa ggc att ctt tta acg aac gcg act Leu Asn Phe Asn Gly Leu Gln Gly Ile Leu Leu Thr Asn Ala Thr 1205 1210 1215			3654
ttg tat aac cgc gcc gct ggc acg caa agc tct tct atg aat ttt			3699

Leu	Tyr	Asn	Arg	Ala	Ala	Gly	Thr	Gln	Ser	Ser	Ser	Met	Asn	Phe	
1220						1225					1230				
ggt	tct	aac	agc	gcg	aac	att	cag	gct	caa	aac	tcc	tat	ttt	ata	3744
Val	Ser	Asn	Ser	Ala	Asn	Ile	Gln	Ala	Gln	Asn	Ser	Tyr	Phe	Ile	
1235						1240					1245				
gac	gat	acc	gca	caa	aat	aaa	ggc	aac	cct	aat	ttt	agt	ttc	aac	3789
Asp	Asp	Thr	Ala	Gln	Asn	Lys	Gly	Asn	Pro	Asn	Phe	Ser	Phe	Asn	
1250						1255					1260				
gct	ttg	aat	ctg	gat	ttt	tct	aac	agc	tct	ttt	aga	ggc	tat	gtg	3834
Ala	Leu	Asn	Leu	Asp	Phe	Ser	Asn	Ser	Ser	Phe	Arg	Gly	Tyr	Val	
1265						1270					1275				
ggg	caa	acg	cag	tct	gtt	ttt	aaa	ttc	aat	gcc	gtt	aat	gcg	atc	3879
Gly	Gln	Thr	Gln	Ser	Val	Phe	Lys	Phe	Asn	Ala	Val	Asn	Ala	Ile	
1280						1285					1290				
agt	ttc	act	aac	agc	tct	aat	tta	agc	tct	ggg	ttg	tat	caa	atg	3924
Ser	Phe	Thr	Asn	Ser	Ser	Asn	Leu	Ser	Ser	Gly	Leu	Tyr	Gln	Met	
1295						1300					1305				
caa	gct	aaa	agc	gtg	ttg	ttt	gac	aat	tcc	aat	tta	agc	gtt	tca	3969
Gln	Ala	Lys	Ser	Val	Leu	Phe	Asp	Asn	Ser	Asn	Leu	Ser	Val	Ser	
1310						1315					1320				
gtg	ggg	aca	agc	agc	att	aaa	gcc	aat	gcg	atc	aat	ctt	tct	caa	4014
Val	Gly	Thr	Ser	Ser	Ile	Lys	Ala	Asn	Ala	Ile	Asn	Leu	Ser	Gln	
1325						1330					1335				
aac	gcc	tct	atc	aat	gcg	agc	aac	cat	tca	acc	tta	gaa	ctt	caa	4059
Asn	Ala	Ser	Ile	Asn	Ala	Ser	Asn	His	Ser	Thr	Leu	Glu	Leu	Gln	
1340						1345					1350				
ggc	gat	ttg	aat	ttg	aac	gac	acc	agc	tcg	ctc	aac	ctc	aac	caa	4104
Gly	Asp	Leu	Asn	Leu	Asn	Asp	Thr	Ser	Ser	Leu	Asn	Leu	Asn	Gln	
1355						1360					1365				
agc	gcc	att	aat	gtt	tct	aac	aac	gcc	acg	atc	aac	gat	tat	gcg	4149
Ser	Ala	Ile	Asn	Val	Ser	Asn	Asn	Ala	Thr	Ile	Asn	Asp	Tyr	Ala	
1370						1375					1380				
agc	ttg	att	gcg	agt	aat	ggc	tct	cac	ctt	aat	ttt	aac	ggg	gcg	4194
Ser	Leu	Ile	Ala	Ser	Asn	Gly	Ser	His	Leu	Asn	Phe	Asn	Gly	Ala	
1385						1390					1395				
gtt	aat	ttc	aat	tca	gcg	aat	att	act	acg	agt	ttg	agt	agt	tcc	4239
Val	Asn	Phe	Asn	Ser	Ala	Asn	Ile	Thr	Thr	Ser	Leu	Ser	Ser	Ser	
1400						1405					1410				
tct	atc	gtg	ttt	aag	ggg	gcg	gtc	tct	tta	cga	ggg	cag	ttt	aat	4284
Ser	Ile	Val	Phe	Lys	Gly	Ala	Val	Ser	Leu	Arg	Gly	Gln	Phe	Asn	
1415						1420					1425				

tta agc aat aat tct tct tta gat ttt caa ggc tct agc gct atc Leu Ser Asn Asn Ser Ser Leu Asp Phe Gln Gly Ser Ser Ala Ile 1430 1435 1440	4329
acc tct aac acg gcg ttt aat ttc tat gat aac gct ttt tct caa Thr Ser Asn Thr Ala Phe Asn Phe Tyr Asp Asn Ala Phe Ser Gln 1445 1450 1455	4374
agc ccc atc act ttc cat caa gcc ctt gac att aaa gtg ccc ttg Ser Pro Ile Thr Phe His Gln Ala Leu Asp Ile Lys Val Pro Leu 1460 1465 1470	4419
agt ttg gga ggc aac ctc tta aac cct aac aac agt agc gtg ctg Ser Leu Gly Gly Asn Leu Leu Asn Pro Asn Asn Ser Ser Val Leu 1475 1480 1485	4464
aat tta aaa aac agc cag ctt gtt ttt agc gat caa ggg agc ttg Asn Leu Lys Asn Ser Gln Leu Val Phe Ser Asp Gln Gly Ser Leu 1490 1495 1500	4509
aat atc gct aac att gat tta cta agc gat ctg aat ggt aat aaa Asn Ile Ala Asn Ile Asp Leu Leu Ser Asp Leu Asn Gly Asn Lys 1505 1510 1515	4554
aat cgt gtg tat aac atc att caa gcg gac atg aat ggt aat tgg Asn Arg Val Tyr Asn Ile Ile Gln Ala Asp Met Asn Gly Asn Trp 1520 1525 1530	4599
tat gag cgt atc aac ttc ttt ggc atg cgc att aat gat ggg att Tyr Glu Arg Ile Asn Phe Phe Gly Met Arg Ile Asn Asp Gly Ile 1535 1540 1545	4644
tat gac gct aaa aac caa act tat agt ttc act aac cct ctc aat Tyr Asp Ala Lys Asn Gln Thr Tyr Ser Phe Thr Asn Pro Leu Asn 1550 1555 1560	4689
aac gcc cta aaa atc acc gag agc ttt aaa aat aac caa ctg agc Asn Ala Leu Lys Ile Thr Glu Ser Phe Lys Asn Asn Gln Leu Ser 1565 1570 1575	4734
gtt acg ctc tct caa atc ccg ggc att aaa aac acg ctc tat aac Val Thr Leu Ser Gln Ile Pro Gly Ile Lys Asn Thr Leu Tyr Asn 1580 1585 1590	4779
att ggc tct gaa atc ttt aac tac caa aag gtt tat aac aac gct Ile Gly Ser Glu Ile Phe Asn Tyr Gln Lys Val Tyr Asn Asn Ala 1595 1600 1605	4824
aat ggc gtg tat tct tat agc gat gac gca caa ggc gtg ttt tat Asn Gly Val Tyr Ser Tyr Ser Asp Asp Ala Gln Gly Val Phe Tyr 1610 1615 1620	4869
ctc acg agc agc gtg aaa ggc tat tac aac ccc aac caa tcc tat Leu Thr Ser Ser Val Lys Gly Tyr Tyr Asn Pro Asn Gln Ser Tyr 1625 1630 1635	4914



caa gcc agc ggc agc aat aac acc acg aaa aat aac aat cta acc	4959
Gln Ala Ser Gly Ser Asn Asn Thr Thr Lys Asn Asn Asn Leu Thr	
1640 1645 1650	
tct gaa tct tct gtc att tcg caa acc tat aac gcg caa ggc aac	5004
Ser Glu Ser Ser Val Ile Ser Gln Thr Tyr Asn Ala Gln Gly Asn	
1655 1660 1665	
cct atc agc gcg tta cac gtc tat aac aag ggc tat aat ttc agt	5049
Pro Ile Ser Ala Leu His Val Tyr Asn Lys Gly Tyr Asn Phe Ser	
1670 1675 1680	
aat atc aaa gcg tta ggg caa atg gcg ctc aaa ctc tac cct gaa	5094
Asn Ile Lys Ala Leu Gly Gln Met Ala Leu Lys Leu Tyr Pro Glu	
1685 1690 1695	
atc aaa aag ata tta ggg aat gat ttt tcg ctt tca agt ttg agc	5139
Ile Lys Lys Ile Leu Gly Asn Asp Phe Ser Leu Ser Ser Leu Ser	
1700 1705 1710	
aat tta aaa ggc gat gcg cta aac cag ctt acc aag ctc atc acg	5184
Asn Leu Lys Gly Asp Ala Leu Asn Gln Leu Thr Lys Leu Ile Thr	
1715 1720 1725	
cct agc gat tgg aaa aac att aac gag ttg att gat aac gca aac	5229
Pro Ser Asp Trp Lys Asn Ile Asn Glu Leu Ile Asp Asn Ala Asn	
1730 1735 1740	
aat tcg gtc gtg caa aat ttc aat aac ggc act ttg att ata gga	5274
Asn Ser Val Val Gln Asn Phe Asn Asn Gly Thr Leu Ile Ile Gly	
1745 1750 1755	
gcg act aaa ata ggg caa aca gac acc aat agt gcg gtg gtt ttt	5319
Ala Thr Lys Ile Gly Gln Thr Asp Thr Asn Ser Ala Val Val Phe	
1760 1765 1770	
ggg ggc ttg ggc tat caa aag cct tgc gat tac act gat att gtg	5364
Gly Gly Leu Gly Tyr Gln Lys Pro Cys Asp Tyr Thr Asp Ile Val	
1775 1780 1785	
tgc caa aaa ttt aga ggc act tat ttg ggg cag ctt ttg gag tcc	5409
Cys Gln Lys Phe Arg Gly Thr Tyr Leu Gly Gln Leu Leu Glu Ser	
1790 1795 1800	
atc tcg gct gat ttg ggc tat att gac acg act ttt aac gct aaa	5454
Ile Ser Ala Asp Leu Gly Tyr Ile Asp Thr Thr Phe Asn Ala Lys	
1805 1810 1815	
gaa att tat ctt acc ggc act tta ggg agc ggg aac gca tgg ggg	5499
Glu Ile Tyr Leu Thr Gly Thr Leu Gly Ser Gly Asn Ala Trp Gly	
1820 1825 1830	
act ggg ggg agt gcg agc gta act ttt aac agc caa act tcg ctc	5544
Thr Gly Gly Ser Ala Ser Val Thr Phe Asn Ser Gln Thr Ser Leu	

1835					1840					1845					
att	ctc	aac	caa	gcg	aat	atc	gta	agc	tcg	caa	acc	gat	ggg	att	5589
Ile	Leu	Asn	Gln	Ala	Asn	Ile	Val	Ser	Ser	Gln	Thr	Asp	Gly	Ile	
1850					1855					1860					
ttt	agc	atg	ctg	ggt	caa	gag	ggc	atc	aat	aag	gtt	ttc	aat	caa	5634
Phe	Ser	Met	Leu	Gly	Gln	Glu	Gly	Ile	Asn	Lys	Val	Phe	Asn	Gln	
1865					1870					1875					
gcc	ggg	ctc	gct	aat	att	ttg	ggc	gaa	gtg	gca	atg	caa	tcc	att	5679
Ala	Gly	Leu	Ala	Asn	Ile	Leu	Gly	Glu	Val	Ala	Met	Gln	Ser	Ile	
1880					1885					1890					
aac	aaa	gcc	ggg	gga	tta	ggg	aat	ttg	ata	gta	aat	acg	cta	ggg	5724
Asn	Lys	Ala	Gly	Gly	Leu	Gly	Asn	Leu	Ile	Val	Asn	Thr	Leu	Gly	
1895					1900					1905					
agt	gat	agc	gtg	att	ggg	ggg	tat	tta	acg	cct	gag	caa	aaa	aat	5769
Ser	Asp	Ser	Val	Ile	Gly	Gly	Tyr	Leu	Thr	Pro	Glu	Gln	Lys	Asn	
1910					1915					1920					
caa	acc	cta	agc	cag	ctt	ttg	ggg	cag	aat	aat	ttt	gat	aac	ctc	5814
Gln	Thr	Leu	Ser	Gln	Leu	Leu	Gly	Gln	Asn	Asn	Phe	Asp	Asn	Leu	
1925					1930					1935					
atg	aac	gat	agc	ggt	ttg	aac	acg	gcg	att	aag	gat	ttg	atc	aga	5859
Met	Asn	Asp	Ser	Gly	Leu	Asn	Thr	Ala	Ile	Lys	Asp	Leu	Ile	Arg	
1940					1945					1950					
caa	aaa	tta	ggc	ttt	tgg	acc	ggg	cta	gtg	ggg	gga	tta	gcc	gga	5904
Gln	Lys	Leu	Gly	Phe	Trp	Thr	Gly	Leu	Val	Gly	Gly	Leu	Ala	Gly	
1955					1960					1965					
ctg	ggg	ggc	att	gat	ttg	caa	aac	cct	gaa	aag	ctt	ata	ggc	agc	5949
Leu	Gly	Gly	Ile	Asp	Leu	Gln	Asn	Pro	Glu	Lys	Leu	Ile	Gly	Ser	
1970					1975					1980					
atg	tcc	atc	aat	gat	tta	ttg	agt	aaa	aag	ggg	ttg	ttc	aat	cag	5994
Met	Ser	Ile	Asn	Asp	Leu	Leu	Ser	Lys	Lys	Gly	Leu	Phe	Asn	Gln	
1985					1990					1995					
atc	acc	ggc	ttt	att	tcc	gct	aac	gat	ata	ggg	caa	gtc	ata	agc	6039
Ile	Thr	Gly	Phe	Ile	Ser	Ala	Asn	Asp	Ile	Gly	Gln	Val	Ile	Ser	
2000					2005					2010					
gtg	atg	ctg	caa	gat	att	gtc	aag	ccg	agc	gac	gct	tta	aaa	aac	6084
Val	Met	Leu	Gln	Asp	Ile	Val	Lys	Pro	Ser	Asp	Ala	Leu	Lys	Asn	
2015					2020					2025					
gat	gta	gcc	gct	ttg	ggc	aag	caa	atg	att	ggc	gaa	ttt	tta	ggc	6129
Asp	Val	Ala	Ala	Leu	Gly	Lys	Gln	Met	Ile	Gly	Glu	Phe	Leu	Gly	
2030					2035					2040					
caa	gac	acg	ctc	aat	tct	tta	gaa	agc	ttg	ctg	caa	aac	cag	cag	6174

Gln	Asp	Thr	Leu	Asn	Ser	Leu	Glu	Ser	Leu	Leu	Gln	Asn	Gln	Gln	
	2045					2050					2055				
att	aaa	agc	gtt	tta	gac	aaa	gtc	tta	gcg	gct	aaa	gga	tta	ggg	6219
Ile	Lys	Ser	Val	Leu	Asp	Lys	Val	Leu	Ala	Ala	Lys	Gly	Leu	Gly	
	2060					2065					2070				
tct	att	tat	gaa	caa	ggt	ttg	ggg	gat	ttg	atc	cct	aat	ctt	ggt	6264
Ser	Ile	Tyr	Glu	Gln	Gly	Leu	Gly	Asp	Leu	Ile	Pro	Asn	Leu	Gly	
	2075					2080					2085				
aaa	aag	ggg	att	ttc	gct	ccc	tat	ggc	ttg	agt	caa	gtg	tgg	caa	6309
Lys	Lys	Gly	Ile	Phe	Ala	Pro	Tyr	Gly	Leu	Ser	Gln	Val	Trp	Gln	
	2090					2095					2100				
aaa	ggg	gat	ttt	agt	ttc	aac	gcg	caa	ggc	aat	gtt	ttt	gtg	caa	6354
Lys	Gly	Asp	Phe	Ser	Phe	Asn	Ala	Gln	Gly	Asn	Val	Phe	Val	Gln	
	2105					2110					2115				
aat	tcc	act	ttc	tct	aac	gct	aat	gga	ggc	acg	ctc	agt	ttt	aac	6399
Asn	Ser	Thr	Phe	Ser	Asn	Ala	Asn	Gly	Gly	Thr	Leu	Ser	Phe	Asn	
	2120					2125					2130				
gca	gga	aat	tcg	ctc	att	ttt	gcc	gga	aac	aac	cac	atc	gct	ttc	6444
Ala	Gly	Asn	Ser	Leu	Ile	Phe	Ala	Gly	Asn	Asn	His	Ile	Ala	Phe	
	2135					2140					2145				
act	aac	cat	tct	gga	acg	ctc	aat	ttg	ttg	tct	aat	caa	gtt	tct	6489
Thr	Asn	His	Ser	Gly	Thr	Leu	Asn	Leu	Leu	Ser	Asn	Gln	Val	Ser	
	2150					2155					2160				
aac	att	aac	gtc	acc	atg	ctt	aac	gct	agc	aac	ggc	ctt	aag	att	6534
Asn	Ile	Asn	Val	Thr	Met	Leu	Asn	Ala	Ser	Asn	Gly	Leu	Lys	Ile	
	2165					2170					2175				
aac	gcc	act	aat	aac	aat	gtt	tcc	gtg	tct	caa	ggc	aat	ctg	ttt	6579
Asn	Ala	Thr	Asn	Asn	Asn	Val	Ser	Val	Ser	Gln	Gly	Asn	Leu	Phe	
	2180					2185					2190				
atc	aac	gct	agc	tgc	gtg	caa	caa	agc	gat	cca	acg	aca	gct	agc	6624
Ile	Asn	Ala	Ser	Cys	Val	Gln	Gln	Ser	Asp	Pro	Thr	Thr	Ala	Ser	
	2195					2200					2205				
gcc	aca	aac	cct	tgc	acc	acc	gct	caa	aat	aac	gct	tct	tct	agt	6669
Ala	Thr	Asn	Pro	Cys	Thr	Thr	Ala	Gln	Asn	Asn	Ala	Ser	Ser	Ser	
	2210					2215					2220				
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Asn	Ala	Ser	Asn	Asn	Ala	Pro	Ile	Ala	Leu	Asn	Asn	Asn	Asp	Glu	
	2225					2230					2235				
agc	ttg	gtg	gtt	acg	gcg	aat	ggg	ttc	aat	ttt	tca	ggc	aat	att	6759
Ser	Leu	Val	Val	Thr	Ala	Asn	Gly	Phe	Asn	Phe	Ser	Gly	Asn	Ile	
	2240					2245					2250				

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aac gtt aaa aac ctg tat ctt tac aat aac gct caa ttc caa gcc Asn Val Lys Asn Leu Tyr Leu Tyr Asn Asn Ala Gln Phe Gln Ala 2270 2275 2280	6849
aac aac ctc acg att tcc aac caa gcg gta tta gag aaa aac gct Asn Asn Leu Thr Ile Ser Asn Gln Ala Val Leu Glu Lys Asn Ala 2285 2290 2295	6894
agc ttt gta acg aat aac tta aac att caa gga gcg ttt aac aac Ser Phe Val Thr Asn Asn Leu Asn Ile Gln Gly Ala Phe Asn Asn 2300 2305 2310	6939
aac gcc acg caa aaa ata gag gtg ctt caa aat tta gtg atc gct Asn Ala Thr Gln Lys Ile Glu Val Leu Gln Asn Leu Val Ile Ala 2315 2320 2325	6984
tca aac gct tct tta agc acc ggg att tat ggg tta gaa gta ggg Ser Asn Ala Ser Leu Ser Thr Gly Ile Tyr Gly Leu Glu Val Gly 2330 2335 2340	7029
ggg gca ttg aat aat ttg gga gcg atc cat ttt aat tta gaa aat Gly Ala Leu Asn Asn Leu Gly Ala Ile His Phe Asn Leu Glu Asn 2345 2350 2355	7074
tct caa acg cct gta aat ccg ctc att caa gta ggg ggg atc att Ser Gln Thr Pro Val Asn Pro Leu Ile Gln Val Gly Gly Ile Ile 2360 2365 2370	7119
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aat ggc gga act tac act tta tta aaa agc agc cgt tat att gat Asn Gly Gly Thr Tyr Thr Leu Leu Lys Ser Ser Arg Tyr Ile Asp 2390 2395 2400	7209
tac aat atc aac cct aac agc ttg caa tcg tat ttg aag ctc tat Tyr Asn Ile Asn Pro Asn Ser Leu Gln Ser Tyr Leu Lys Leu Tyr 2405 2410 2415	7254
acc tta atc aat atc aac gga aac cac ata gag gaa aaa aac ggc Thr Leu Ile Asn Ile Asn Gly Asn His Ile Glu Glu Lys Asn Gly 2420 2425 2430	7299
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tta tta ttg agt gta gca cta cct aac tca aac aac gcc tct caa Leu Leu Leu Ser Val Ala Leu Pro Asn Ser Asn Asn Ala Ser Gln 2450 2455 2460	7389

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Asn Asn Ile Leu Ser Leu Ser Val Leu His Asn Gln Ile Lys Met	
2465 2470 2475	
tct tat ggt aat aaa gtg atg gac ttt acc cct ccc acc tta cag	7479
Ser Tyr Gly Asn Lys Val Met Asp Phe Thr Pro Pro Thr Leu Gln	
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gat tac att gtg ggc att caa gga caa agc gca ctc aat caa att	7524
Asp Tyr Ile Val Gly Ile Gln Gly Gln Ser Ala Leu Asn Gln Ile	
2495 2500 2505	
gaa gct gtt ggg ggg aat aac gct atc aag tgg ctt tca aca ttg	7569
Glu Ala Val Gly Gly Asn Asn Ala Ile Lys Trp Leu Ser Thr Leu	
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atg atg gag act aaa gaa aac ccg ctt ttt gcg ccg att tat tta	7614
Met Met Glu Thr Lys Glu Asn Pro Leu Phe Ala Pro Ile Tyr Leu	
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gaa aac cac tct tta aat gaa atc tta ggc gta aca aaa gat ctt	7659
Glu Asn His Ser Leu Asn Glu Ile Leu Gly Val Thr Lys Asp Leu	
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Gln Asn Thr Ala Ser Leu Ile Ser Asn Pro Asn Phe Arg Asn Asn	
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gct acc agc ctt tta gaa atg gcg agt tac acc caa caa acc agc	7749
Ala Thr Ser Leu Leu Glu Met Ala Ser Tyr Thr Gln Gln Thr Ser	
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Arg Leu Thr Lys Leu Ser Asp Phe Arg Ala Arg Glu Gly Glu Ser	
2585 2590 2595	
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Asn Phe Ser Glu Arg Leu Leu Glu Leu Lys Asn Lys Arg Phe Ser	
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Asp Pro Asn Pro Ser Glu Val Phe Val Lys Tyr Ser Gln Leu Ser	
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Lys His Pro Asn Asn Leu Trp Ile Gln Gly Val Gly Gly Ala Ser	
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Phe Ile Ser Gly Gly Asn Gly Thr Leu Tyr Gly Leu Asn Val Gly	
2645 2650 2655	
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Tyr Asp Arg Leu Val Lys Ser Val Ile Leu Gly Gly Tyr Val Ala	

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Tyr	Gly	Tyr	Ser	Gly	Phe	Asn	Gly	Asn	Ile	Met	His	Ser	Leu	Ala	
	2675					2680					2685				
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Asn	Asn	Val	Asp	Val	Gly	Met	Tyr	Ala	Arg	Ala	Phe	Leu	Lys	Arg	
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Asn	Glu	Phe	Thr	Leu	Ser	Ala	Asn	Glu	Thr	Tyr	Gly	Gly	Asn	Ala	
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Ser	His	Ile	Asn	Ser	Ser	Asn	Ser	Leu	Leu	Ser	Val	Leu	Asn	Gln	
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Arg	Tyr	Asn	Tyr	Asn	Thr	Trp	Thr	Thr	Ser	Val	Asn	Gly	Asn	Tyr	
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Gly	Tyr	Asp	Phe	Met	Phe	Lys	Gln	Lys	Ser	Val	Val	Leu	Lys	Pro	
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Gln	Val	Gly	Leu	Ser	Tyr	His	Phe	Ile	Gly	Leu	Ser	Gly	Met	Lys	
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Gly	Lys	Met	Gln	Asn	Pro	Ala	Tyr	Gln	Gln	Phe	Val	Met	His	Ser	
	2780					2785					2790				
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Asn	Pro	Ser	Asn	Glu	Ser	Val	Leu	Thr	Leu	Asn	Met	Gly	Leu	Glu	
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Ser	Arg	Lys	Tyr	Phe	Gly	Lys	Asn	Ser	Tyr	Tyr	Phe	Val	Thr	Ala	
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Arg	Leu	Gly	Arg	Asp	Leu	Leu	Ile	Lys	Ala	Lys	Gly	Asp	Asn	Val	
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Val	Arg	Phe	Val	Gly	Glu	Asn	Thr	Leu	Leu	Tyr	Arg	Lys	Gly	Glu	
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Ile	Phe	Asn	Thr	Phe	Ala	Ser	Val	Ile	Thr	Gly	Gly	Glu	Met	His	
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Leu Trp Arg Leu Met Tyr Val Asn Ala Gly Val Gly Leu Lys Met  
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ggc ttg caa tac caa gat ctt aat atc act ggg aat gtg ggc atg 8694  
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 <213> Helicobacter pylori

<400> 116

Met Lys Gln Phe Lys Lys Lys Pro Lys Lys Ile Lys Arg Ser His Gln  
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Asn Gln Lys Thr Ile Leu Lys Arg Pro Leu Trp Leu Met Pro Leu Leu  
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Ile Gly Gly Phe Ala Ser Gly Val Tyr Ala Asp Gly Thr Asp Ile Leu  
 35 40 45

Gly Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro  
 50 55 60

Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln  
 65 70 75 80

Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala  
 85 90 95

Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu  
 100 105 110

Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr  
 115 120 125

Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn  
 130 135 140

Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp  
 145 150 155 160

Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn  
 165 170 175

Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly  
 180 185 190

Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr  
 195 200 205

Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly  
 210 215 220

Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Asp  
 225 230 235 240

Thr Cys Ser Ser Leu Ala Arg Val Gly Val Gly Ala Asn Cys Ser Thr  
 245 250 255

Ser Gly Pro Ser Tyr Ser Phe Lys Gly Thr Thr Asn Ala Thr Asn Thr  
 260 265 270

Thr Phe Ser Asn Ser Ser Gly Ser Phe Thr Phe Glu Glu Asn Ala Thr  
 275 280 285

Phe Ser Gly Ala Lys Leu Asn Gly Gly Ala Phe Thr Phe Asn Lys Lys  
 290 295 300

Phe Asn Ala Thr Asn Asn Thr Ala Phe Asn Ser Gly Ser Phe Thr Phe  
 305 310 315 320

Lys Gly Thr Ser Ser Phe Asn Gly Ala Asn Phe Ser Asn Ala Ser Tyr  
 325 330 335

Thr Phe Asn Asn Gln Ala Thr Phe Gln Asn Ser Ser Phe Asn Gly Gly  
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Thr Phe Thr Phe Asn Asp Gln Thr Asn Gln Ser Thr Gln His Pro Gln  
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Ile Gln Asn Ser Ser Phe Ser Gly Ser Ala Thr Thr Leu Lys Gly Phe  
370 375 380

Ala Thr Phe Glu Gln Ala Phe Asn Asn Ser Asn His Gln Leu Thr Ile  
385 390 395 400

Gln Asn Ala Ser Phe Asn Asn Ala Thr Phe Asn Asn Thr Gly Lys Ile  
405 410 415

Thr Ile Glu Lys Asp Ala Ser Phe Asn Asn Thr Ser Phe Asn Thr Pro  
420 425 430

Val Asp Thr Asn Asn Met Thr Ile Ser Gly Gly Val Thr Leu Ser Gly  
435 440 445

Lys Asn Asp Leu Lys Asn Gly Ala Thr Leu Asp Phe Gly Ser Ser Lys  
450 455 460

Ile Thr Leu Thr Gln Gly Thr Thr Phe Asn Leu Thr Ser Leu Gly Ser  
465 470 475 480

Glu Lys Ser Val Thr Ile Leu Asn Ser Arg Gly Gly Ile Thr Tyr Asn  
485 490 495

His Leu Leu Asn His Ala Ile Asn Ser Leu Thr Asn Ala Leu Lys Thr  
500 505 510

Asn Glu Ser Ser Ser Lys Pro Gln Ser Phe Ala Gln Gly Leu Trp Asp  
515 520 525

Met Ile Thr Tyr Asn Gly Val Thr Gly Gln Leu Leu Asn Glu Asn Ala  
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Ala Thr Ser Lys Pro Thr Asp Ser Ser Pro Ser Lys Ser Ser Thr Asn  
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Ser Thr Gln Val Tyr Gln Val Gly Tyr Lys Ile Gly Asp Thr Ile Tyr  
565 570 575

Lys Leu Gln Glu Thr Phe Ser His Asn Ser Ile Ile Ile Gln Ala Leu  
580 585 590

Glu Ser Gly Thr Tyr Thr Pro Pro Val Ile Asn Gly Ser Lys Phe  
595 600 605

Asp Leu Ser Ala Ser Asn Tyr Ile Asn Ala Asp Met Pro Trp Tyr Asn  
610 615 620

His Lys Tyr Tyr Ile Pro Lys Ser Gln Asn Phe Thr Glu Ser Gly Thr  
625 630 635 640

Tyr Tyr Leu Pro Ser Val Gln Ile Trp Gly Ser Tyr Thr Asn Ser Phe  
645 650 655

Lys Gln Thr Phe Ser Ala Ser Asn Ser Asn Leu Val Ile Gly Tyr Asn  
660 665 670

Ala Thr Trp Thr Asp His Asn Val Ser Ser Ser Asp Thr Val Ala Phe  
675 680 685

Gly Asp Thr Ser Gly Ser Ala Leu Asn Gly His Cys Gly Pro Trp Pro  
690 695 700

Tyr Tyr Gln Cys Thr Gly Thr Thr Asn Gly Thr Tyr Ser Ala Tyr His  
705 710 715 720

Val Tyr Ile Thr Ala Asn Leu Arg Ser Gly Asn Arg Ile Gly Thr Gly  
725 730 735

Gly Ala Ala Asn Leu Ile Phe Asn Gly Val Asp Ser Ile Asn Ile Ala  
740 745 750

Asn Ala Thr Ile Thr Gln His Asn Ala Gly Ala Tyr Ser Ser Ser Met  
755 760 765

Thr Phe Ser Thr Gln Asn Met Asp Asn Ser Gln Asn Leu Asn Gly Leu  
770 775 780

Asn Ser Asn Gly Lys Leu Leu Val Tyr Gly Thr Thr Phe Thr Asn Gln  
785 790 795 800

Ala Lys Asp Gly Lys Phe Ile Phe Asn Ala Gly Gln Ala Thr Phe Glu

805

810

815

Asn Thr Asn Phe Asn Gly Gly Ser Tyr Gln Phe Ser Gly Asp Ser Leu  
                   820                  825                  830

Asn Phe Ser Asn Asn Asn Gln Phe Asn Ser Gly Ser Phe Glu Ile Gly  
                   835                  840                  845

Ala Lys Asn Thr Ile Phe Asn Asn Ala Asn Phe Asn Asn Ser Thr Ser  
                   850                  855                  860

Phe Asn Phe Asn Asn Ser Ser Ala Thr Thr Ser Phe Val Gly Asp Phe  
                   865                  870                  875                  880

Thr Asn Ala Asn Ser Asn Leu Gln Ile Ala Gly Asn Ala Val Phe Gly  
                   885                  890

Asn Ser Thr Asn Gly Ser Gln Asn Thr Ala Asn Phe Asn Asn Thr Gly  
                   900                  905                  910

Ser Val Asn Ile Ala Gly Asn Ala Thr Phe Asp Asn Val Val Phe Asn  
                   915                  920                  925

Ser Pro Thr Asn Thr Ser Val Lys Gly Lys Val Thr Leu Asn Asn Ile  
                   930                  935                  940

Thr Leu Lys Asn Leu Asn Ala Pro Leu Ser Phe Gly Asp Gly Thr Ile  
                   945                  950                  955                  960

Val Phe Ser Ala His Ser Val Ile Asn Ile Gly Glu Ala Ile Thr Asn  
                   965                  970                  975

Gly Asn Pro Ile Thr Leu Val Ser Ser Ser Lys Ala Ile Glu Tyr Asn  
                   980                  985                  990

Asp Ala Phe Ser Lys Asn Leu Trp Gln Leu Ile Asn Tyr Gln Gly His  
                   995                  1000                  1005

Gly Ala Ser Ser Glu Lys Leu Val Ser Ser Ala Gly Asn Gly Val  
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1055						1060					1065			
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1070						1075					1080			
Tyr	Asn	Asn	Asn	Leu	Gly	Asn	Leu	Asn	Asn	Thr	Ile	Tyr	Tyr	Tyr
1085						1090					1095			
Asp	Asn	Ser	Ile	Asp	Phe	Tyr	Ala	Ser	Gly	Lys	Thr	Leu	Phe	Thr
1100						1105					1110			
Lys	Ala	Glu	Phe	Ser	Gln	Thr	Phe	Thr	Gly	Gln	Asn	Ser	Ala	Ile
1115						1120					1125			
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1130						1135					1140			
Gln	Ser	Asn	Val	Ile	Ile	Arg	Phe	Gly	Asp	Asn	Lys	Gly	Ala	Gly
1145						1150					1155			
Ser	Asn	Asp	Ala	Ser	Gly	His	Cys	Trp	Asn	Leu	Gln	Cys	Ile	Gly
1160						1165					1170			
Phe	Ile	Thr	Gly	His	Tyr	Glu	Ala	Gln	Lys	Ile	Tyr	Ile	Thr	Gly
1175						1180					1185			
Ser	Ile	Glu	Ser	Gly	Asn	Arg	Ile	Ser	Ser	Gly	Gly	Gly	Ala	Ser
1190						1195					1200			
Leu	Asn	Phe	Asn	Gly	Leu	Gln	Gly	Ile	Leu	Leu	Thr	Asn	Ala	Thr
1205						1210					1215			
Leu	Tyr	Asn	Arg	Ala	Ala	Gly	Thr	Gln	Ser	Ser	Ser	Met	Asn	Phe
1220						1225					1230			

Val	Ser	Asn	Ser	Ala	Asn	Ile	Gln	Ala	Gln	Asn	Ser	Tyr	Phe	Ile
1235						1240					1245			
Asp	Asp	Thr	Ala	Gln	Asn	Lys	Gly	Asn	Pro	Asn	Phe	Ser	Phe	Asn
1250						1255					1260			
Ala	Leu	Asn	Leu	Asp	Phe	Ser	Asn	Ser	Ser	Phe	Arg	Gly	Tyr	Val
1265						1270					1275			
Gly	Gln	Thr	Gln	Ser	Val	Phe	Lys	Phe	Asn	Ala	Val	Asn	Ala	Ile
1280						1285					1290			
Ser	Phe	Thr	Asn	Ser	Ser	Asn	Leu	Ser	Ser	Gly	Leu	Tyr	Gln	Met
1295						1300					1305			
Gln	Ala	Lys	Ser	Val	Leu	Phe	Asp	Asn	Ser	Asn	Leu	Ser	Val	Ser
1310						1315					1320			
Val	Gly	Thr	Ser	Ser	Ile	Lys	Ala	Asn	Ala	Ile	Asn	Leu	Ser	Gln
1325						1330					1335			
Asn	Ala	Ser	Ile	Asn	Ala	Ser	Asn	His	Ser	Thr	Leu	Glu	Leu	Gln
1340						1345					1350			
Gly	Asp	Leu	Asn	Leu	Asn	Asp	Thr	Ser	Ser	Leu	Asn	Leu	Asn	Gln
1355						1360					1365			
Ser	Ala	Ile	Asn	Val	Ser	Asn	Asn	Ala	Thr	Ile	Asn	Asp	Tyr	Ala
1370						1375					1380			
Ser	Leu	Ile	Ala	Ser	Asn	Gly	Ser	His	Leu	Asn	Phe	Asn	Gly	Ala
1385						1390					1395			
Val	Asn	Phe	Asn	Ser	Ala	Asn	Ile	Thr	Thr	Ser	Leu	Ser	Ser	Ser
1400						1405					1410			
Ser	Ile	Val	Phe	Lys	Gly	Ala	Val	Ser	Leu	Arg	Gly	Gln	Phe	Asn
1415						1420					1425			
Leu	Ser	Asn	Asn	Ser	Ser	Leu	Asp	Phe	Gln	Gly	Ser	Ser	Ala	Ile
1430						1435					1440			

Thr	Ser	Asn	Thr	Ala	Phe	Asn	Phe	Tyr	Asp	Asn	Ala	Phe	Ser	Gln
	1445					1450					1455			
Ser	Pro	Ile	Thr	Phe	His	Gln	Ala	Leu	Asp	Ile	Lys	Val	Pro	Leu
	1460					1465					1470			
Ser	Leu	Gly	Gly	Asn	Leu	Leu	Asn	Pro	Asn	Asn	Ser	Ser	Val	Leu
	1475					1480					1485			
Asn	Leu	Lys	Asn	Ser	Gln	Leu	Val	Phe	Ser	Asp	Gln	Gly	Ser	Leu
	1490					1495					1500			
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Asn	Arg	Val	Tyr	Asn	Ile	Ile	Gln	Ala	Asp	Met	Asn	Gly	Asn	Trp
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Tyr	Glu	Arg	Ile	Asn	Phe	Phe	Gly	Met	Arg	Ile	Asn	Asp	Gly	Ile
	1535					1540					1545			
Tyr	Asp	Ala	Lys	Asn	Gln	Thr	Tyr	Ser	Phe	Thr	Asn	Pro	Leu	Asn
	1550					1555					1560			
Asn	Ala	Leu	Lys	Ile	Thr	Glu	Ser	Phe	Lys	Asn	Asn	Gln	Leu	Ser
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Val	Thr	Leu	Ser	Gln	Ile	Pro	Gly	Ile	Lys	Asn	Thr	Leu	Tyr	Asn
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Gln	Ala	Ser	Gly	Ser	Asn	Asn	Thr	Thr	Lys	Asn	Asn	Asn	Leu	Thr

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Pro Ile 1670	Ser Ala Leu His	Val 1675	Tyr Asn Lys Gly	Tyr 1680 Asn Phe Ser
Asn Ile 1685	Lys Ala Leu Gly	Gln 1690	Met Ala Leu Lys	Leu 1695 Tyr Pro Glu
Ile Lys 1700	Lys Ile Leu Gly	Asn 1705	Asp Phe Ser Leu	Ser 1710 Ser Leu Ser
Asn Leu 1715	Lys Gly Asp Ala	Leu 1720	Asn Gln Leu Thr	Lys 1725 Leu Ile Thr
Pro Ser 1730	Asp Trp Lys Asn	Ile 1735	Asn Glu Leu Ile	Asp 1740 Asn Ala Asn
Asn Ser 1745	Val Val Gln Asn	Phe 1750	Asn Asn Gly Thr	Leu 1755 Ile Ile Gly
Ala Thr 1760	Lys Ile Gly Gln	Thr 1765	Asp Thr Asn Ser	Ala 1770 Val Val Phe
Gly Gly 1775	Leu Gly Tyr Gln	Lys 1780	Pro Cys Asp Tyr	Thr 1785 Asp Ile Val
Cys Gln 1790	Lys Phe Arg Gly	Thr 1795	Tyr Leu Gly Gln	Leu 1800 Leu Glu Ser
Ile Ser 1805	Ala Asp Leu Gly	Tyr 1810	Ile Asp Thr Thr	Phe 1815 Asn Ala Lys
Glu Ile 1820	Tyr Leu Thr Gly	Thr 1825	Leu Gly Ser Gly	Asn 1830 Ala Trp Gly
Thr Gly 1835	Gly Ser Ala Ser	Val 1840	Thr Phe Asn Ser	Gln 1845 Thr Ser Leu

Ile	Leu	Asn	Gln	Ala	Asn	Ile	Val	Ser	Ser	Gln	Thr	Asp	Gly	Ile
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1895						1900					1905			
Ser	Asp	Ser	Val	Ile	Gly	Gly	Tyr	Leu	Thr	Pro	Glu	Gln	Lys	Asn
1910						1915					1920			
Gln	Thr	Leu	Ser	Gln	Leu	Leu	Gly	Gln	Asn	Asn	Phe	Asp	Asn	Leu
1925						1930					1935			
Met	Asn	Asp	Ser	Gly	Leu	Asn	Thr	Ala	Ile	Lys	Asp	Leu	Ile	Arg
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Gln	Lys	Leu	Gly	Phe	Trp	Thr	Gly	Leu	Val	Gly	Gly	Leu	Ala	Gly
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1970						1975					1980			
Met	Ser	Ile	Asn	Asp	Leu	Leu	Ser	Lys	Lys	Gly	Leu	Phe	Asn	Gln
1985						1990					1995			
Ile	Thr	Gly	Phe	Ile	Ser	Ala	Asn	Asp	Ile	Gly	Gln	Val	Ile	Ser
2000						2005					2010			
Val	Met	Leu	Gln	Asp	Ile	Val	Lys	Pro	Ser	Asp	Ala	Leu	Lys	Asn
2015						2020					2025			
Asp	Val	Ala	Ala	Leu	Gly	Lys	Gln	Met	Ile	Gly	Glu	Phe	Leu	Gly
2030						2035					2040			
Gln	Asp	Thr	Leu	Asn	Ser	Leu	Glu	Ser	Leu	Leu	Gln	Asn	Gln	Gln
2045						2050					2055			



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Ser	Ile	Tyr	Glu	Gln	Gly	Leu	Gly	Asp	Leu	Ile	Pro	Asn	Leu	Gly
	2075					2080					2085			
Lys	Lys	Gly	Ile	Phe	Ala	Pro	Tyr	Gly	Leu	Ser	Gln	Val	Trp	Gln
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Ala	Gly	Asn	Ser	Leu	Ile	Phe	Ala	Gly	Asn	Asn	His	Ile	Ala	Phe
	2135					2140					2145			
Thr	Asn	His	Ser	Gly	Thr	Leu	Asn	Leu	Leu	Ser	Asn	Gln	Val	Ser
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	2225					2230					2235			
Ser	Leu	Val	Val	Thr	Ala	Asn	Gly	Phe	Asn	Phe	Ser	Gly	Asn	Ile
	2240					2245					2250			
Tyr	Ala	Asn	Gly	Val	Val	Asp	Phe	Ser	Lys	Ile	Lys	Gly	Ser	Ala
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Asn	Val	Lys	Asn	Leu	Tyr	Leu	Tyr	Asn	Asn	Ala	Gln	Phe	Gln	Ala
2270						2275					2280			
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2285						2290					2295			
Ser	Phe	Val	Thr	Asn	Asn	Leu	Asn	Ile	Gln	Gly	Ala	Phe	Asn	Asn
2300						2305					2310			
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2345						2350					2355			
Ser	Gln	Thr	Pro	Val	Asn	Pro	Leu	Ile	Gln	Val	Gly	Gly	Ile	Ile
2360						2365					2370			
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2375						2380					2385			
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2390						2395					2400			
Tyr	Asn	Ile	Asn	Pro	Asn	Ser	Leu	Gln	Ser	Tyr	Leu	Lys	Leu	Tyr
2405						2410					2415			
Thr	Leu	Ile	Asn	Ile	Asn	Gly	Asn	His	Ile	Glu	Glu	Lys	Asn	Gly
2420						2425					2430			
Val	Leu	Thr	Tyr	Leu	Gly	Gln	Arg	Val	Leu	Leu	Gln	Asp	Lys	Gly
2435						2440					2445			
Leu	Leu	Leu	Ser	Val	Ala	Leu	Pro	Asn	Ser	Asn	Asn	Ala	Ser	Gln
2450						2455					2460			
Asn	Asn	Ile	Leu	Ser	Leu	Ser	Val	Leu	His	Asn	Gln	Ile	Lys	Met

2465						2470						2475			
Ser	Tyr	Gly	Asn	Lys	Val	Met	Asp	Phe	Thr	Pro	Pro	Thr	Leu	Gln	
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2495						2500					2505				
Glu	Ala	Val	Gly	Gly	Asn	Asn	Ala	Ile	Lys	Trp	Leu	Ser	Thr	Leu	
2510						2515					2520				
Met	Met	Glu	Thr	Lys	Glu	Asn	Pro	Leu	Phe	Ala	Pro	Ile	Tyr	Leu	
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Glu	Asn	His	Ser	Leu	Asn	Glu	Ile	Leu	Gly	Val	Thr	Lys	Asp	Leu	
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Gln	Asn	Thr	Ala	Ser	Leu	Ile	Ser	Asn	Pro	Asn	Phe	Arg	Asn	Asn	
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Ala	Thr	Ser	Leu	Leu	Glu	Met	Ala	Ser	Tyr	Thr	Gln	Gln	Thr	Ser	
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Arg	Leu	Thr	Lys	Leu	Ser	Asp	Phe	Arg	Ala	Arg	Glu	Gly	Glu	Ser	
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Asn	Phe	Ser	Glu	Arg	Leu	Leu	Glu	Leu	Lys	Asn	Lys	Arg	Phe	Ser	
2600						2605					2610				
Asp	Pro	Asn	Pro	Ser	Glu	Val	Phe	Val	Lys	Tyr	Ser	Gln	Leu	Ser	
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Lys	His	Pro	Asn	Asn	Leu	Trp	Ile	Gln	Gly	Val	Gly	Gly	Ala	Ser	
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Phe	Ile	Ser	Gly	Gly	Asn	Gly	Thr	Leu	Tyr	Gly	Leu	Asn	Val	Gly	
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Tyr	Asp	Arg	Leu	Val	Lys	Ser	Val	Ile	Leu	Gly	Gly	Tyr	Val	Ala	
2660						2665					2670				

Tyr	Gly	Tyr	Ser	Gly	Phe	Asn	Gly	Asn	Ile	Met	His	Ser	Leu	Ala
2675						2680					2685			
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2690						2695					2700			
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2705						2710					2715			
Ser	His	Ile	Asn	Ser	Ser	Asn	Ser	Leu	Leu	Ser	Val	Leu	Asn	Gln
2720						2725					2730			
Arg	Tyr	Asn	Tyr	Asn	Thr	Trp	Thr	Thr	Ser	Val	Asn	Gly	Asn	Tyr
2735						2740					2745			
Gly	Tyr	Asp	Phe	Met	Phe	Lys	Gln	Lys	Ser	Val	Val	Leu	Lys	Pro
2750						2755					2760			
Gln	Val	Gly	Leu	Ser	Tyr	His	Phe	Ile	Gly	Leu	Ser	Gly	Met	Lys
2765						2770					2775			
Gly	Lys	Met	Gln	Asn	Pro	Ala	Tyr	Gln	Gln	Phe	Val	Met	His	Ser
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2795						2800					2805			
Ser	Arg	Lys	Tyr	Phe	Gly	Lys	Asn	Ser	Tyr	Tyr	Phe	Val	Thr	Ala
2810						2815					2820			
Arg	Leu	Gly	Arg	Asp	Leu	Leu	Ile	Lys	Ala	Lys	Gly	Asp	Asn	Val
2825						2830					2835			
Val	Arg	Phe	Val	Gly	Glu	Asn	Thr	Leu	Leu	Tyr	Arg	Lys	Gly	Glu
2840						2845					2850			
Ile	Phe	Asn	Thr	Phe	Ala	Ser	Val	Ile	Thr	Gly	Gly	Glu	Met	His
2855						2860					2865			
Leu	Trp	Arg	Leu	Met	Tyr	Val	Asn	Ala	Gly	Val	Gly	Leu	Lys	Met
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 2885 2890 2895

Arg Val Ala Phe  
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 <222> (1)..(873)

<220>  
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 acg att gtt att gtg ctg ttg gtt anc ttt ttt gtc gcg caa gcc ttt 96  
 Thr Ile Val Ile Val Leu Leu Val Xaa Phe Phe Val Ala Gln Ala Phe  
 20 25 30  
 atc att ccc tct cgc tct atg gta ggc acg ctc tat gag ggc gat atg 144  
 Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr Glu Gly Asp Met  
 35 40 45  
 ctc ttt gtc aaa aaa ttt tct tac ggc atc ccc att cct aaa atc cca 192  
 Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile Pro Lys Ile Pro  
 50 55 60  
 tgg att gag ctt cct gtt atg cct gat ttt aaa aat aac ggg cat ttg 240  
 Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn Gly His Leu  
 65 70 75 80  
 ata gag ggg gat cgc cct aaa cgc ggc gaa gtg gtg gtg ttt atc cct 288  
 Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val Val Phe Ile Pro  
 85 90 95  
 ccc cat gaa aaa aaa tct tac tat gtc aaa agg aat ttt gct att ggg 336  
 Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe Ala Ile Gly  
 100 105 110  
 ggc gat gag gtg tta ttc act agt gag ggg ttt tat ttg cac cct ttt 384

Gly	Asp	Glu	Val	Leu	Phe	Thr	Ser	Glu	Gly	Phe	Tyr	Leu	His	Pro	Phe		
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Glu	Ser	Gly	Thr	Asp	Lys	Thr	Tyr	Ile	Ala	Lys	His	Tyr	Pro	Asp	Ala		
	130					135					140						
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Met	Thr	Lys	Glu	Phe	Met	Gly	Lys	Ile	Phe	Val	Leu	Asn	Pro	Tyr	Lys		
	145				150					155					160		
agt	aag	cat	ccg	ggg	atc	cat	tac	caa	aaa	gac	aat	gaa	acc	ttc	cat		528
Ser	Lys	His	Pro	Gly	Ile	His	Tyr	Gln	Lys	Asp	Asn	Glu	Thr	Phe	His		
				165					170					175			
tta	atg	gag	cag	tta	gcc	act	caa	ggc	gcg	gaa	gct	aat	atc	agc	atg		576
Leu	Met	Glu	Gln	Leu	Ala	Thr	Gln	Gly	Ala	Glu	Ala	Asn	Ile	Ser	Met		
			180					185					190				
caa	ctc	att	caa	atg	gag	ggc	gaa	aag	gtg	ttt	tat	aaa	aaa	atc	aat		624
Gln	Leu	Ile	Gln	Met	Glu	Gly	Glu	Lys	Val	Phe	Tyr	Lys	Lys	Ile	Asn		
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gac	gat	gaa	ttt	ttc	atg	atc	ggc	gat	aac	agg	gat	aat	tct	agc	gac		672
Asp	Asp	Glu	Phe	Phe	Met	Ile	Gly	Asp	Asn	Arg	Asp	Asn	Ser	Ser	Asp		
	210					215					220						
tcg	cgc	ttt	tgg	ggg	agt	gtg	gct	tat	aaa	aat	atc	gtg	ggg	tcg	cca		720
Ser	Arg	Phe	Trp	Gly	Ser	Val	Ala	Tyr	Lys	Asn	Ile	Val	Gly	Ser	Pro		
	225				230					235					240		
tgg	ttt	gtt	tat	ttc	agt	ttg	agt	tta	aaa	aat	agc	ctg	gaa	atg	gat		768
Trp	Phe	Val	Tyr	Phe	Ser	Leu	Ser	Leu	Lys	Asn	Ser	Leu	Glu	Met	Asp		
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gca	gaa	aat	aac	ccc	aaa	aaa	cgc	tat	ttg	gtg	cgt	tgg	gag	cgc	atg		816
Ala	Glu	Asn	Asn	Pro	Lys	Lys	Arg	Tyr	Leu	Val	Arg	Trp	Glu	Arg	Met		
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ttt	aaa	agc	gtt	gaa	ggc	tta	gaa	aaa	atc	att	aaa	aaa	gaa	aaa	gca		864
Phe	Lys	Ser	Val	Glu	Gly	Leu	Glu	Lys	Ile	Ile	Lys	Lys	Glu	Lys	Ala		
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acg	cat	taa															873
Thr	His																
	290																

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 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <221> misc\_feature

<222> (25)..(25)

<223> The 'Xaa' at location 25 stands for Asn, Ser, Thr, or Ile.

<400> 118

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Thr Ile Val Ile Val Leu Leu Val Xaa Phe Phe Val Ala Gln Ala Phe  
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Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr Glu Gly Asp Met  
35 40 45

Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile Pro Lys Ile Pro  
50 55 60

Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn Gly His Leu  
65 70 75 80

Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val Val Phe Ile Pro  
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Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe Ala Ile Gly  
100 105 110

Gly Asp Glu Val Leu Phe Thr Ser Glu Gly Phe Tyr Leu His Pro Phe  
115 120 125

Glu Ser Gly Thr Asp Lys Thr Tyr Ile Ala Lys His Tyr Pro Asp Ala  
130 135 140

Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu Asn Pro Tyr Lys  
145 150 155 160

Ser Lys His Pro Gly Ile His Tyr Gln Lys Asp Asn Glu Thr Phe His  
165 170 175

Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala Asn Ile Ser Met  
180 185 190

Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr Lys Lys Ile Asn  
195 200 205

Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp Asn Ser Ser Asp  
 210 215 220

Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile Val Gly Ser Pro  
 225 230 235 240

Trp Phe Val Tyr Phe Ser Leu Ser Leu Lys Asn Ser Leu Glu Met Asp  
 245 250 255

Ala Glu Asn Asn Pro Lys Lys Arg Tyr Leu Val Arg Trp Glu Arg Met  
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Phe Lys Ser Val Glu Gly Leu Glu Lys Ile Ile Lys Lys Glu Lys Ala  
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Thr His  
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<220>  
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 Ile Tyr Tyr Gly Val Glu Pro Tyr Ala His Ser Val Met His Pro Lys  
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 gtc gct ccg gca gat ttt gct ttc aag gat tta gag ccg atg gat tta 144  
 Val Ala Pro Ala Asp Phe Ala Phe Lys Asp Leu Glu Pro Met Asp Leu  
 35 40 45  
 aaa aat ggc gat gct aat aag ggc aaa cag ctt gta gcc gaa aat tgc 192  
 Lys Asn Gly Asp Ala Asn Lys Gly Lys Gln Leu Val Ala Glu Asn Cys  
 50 55 60  
 acc gct tgc cat ggc att aaa tcc caa aac att cca gcc cct atg gac 240  
 Thr Ala Cys His Gly Ile Lys Ser Gln Asn Ile Pro Ala Pro Met Asp



65		70		75		80	
agc ctt agc gcg agc aac tct ttt ggg gtc gtg cca ccg gat tta agc							288
Ser Leu Ser Ala Ser Asn Ser Phe Gly Val Val Pro Pro Asp Leu Ser							
		85		90		95	
cat gtg gct ggg gtt ttg aac gcg aat ttc tta gcc cac ttc atc aaa							336
His Val Ala Gly Val Leu Asn Ala Asn Phe Leu Ala His Phe Ile Lys							
		100		105		110	
gac ccc gtg aaa acg gcg aaa ttg agc cat aag ttc aac gat gaa agg							384
Asp Pro Val Lys Thr Ala Lys Leu Ser His Lys Phe Asn Asp Glu Arg							
		115		120		125	
ccc tat cct atg ccg gcg ttt tct caa ttt agc gat caa gat ttg agc							432
Pro Tyr Pro Met Pro Ala Phe Ser Gln Phe Ser Asp Gln Asp Leu Ser							
		130		135		140	
gat att gtg gcg tat ctc act tct att ttg cct aaa agt ttg agc gat							480
Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys Ser Leu Ser Asp							
		145		150		155	160
aag gaa gtg ttc gca caa agc tgt caa agg tgc cat agc ttg gat tat							528
Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His Ser Leu Asp Tyr							
		165		170		175	
gct aaa gat aag gcc ttt agc gat cct aaa gat cta gcc aat tat tta							576
Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu Ala Asn Tyr Leu							
		180		185		190	
ggc tct cat gca cct gat ttg tcc atg atg att aga gct aaa ggc gaa							624
Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg Ala Lys Gly Glu							
		195		200		205	
cat ggc ttg aat att ttc atc aac gat ccg caa aag ctt							663
His Gly Leu Asn Ile Phe Ile Asn Asp Pro Gln Lys Leu							
		210		215		220	

<210> 120

<211> 221

<212> PRT

<213> Helicobacter pylori

<400> 120

Met Lys Glu Phe Lys Ile Leu Ile Ile Leu Ile Val Val Val Gly Val
1 5 10 15

Ile Tyr Tyr Gly Val Glu Pro Tyr Ala His Ser Val Met His Pro Lys
20 25 30

Val Ala Pro Ala Asp Phe Ala Phe Lys Asp Leu Glu Pro Met Asp Leu

35	40	45
Lys Asn Gly Asp Ala Asn Lys Gly Lys Gln Leu Val Ala Glu Asn Cys		
50	55	60
Thr Ala Cys His Gly Ile Lys Ser Gln Asn Ile Pro Ala Pro Met Asp		
65	70	75
Ser Leu Ser Ala Ser Asn Ser Phe Gly Val Val Pro Pro Asp Leu Ser		
	85	90
His Val Ala Gly Val Leu Asn Ala Asn Phe Leu Ala His Phe Ile Lys		
	100	105
Asp Pro Val Lys Thr Ala Lys Leu Ser His Lys Phe Asn Asp Glu Arg		
	115	120
Pro Tyr Pro Met Pro Ala Phe Ser Gln Phe Ser Asp Gln Asp Leu Ser		
	130	135
Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys Ser Leu Ser Asp		
145	150	155
Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His Ser Leu Asp Tyr		
	165	170
Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu Ala Asn Tyr Leu		
	180	185
Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg Ala Lys Gly Glu		
	195	200
His Gly Leu Asn Ile Phe Ile Asn Asp Pro Gln Lys Leu		
	210	215
		220

<210> 121  
 <211> 1674  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS

<222> (1)..(1674)

<400> 121

atg	aat	aaa	cca	ttt	tta	atc	tta	ctc	ata	gcc	cta	att	gtc	ttt	agc	48
Met	Asn	Lys	Pro	Phe	Leu	Ile	Leu	Leu	Ile	Ala	Leu	Ile	Val	Phe	Ser	
1				5					10					15		

ggc	tgt	aac	atg	aga	aaa	tat	ttc	aaa	ccc	gct	aaa	cac	caa	ggt	aaa	96
Gly	Cys	Asn	Met	Arg	Lys	Tyr	Phe	Lys	Pro	Ala	Lys	His	Gln	Val	Lys	
			20					25					30			

ggc	gaa	gcg	tat	ttc	cct	aat	cat	ttg	caa	gaa	agt	atc	ggt	tcg	tct	144
Gly	Glu	Ala	Tyr	Phe	Pro	Asn	His	Leu	Gln	Glu	Ser	Ile	Val	Ser	Ser	
		35					40					45				

aat	cgt	tat	gga	gcc	att	ttg	aaa	aat	gga	gcg	ggt	ata	ggc	gat	aaa	192
Asn	Arg	Tyr	Gly	Ala	Ile	Leu	Lys	Asn	Gly	Ala	Val	Ile	Gly	Asp	Lys	
	50					55					60					

ggc	tta	acg	cag	cta	aga	atc	ggc	aag	aat	ttc	aat	tat	gaa	agc	agt	240
Gly	Leu	Thr	Gln	Leu	Arg	Ile	Gly	Lys	Asn	Phe	Asn	Tyr	Glu	Ser	Ser	
65					70					75					80	

ttt	tta	aat	gag	agt	cag	ggg	ttt	ttc	atc	ctt	gcg	caa	gat	tgt	ttg	288
Phe	Leu	Asn	Glu	Ser	Gln	Gly	Phe	Phe	Ile	Leu	Ala	Gln	Asp	Cys	Leu	
				85					90					95		

aac	aag	att	gat	aaa	aaa	aca	agc	aaa	aac	aag	gtg	gct	aaa	agt	gag	336
Asn	Lys	Ile	Asp	Lys	Lys	Thr	Ser	Lys	Asn	Lys	Val	Ala	Lys	Ser	Glu	
			100					105					110			

gaa	acg	gag	ctg	aaa	tta	aag	ggc	ggt	gaa	gcc	gaa	gtc	caa	gat	aaa	384
Glu	Thr	Glu	Leu	Lys	Leu	Lys	Gly	Val	Glu	Ala	Glu	Val	Gln	Asp	Lys	
		115					120					125				

gtc	tgt	cat	caa	gtg	gaa	ttg	att	agc	aat	aac	cct	aac	gcc	agc	caa	432
Val	Cys	His	Gln	Val	Glu	Leu	Ile	Ser	Asn	Asn	Pro	Asn	Ala	Ser	Gln	
	130					135					140					

caa	tct	atc	ggt	atc	cct	ttg	gag	act	ttt	gcc	ttg	agc	gca	agc	ggt	480
Gln	Ser	Ile	Val	Ile	Pro	Leu	Glu	Thr	Phe	Ala	Leu	Ser	Ala	Ser	Val	
145					150					155					160	

aaa	ggg	aat	ctt	tta	gcg	gtg	gtg	tta	gcg	gac	aat	tca	gcg	aat	tta	528
Lys	Gly	Asn	Leu	Leu	Ala	Val	Val	Leu	Ala	Asp	Asn	Ser	Ala	Asn	Leu	
				165					170					175		

tac	gac	atc	act	tct	caa	aaa	ttg	ctt	ttt	agt	gag	aaa	ggc	tcc	cca	576
Tyr	Asp	Ile	Thr	Ser	Gln	Lys	Leu	Leu	Phe	Ser	Glu	Lys	Gly	Ser	Pro	
			180					185					190			

agc	acc	acg	atc	aat	tct	tta	atg	gcg	atg	cct	att	ttt	atg	gat	acg	624
Ser	Thr	Thr	Ile	Asn	Ser	Leu	Met	Ala	Met	Pro	Ile	Phe	Met	Asp	Thr	
		195					200					205				

gtc	gtg	gtg	ttc	ccc	atg	cta	gat	ggg	cgt	ttg	ttg	gtc	gtg	gat	tat	672
Val	Val	Val	Phe	Pro	Met	Leu	Asp	Gly	Arg	Leu	Leu	Val	Val	Asp	Tyr	
	210					215					220					
gtg	cat	gga	aac	cct	acg	cct	att	aga	aac	att	gtt	atc	agc	agc	gat	720
Val	His	Gly	Asn	Pro	Thr	Pro	Ile	Arg	Asn	Ile	Val	Ile	Ser	Ser	Asp	
	225				230					235					240	
aag	ttt	ttt	aac	aat	atc	act	tac	ctt	atc	gta	gat	ggc	aat	aac	atg	768
Lys	Phe	Phe	Asn	Asn	Ile	Thr	Tyr	Leu	Ile	Val	Asp	Gly	Asn	Asn	Met	
				245					250					255		
atc	gct	tct	aca	ggg	aaa	aga	ata	ctc	tca	gtc	gtg	agc	ggg	caa	gag	816
Ile	Ala	Ser	Thr	Gly	Lys	Arg	Ile	Leu	Ser	Val	Val	Ser	Gly	Gln	Glu	
			260					265					270			
ttc	aac	tat	gat	ggg	gat	att	ata	gat	ttg	ctt	tat	gat	aag	ggg	act	864
Phe	Asn	Tyr	Asp	Gly	Asp	Ile	Ile	Asp	Leu	Leu	Tyr	Asp	Lys	Gly	Thr	
		275					280					285				
tta	tac	gtg	ctc	acg	cta	gac	ggg	cag	att	ttg	caa	atg	gat	aag	agt	912
Leu	Tyr	Val	Leu	Thr	Leu	Asp	Gly	Gln	Ile	Leu	Gln	Met	Asp	Lys	Ser	
	290					295					300					
ttg	agg	gaa	tta	aac	agc	gtg	aaa	ctg	ccc	ttt	gct	tcg	ctc	aat	acc	960
Leu	Arg	Glu	Leu	Asn	Ser	Val	Lys	Leu	Pro	Phe	Ala	Ser	Leu	Asn	Thr	
	305				310					315					320	
att	gta	tta	aac	cat	aat	aaa	ttg	tat	tct	tta	gaa	aag	cgt	ggg	tat	1008
Ile	Val	Leu	Asn	His	Asn	Lys	Leu	Tyr	Ser	Leu	Glu	Lys	Arg	Gly	Tyr	
				325					330					335		
gtg	ata	gaa	gtg	gat	ttg	aat	gat	ttt	gat	tcg	tat	aat	gtc	tat	aaa	1056
Val	Ile	Glu	Val	Asp	Leu	Asn	Asp	Phe	Asp	Ser	Tyr	Asn	Val	Tyr	Lys	
			340					345					350			
acg	cca	act	ata	ggc	agt	ttt	arg	ttt	ttt	tca	tcc	aat	cgt	ttg	gat	1104
Thr	Pro	Thr	Ile	Gly	Ser	Phe	Xaa	Phe	Phe	Ser	Ser	Asn	Arg	Leu	Asp	
			355				360						365			
aaa	ggg	gtg	ttt	tat	gat	aaa	aat	cgg	gtg	tat	tac	gat	cgc	tac	tat	1152
Lys	Gly	Val	Phe	Tyr	Asp	Lys	Asn	Arg	Val	Tyr	Tyr	Asp	Arg	Tyr	Tyr	
	370					375					380					
tta	gat	tat	aac	gat	ttt	aaa	cca	aaa	ctt	tat	ccc	gtt	gtg	gaa	aaa	1200
Leu	Asp	Tyr	Asn	Asp	Phe	Lys	Pro	Lys	Leu	Tyr	Pro	Val	Val	Glu	Lys	
	385				390					395				400		
tcg	gca	tct	aaa	aaa	tct	caa	aaa	ggc	gaa	aaa	ggg	aac	act	ccc	att	1248
Ser	Ala	Ser	Lys	Lys	Ser	Gln	Lys	Gly	Glu	Lys	Gly	Asn	Thr	Pro	Ile	
				405				410						415		
tat	ttg	caa	gaa	agg	cat	aaa	gct	aaa	gaa	aag	cct	tta	gaa	gaa	aac	1296
Tyr	Leu	Gln	Glu	Arg	His	Lys	Ala	Lys	Glu	Lys	Pro	Leu	Glu	Glu	Asn	
			420				425						430			

aaa gtt aag cca aga aat agc ggg ttt gaa gaa gaa gaa gtt aaa acc	1344
Lys Val Lys Pro Arg Asn Ser Gly Phe Glu Glu Glu Glu Val Lys Thr	
435 440 445	
gga agc cgt gat atg gag cct act aac aat caa aat aac gct atc caa	1392
Gly Ser Arg Asp Met Glu Pro Thr Asn Asn Gln Asn Asn Ala Ile Gln	
450 455 460	
aaa ggc ata aaa gaa agt caa gaa aac aaa aac gct cct gct tca aaa	1440
Lys Gly Ile Lys Glu Ser Gln Glu Asn Lys Asn Ala Pro Ala Ser Lys	
465 470 475 480	
gag ggt aac caa aaa ggt gca gaa aac gct cct gtt tca aaa gag gat	1488
Glu Gly Asn Gln Lys Gly Ala Glu Asn Ala Pro Val Ser Lys Glu Asp	
485 490 495	
aac gct att aaa gaa gcg cca aaa ctc agc cct aaa gaa gaa aaa cgc	1536
Asn Ala Ile Lys Glu Ala Pro Lys Leu Ser Pro Lys Glu Glu Lys Arg	
500 505 510	
cgc ttg aaa gaa gaa aag aaa aaa gcc aaa gcc gaa caa aga gcg aga	1584
Arg Leu Lys Glu Glu Lys Lys Lys Ala Lys Ala Glu Gln Arg Ala Arg	
515 520 525	
gaa ttt gaa caa aga gcg aga gag cat caa gaa aga gat gaa aaa gag	1632
Glu Phe Glu Gln Arg Ala Arg Glu His Gln Glu Arg Asp Glu Lys Glu	
530 535 540	
ctt gaa gaa aga aga aaa gct tta gaa atg aat aag aag tag	1674
Leu Glu Glu Arg Arg Lys Ala Leu Glu Met Asn Lys Lys	
545 550 555	

<210> 122  
 <211> 557  
 <212> PRT  
 <213> *Helicobacter pylori*

<220>  
 <221> misc\_feature  
 <222> (360)..(360)

<223> The 'Xaa' at location 360 stands for Arg, or Lys.

<400> 122

Met Asn Lys Pro Phe Leu Ile Leu Leu Ile Ala Leu Ile Val Phe Ser
1 5 10 15

Gly Cys Asn Met Arg Lys Tyr Phe Lys Pro Ala Lys His Gln Val Lys
20 25 30

Gly	Glu	Ala	Tyr	Phe	Pro	Asn	His	Leu	Gln	Glu	Ser	Ile	Val	Ser	Ser	
		35					40					45				
Asn	Arg	Tyr	Gly	Ala	Ile	Leu	Lys	Asn	Gly	Ala	Val	Ile	Gly	Asp	Lys	
	50					55					60					
Gly	Leu	Thr	Gln	Leu	Arg	Ile	Gly	Lys	Asn	Phe	Asn	Tyr	Glu	Ser	Ser	
65					70					75					80	
Phe	Leu	Asn	Glu	Ser	Gln	Gly	Phe	Phe	Ile	Leu	Ala	Gln	Asp	Cys	Leu	
				85					90					95		
Asn	Lys	Ile	Asp	Lys	Lys	Thr	Ser	Lys	Asn	Lys	Val	Ala	Lys	Ser	Glu	
			100					105					110			
Glu	Thr	Glu	Leu	Lys	Leu	Lys	Gly	Val	Glu	Ala	Glu	Val	Gln	Asp	Lys	
		115					120					125				
Val	Cys	His	Gln	Val	Glu	Leu	Ile	Ser	Asn	Asn	Pro	Asn	Ala	Ser	Gln	
	130					135					140					
Gln	Ser	Ile	Val	Ile	Pro	Leu	Glu	Thr	Phe	Ala	Leu	Ser	Ala	Ser	Val	
145					150					155					160	
Lys	Gly	Asn	Leu	Leu	Ala	Val	Val	Leu	Ala	Asp	Asn	Ser	Ala	Asn	Leu	
				165					170					175		
Tyr	Asp	Ile	Thr	Ser	Gln	Lys	Leu	Leu	Phe	Ser	Glu	Lys	Gly	Ser	Pro	
			180					185					190			
Ser	Thr	Thr	Ile	Asn	Ser	Leu	Met	Ala	Met	Pro	Ile	Phe	Met	Asp	Thr	
		195					200					205				
Val	Val	Val	Phe	Pro	Met	Leu	Asp	Gly	Arg	Leu	Leu	Val	Val	Asp	Tyr	
	210					215					220					
Val	His	Gly	Asn	Pro	Thr	Pro	Ile	Arg	Asn	Ile	Val	Ile	Ser	Ser	Asp	
225					230					235					240	
Lys	Phe	Phe	Asn	Asn	Ile	Thr	Tyr	Leu	Ile	Val	Asp	Gly	Asn	Asn	Met	
				245					250					255		

Ile Ala Ser Thr Gly Lys Arg Ile Leu Ser Val Val Ser Gly Gln Glu  
260 265 270

Phe Asn Tyr Asp Gly Asp Ile Ile Asp Leu Leu Tyr Asp Lys Gly Thr  
275 280 285

Leu Tyr Val Leu Thr Leu Asp Gly Gln Ile Leu Gln Met Asp Lys Ser  
290 295 300

Leu Arg Glu Leu Asn Ser Val Lys Leu Pro Phe Ala Ser Leu Asn Thr  
305 310 315 320

Ile Val Leu Asn His Asn Lys Leu Tyr Ser Leu Glu Lys Arg Gly Tyr  
325 330 335

Val Ile Glu Val Asp Leu Asn Asp Phe Asp Ser Tyr Asn Val Tyr Lys  
340 345 350

Thr Pro Thr Ile Gly Ser Phe Xaa Phe Phe Ser Ser Asn Arg Leu Asp  
355 360 365

Lys Gly Val Phe Tyr Asp Lys Asn Arg Val Tyr Tyr Asp Arg Tyr Tyr  
370 375 380

Leu Asp Tyr Asn Asp Phe Lys Pro Lys Leu Tyr Pro Val Val Glu Lys  
385 390 395 400

Ser Ala Ser Lys Lys Ser Gln Lys Gly Glu Lys Gly Asn Thr Pro Ile  
405 410 415

Tyr Leu Gln Glu Arg His Lys Ala Lys Glu Lys Pro Leu Glu Glu Asn  
420 425 430

Lys Val Lys Pro Arg Asn Ser Gly Phe Glu Glu Glu Glu Val Lys Thr  
435 440 445

Gly Ser Arg Asp Met Glu Pro Thr Asn Asn Gln Asn Asn Ala Ile Gln  
450 455 460

Lys Gly Ile Lys Glu Ser Gln Glu Asn Lys Asn Ala Pro Ala Ser Lys

465						470				475				480			
Glu	Gly	Asn	Gln	Lys 485	Gly	Ala	Glu	Asn	Ala 490	Pro	Val	Ser	Lys	Glu 495	Asp		
Asn	Ala	Ile	Lys 500	Glu	Ala	Pro	Lys	Leu 505	Ser	Pro	Lys	Glu	Glu 510	Lys	Arg		
Arg	Leu	Lys 515	Glu	Glu	Lys	Lys	Lys 520	Ala	Lys	Ala	Glu	Gln 525	Arg	Ala	Arg		
Glu	Phe 530	Glu	Gln	Arg	Ala	Arg 535	Glu	His	Gln	Glu	Arg 540	Asp	Glu	Lys	Glu		
Leu 545	Glu	Glu	Arg	Arg	Lys 550	Ala	Leu	Glu	Met	Asn 555	Lys	Lys					



cat ctc ttc ccc tta ccc ccc aaa aaa cgc agc cca gaa aac gaa tgc	240
His Leu Phe Pro Leu Pro Pro Lys Lys Arg Ser Pro Glu Asn Glu Cys	
65 70 75 80	
gtg aat tgc ttg cat tgc gtg cag gtt tgc ccc aca cat att gat att	288
Val Asn Cys Leu His Cys Val Gln Val Cys Pro Thr His Ile Asp Ile	
85 90 95	
agg aaa ggc ttg caa tta gaa tgc atc aat tgt tta gaa tgc gtg nat	336
Arg Lys Gly Leu Gln Leu Glu Cys Ile Asn Cys Leu Glu Cys Val Xaa	
100 105 110	
gca tgc acc att acc atg gct aaa tac aac cgc cct tca ctc atc caa	384
Ala Cys Thr Ile Thr Met Ala Lys Tyr Asn Arg Pro Ser Leu Ile Gln	
115 120 125	
tgg tct tca acc aac gcc att aac acg cgc caa aaa gtg cgc ctg gtg	432
Trp Ser Ser Thr Asn Ala Ile Asn Thr Arg Gln Lys Val Arg Leu Val	
130 135 140	
cgt tta aaa acg atc gct tac atg ggg gtt atc gct gtt gtg atc gct	480
Arg Leu Lys Thr Ile Ala Tyr Met Gly Val Ile Ala Val Val Ile Ala	
145 150 155 160	
ctt tta gcc atc act tcg ttt aaa aaa gaa cgc atg ctc tta gac att	528
Leu Leu Ala Ile Thr Ser Phe Lys Lys Glu Arg Met Leu Leu Asp Ile	
165 170 175	
aac cgc aac agc gat ctg tat gaa ttg cgc tct agt ggg tat gtg gat	576
Asn Arg Asn Ser Asp Leu Tyr Glu Leu Arg Ser Ser Gly Tyr Val Asp	
180 185 190	
aac gat tat gtg ttt tta ttc cac aac acg gac aat aaa gac cat gag	624
Asn Asp Tyr Val Phe Leu Phe His Asn Thr Asp Asn Lys Asp His Glu	
195 200 205	
ttt tat ttc aaa att tta ggg caa aaa gac atc caa atc aaa aag cct	672
Phe Tyr Phe Lys Ile Leu Gly Gln Lys Asp Ile Gln Ile Lys Lys Pro	
210 215 220	
tta aat cct atc gcc att aaa gcc g	697
Leu Asn Pro Ile Ala Ile Lys Ala	
225 230	

<210> 124

<211> 232

<212> PRT

<213> Helicobacter pylori

<220>

<221> misc\_feature

<222> (112)..(112)

<223> The 'Xaa' at location 112 stands for Asn, Asp, His, or Tyr.

<400> 124

Asp His Pro Ile Ala Met Gly Phe Trp Leu Phe Ser Thr Thr Val Val  
1 5 10 15

Leu Phe Asp Ile Val Val Val Ala Glu Arg Phe Cys Ile Tyr Leu Cys  
20 25 30

Pro Tyr Ala Arg Val Gln Ser Val Leu Tyr Asp Asn Asp Thr Leu Asn  
35 40 45

Pro Ile Tyr Asp Glu Lys Arg Gly Gly Val Leu Tyr Asn Asn Gln Gly  
50 55 60

His Leu Phe Pro Leu Pro Pro Lys Lys Arg Ser Pro Glu Asn Glu Cys  
65 70 75 80

Val Asn Cys Leu His Cys Val Gln Val Cys Pro Thr His Ile Asp Ile  
85 90 95

Arg Lys Gly Leu Gln Leu Glu Cys Ile Asn Cys Leu Glu Cys Val Xaa  
100 105 110

Ala Cys Thr Ile Thr Met Ala Lys Tyr Asn Arg Pro Ser Leu Ile Gln  
115 120 125

Trp Ser Ser Thr Asn Ala Ile Asn Thr Arg Gln Lys Val Arg Leu Val  
130 135 140

Arg Leu Lys Thr Ile Ala Tyr Met Gly Val Ile Ala Val Val Ile Ala  
145 150 155 160

Leu Leu Ala Ile Thr Ser Phe Lys Lys Glu Arg Met Leu Leu Asp Ile  
165 170 175

Asn Arg Asn Ser Asp Leu Tyr Glu Leu Arg Ser Ser Gly Tyr Val Asp  
180 185 190

Asn Asp Tyr Val Phe Leu Phe His Asn Thr Asp Asn Lys Asp His Glu  
195 200 205

Phe Tyr Phe Lys Ile Leu Gly Gln Lys Asp Ile Gln Ile Lys Lys Pro

210

215

220

Leu Asn Pro Ile Ala Ile Lys Ala  
 225 230

<210> 125  
 <211> 519  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(519)

<220>  
 <221> misc\_feature  
 <222> (490)..(493)  
 <223> n = any nucleotide

<400> 125  
 gat caa aat aac gat ttg gcg ttt gtg gtg tgc ttg caa atc cct ttg 48  
 Asp Gln Asn Asn Asp Leu Ala Phe Val Val Cys Leu Gln Ile Pro Leu  
 1 5 10 15  
 agg gta gcg att gaa atc agc tcg cct tca aag tat ttc aga acc ttt 96  
 Arg Val Ala Ile Glu Ile Ser Ser Pro Ser Lys Tyr Phe Arg Thr Phe  
 20 25 30  
 agc gaa ggg agc atg gtc atg tat ttt tcg cct tca aag tat ttc aga 144  
 Ser Glu Gly Ser Met Val Met Tyr Phe Ser Pro Ser Lys Tyr Phe Arg  
 35 40 45  
 acc ttt agc gaa ggg agc atg gtc atg tat ttt atg att tct atc atg 192  
 Thr Phe Ser Glu Gly Ser Met Val Met Tyr Phe Met Ile Ser Ile Met  
 50 55 60  
 ctc act tta gtg tcg ttg ctt tta ttt gtg aaa tgc att tct agc ttt 240  
 Leu Thr Leu Val Ser Leu Leu Leu Phe Val Lys Cys Ile Ser Ser Phe  
 65 70 75 80  
 tgg aca gcg att gtc aat ttt agc agt ttt gat att aaa gaa gtg ttc 288  
 Trp Thr Ala Ile Val Asn Phe Ser Ser Phe Asp Ile Lys Glu Val Phe  
 85 90 95  
 cac ccc att gtg ctt tta acc cta gcc tta gcc acc ttt gat ctg gtc 336  
 His Pro Ile Val Leu Leu Thr Leu Ala Leu Ala Thr Phe Asp Leu Val  
 100 105 110  
 aag gcg att ttt gaa gag gaa gtt ttg ggt aaa aat agc ggg gac aac 384  
 Lys Ala Ile Phe Glu Glu Glu Val Leu Gly Lys Asn Ser Gly Asp Asn  
 115 120 125

cac	cat	gcg	atc	cac	cgc	acg	atg	atc	aga	ttt	tta	ggc	tct	atc	att	432
His	His	Ala	Ile	His	Arg	Thr	Met	Ile	Arg	Phe	Leu	Gly	Ser	Ile	Ile	
	130					135					140					

atc	gca	tta	gcc	att	gaa	gcg	tta	atg	tta	gtg	ttt	aaa	ttc	agc	gtg	480
Ile	Ala	Leu	Ala	Ile	Glu	Ala	Leu	Met	Leu	Val	Phe	Lys	Phe	Ser	Val	
145					150					155					160	

agc	gaa	ccg	nnn	naa	atc	act	tat	gcg	gtg	tat	ttg	gct				519
Ser	Glu	Pro	Xaa	Xaa	Ile	Thr	Tyr	Ala	Val	Tyr	Leu	Ala				
			165						170							

<210> 126  
 <211> 173  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <221> misc\_feature  
 <222> (164)..(164)  
 <223> The 'Xaa' at location 164 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (165)..(165)  
 <223> The 'Xaa' at location 165 stands for Lys, Glu, or Gln.

<400> 126

Asp	Gln	Asn	Asn	Asp	Leu	Ala	Phe	Val	Val	Cys	Leu	Gln	Ile	Pro	Leu
1				5					10					15	

Arg	Val	Ala	Ile	Glu	Ile	Ser	Ser	Pro	Ser	Lys	Tyr	Phe	Arg	Thr	Phe
			20					25					30		

Ser	Glu	Gly	Ser	Met	Val	Met	Tyr	Phe	Ser	Pro	Ser	Lys	Tyr	Phe	Arg
		35					40					45			

Thr	Phe	Ser	Glu	Gly	Ser	Met	Val	Met	Tyr	Phe	Met	Ile	Ser	Ile	Met
	50					55					60				

Leu	Thr	Leu	Val	Ser	Leu	Leu	Leu	Phe	Val	Lys	Cys	Ile	Ser	Ser	Phe
65					70					75					80

Trp	Thr	Ala	Ile	Val	Asn	Phe	Ser	Ser	Phe	Asp	Ile	Lys	Glu	Val	Phe
				85					90					95	

His Pro Ile Val Leu Leu Thr Leu Ala Leu Ala Thr Phe Asp Leu Val  
100 105 110

Lys Ala Ile Phe Glu Glu Glu Val Leu Gly Lys Asn Ser Gly Asp Asn  
115 120 125

His His Ala Ile His Arg Thr Met Ile Arg Phe Leu Gly Ser Ile Ile  
130 135 140

Ile Ala Leu Ala Ile Glu Ala Leu Met Leu Val Phe Lys Phe Ser Val  
145 150 155 160

Ser Glu Pro Xaa Xaa Ile Thr Tyr Ala Val Tyr Leu Ala  
165 170

<210> 127

<211> 480

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(480)

<400> 127

atg cgc tct cca aat tta gaa aaa gaa gaa act gaa atc ata gaa aca 48

Met Arg Ser Pro Asn Leu Glu Lys Glu Glu Thr Glu Ile Ile Glu Thr

1 5 10 15

ctc ctt atg cgt gaa aaa atg cgt tta tgc ccc ttg tat tgg cgc atc 96

Leu Leu Met Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile

20 25 30

tta gcg ttt tta acc gat ggt ttg ttg gtg gcg ttt tta ttg agc gat 144

Leu Ala Phe Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp

35 40 45

ctt tta gac gca tgc gat ttc ttg cat tct tta tat tgg ctg act aac 192

Leu Leu Asp Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Thr Asn

50 55 60

ccc att tac cac agc gtg ttt gtt gta atg agt ttt atc gtc ttg tat 240

Pro Ile Tyr His Ser Val Phe Val Val Met Ser Phe Ile Val Leu Tyr

65 70 75 80

ggc gtt tat gaa atc ttt ttt gtg tgt ttg tgc aag atg agt ttg gct 288

Gly	Val	Tyr	Glu	Ile	Phe	Phe	Val	Cys	Leu	Cys	Lys	Met	Ser	Leu	Ala		
				85					90					95			
aaa	ctg	gtt	ttt	agg	att	aaa	att	att	gat	att	tat	tta	gca	gat	tgc		336
Lys	Leu	Val	Phe	Arg	Ile	Lys	Ile	Ile	Asp	Ile	Tyr	Leu	Ala	Asp	Cys		
			100					105					110				
ccc	agt	agg	gct	att	tta	ttg	aag	cgt	tta	ggg	tta	aag	atc	gtg	gtt		384
Pro	Ser	Arg	Ala	Ile	Leu	Leu	Lys	Arg	Leu	Gly	Leu	Lys	Ile	Val	Val		
			115				120					125					
ttt	cta	tgc	ccc	ttt	tta	tgg	ttt	gta	gtg	ttt	aaa	aac	ccc	tat	cat		432
Phe	Leu	Cys	Pro	Phe	Leu	Trp	Phe	Val	Val	Phe	Lys	Asn	Pro	Tyr	His		
	130						135					140					
agg	gca	tgg	cat	gaa	gaa	aaa	agc	aaa	agt	ctt	ttg	gtg	ttg	ttt	taa		480
Arg	Ala	Trp	His	Glu	Glu	Lys	Ser	Lys	Ser	Leu	Leu	Val	Leu	Phe			
145					150					155							
<210> 128																	
<211> 159																	
<212> PRT																	
<213> Helicobacter pylori																	
<400> 128																	
Met	Arg	Ser	Pro	Asn	Leu	Glu	Lys	Glu	Glu	Thr	Glu	Ile	Ile	Glu	Thr		
1				5					10					15			
Leu	Leu	Met	Arg	Glu	Lys	Met	Arg	Leu	Cys	Pro	Leu	Tyr	Trp	Arg	Ile		
			20					25					30				
Leu	Ala	Phe	Leu	Thr	Asp	Gly	Leu	Leu	Val	Ala	Phe	Leu	Leu	Ser	Asp		
	35					40						45					
Leu	Leu	Asp	Ala	Cys	Asp	Phe	Leu	His	Ser	Leu	Tyr	Trp	Leu	Thr	Asn		
50						55				60							
Pro	Ile	Tyr	His	Ser	Val	Phe	Val	Val	Met	Ser	Phe	Ile	Val	Leu	Tyr		
65					70					75				80			
Gly	Val	Tyr	Glu	Ile	Phe	Phe	Val	Cys	Leu	Cys	Lys	Met	Ser	Leu	Ala		
				85					90					95			
Lys	Leu	Val	Phe	Arg	Ile	Lys	Ile	Ile	Asp	Ile	Tyr	Leu	Ala	Asp	Cys		
			100					105					110				

Pro Ser Arg Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val  
115 120 125

Phe Leu Cys Pro Phe Leu Trp Phe Val Val Phe Lys Asn Pro Tyr His  
130 135 140

Arg Ala Trp His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe  
145 150 155

<210> 129  
<211> 1983  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(1983)

<400> 129  
atg att tat tgg ttg tat ttg gcg gtc ttt ttt ttg ttg ggt gca tta 48  
Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Gly Ala Leu  
1 5 10 15  
gac gct aaa gaa atc gct atg caa cga ttt gac aaa caa aac cat aag 96  
Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys  
20 25 30  
att ttt gaa atc ctt gcg gat aaa gtg agc gct aaa gac aat gtg ata 144  
Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile  
35 40 45  
acc gca tca ggg aat gcg atc tta ttg aat tat gat gtg tat att tta 192  
Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu  
50 55 60  
gcg gac aag gtg cgt tat gac act aaa acc aaa gaa gcg tta tta gag 240  
Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu  
65 70 75 80  
ggg aat atc aag gtt tat agg ggc gag ggt ttg ctc gtt aaa acc gat 288  
Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp  
85 90 95  
tat gtg aaa ttg agc ttg aat gaa aaa tat gaa atc att ttc ccc ttt 336  
Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe  
100 105 110  
tat gtc caa gac agc gtg agc ggg att tgg gtg agc gcg gat att gct 384

Tyr	Val	Gln	Asp	Ser	Val	Ser	Gly	Ile	Trp	Val	Ser	Ala	Asp	Ile	Ala	
		115					120					125				
agc	ggg	aag	gat	caa	aaa	tat	aag	gtt	aaa	aac	atg	agc	gct	tca	ggg	432
Ser	Gly	Lys	Asp	Gln	Lys	Tyr	Lys	Val	Lys	Asn	Met	Ser	Ala	Ser	Gly	
	130					135				140						
tgc	agc	att	gat	aac	ccc	att	tgg	cat	gtc	aat	gcg	act	tca	ggc	tca	480
Cys	Ser	Ile	Asp	Asn	Pro	Ile	Trp	His	Val	Asn	Ala	Thr	Ser	Gly	Ser	
145					150					155				160		
ttc	aac	atg	caa	aaa	tcg	cat	ttg	tct	atg	tgg	aat	cct	aag	atc	tat	528
Phe	Asn	Met	Gln	Lys	Ser	His	Leu	Ser	Met	Trp	Asn	Pro	Lys	Ile	Tyr	
				165					170					175		
gtc	ggg	gat	att	cct	gta	ttg	tat	ttg	ccc	tat	att	ttc	atg	tcc	act	576
Val	Gly	Asp	Ile	Pro	Val	Leu	Tyr	Leu	Pro	Tyr	Ile	Phe	Met	Ser	Thr	
			180					185					190			
agc	aat	aaa	aga	act	acc	ggg	ttt	tta	tac	cct	gag	ttt	ggg	act	tcc	624
Ser	Asn	Lys	Arg	Thr	Thr	Gly	Phe	Leu	Tyr	Pro	Glu	Phe	Gly	Thr	Ser	
		195					200					205				
aac	tta	gac	ggc	ttt	att	tat	ttg	caa	ccc	ttt	tat	tta	gcc	ccc	aaa	672
Asn	Leu	Asp	Gly	Phe	Ile	Tyr	Leu	Gln	Pro	Phe	Tyr	Leu	Ala	Pro	Lys	
	210					215					220					
aac	tca	tgg	gat	atg	acc	ttt	acc	cca	caa	atc	cgc	tat	aaa	agg	ggg	720
Asn	Ser	Trp	Asp	Met	Thr	Phe	Thr	Pro	Gln	Ile	Arg	Tyr	Lys	Arg	Gly	
225					230					235					240	
ttt	ggc	ttg	aat	ttt	gaa	gcg	cgc	tac	att	aac	tct	aaa	gac	gac	agg	768
Phe	Gly	Leu	Asn	Phe	Glu	Ala	Arg	Tyr	Ile	Asn	Ser	Lys	Asp	Asp	Arg	
				245					250					255		
ttt	tta	ttc	aat	gcg	cgc	tat	ttt	agg	aat	tac	acc	caa	tat	gtc	aaa	816
Phe	Leu	Phe	Asn	Ala	Arg	Tyr	Phe	Arg	Asn	Tyr	Thr	Gln	Tyr	Val	Lys	
			260					265					270			
cgc	tac	gat	ttg	agg	aat	caa	aat	atc	tat	ggg	ttt	gaa	ttt	tta	agc	864
Arg	Tyr	Asp	Leu	Arg	Asn	Gln	Asn	Ile	Tyr	Gly	Phe	Glu	Phe	Leu	Ser	
		275					280					285				
tct	agc	agg	gac	act	tta	caa	aaa	tac	ttt	cat	ctt	aag	tct	aat	att	912
Ser	Ser	Arg	Asp	Thr	Leu	Gln	Lys	Tyr	Phe	His	Leu	Lys	Ser	Asn	Ile	
	290					295					300					
gat	aac	ggg	cat	tac	att	gac	ttt	tta	tac	atg	aac	gat	ttg	gat	tat	960
Asp	Asn	Gly	His	Tyr	Ile	Asp	Phe	Leu	Tyr	Met	Asn	Asp	Leu	Asp	Tyr	
305					310					315					320	
gtg	cgt	ttt	gaa	aag	gtt	aat	aag	cgc	atc	aca	gac	gcc	acg	cac	atg	1008
Val	Arg	Phe	Glu	Lys	Val	Asn	Lys	Arg	Ile	Thr	Asp	Ala	Thr	His	Met	



325								330				335				
tct	agg	gcg	aat	tac	tat	ttg	caa	aca	gaa	aac	aat	tat	tac	ggc	ttg	1056
Ser	Arg	Ala	Asn	Tyr	Tyr	Leu	Gln	Thr	Glu	Asn	Asn	Tyr	Tyr	Gly	Leu	
			340					345					350			
aat	atc	aag	tat	ttt	tta	aac	ctg	aat	aaa	atc	aac	aac	aac	cgc	act	1104
Asn	Ile	Lys	Tyr	Phe	Leu	Asn	Leu	Asn	Lys	Ile	Asn	Asn	Asn	Arg	Thr	
		355					360					365				
ttc	caa	tct	gtc	cct	aat	ttg	caa	tac	cat	aaa	tat	tta	aat	tct	ttg	1152
Phe	Gln	Ser	Val	Pro	Asn	Leu	Gln	Tyr	His	Lys	Tyr	Leu	Asn	Ser	Leu	
	370					375					380					
tat	ttt	aga	aat	tta	ttg	tat	tcg	gtg	gat	tat	cag	ttt	aga	aac	acc	1200
Tyr	Phe	Arg	Asn	Leu	Leu	Tyr	Ser	Val	Asp	Tyr	Gln	Phe	Arg	Asn	Thr	
385					390					395					400	
gca	aga	gas	atc	ggc	tat	ggc	tat	gtg	caa	aac	gct	ttg	aat	gtg	ccg	1248
Ala	Arg	Xaa	Ile	Gly	Tyr	Gly	Tyr	Val	Gln	Asn	Ala	Leu	Asn	Val	Pro	
				405					410					415		
gtg	ggc	ttg	caa	ttt	tct	ttg	ttt	aaa	aag	tat	ttg	tct	tta	ggg	ctt	1296
Val	Gly	Leu	Gln	Phe	Ser	Leu	Phe	Lys	Lys	Tyr	Leu	Ser	Leu	Gly	Leu	
			420					425					430			
tgg	aac	gat	ctc	caa	cta	tct	aat	gtg	gct	tta	atg	caa	tct	aac	aat	1344
Trp	Asn	Asp	Leu	Gln	Leu	Ser	Asn	Val	Ala	Leu	Met	Gln	Ser	Asn	Asn	
		435					440					445				
tcc	ttc	gtg	cct	acg	atc	cct	aat	gaa	tca	agg	gaa	ttt	ggg	aac	ttt	1392
Ser	Phe	Val	Pro	Thr	Ile	Pro	Asn	Glu	Ser	Arg	Glu	Phe	Gly	Asn	Phe	
	450					455					460					
gtg	tct	tca	aat	ttt	tcc	atg	tat	gtc	aat	atg	gat	tta	gcc	aga	gaa	1440
Val	Ser	Ser	Asn	Phe	Ser	Met	Tyr	Val	Asn	Met	Asp	Leu	Ala	Arg	Glu	
465					470				475						480	
tac	aac	aag	ctt	ttc	cac	acg	atc	caa	ttg	gaa	gcg	att	ttc	aac	atc	1488
Tyr	Asn	Lys	Leu	Phe	His	Thr	Ile	Gln	Leu	Glu	Ala	Ile	Phe	Asn	Ile	
			485					490						495		
cct	tat	tac	mcc	ttt	aaa	aac	ggc	tta	ttt	tct	caa	aac	atg	tat	gct	1536
Pro	Tyr	Tyr	Xaa	Phe	Lys	Asn	Gly	Leu	Phe	Ser	Gln	Asn	Met	Tyr	Ala	
			500				505						510			
tta	agc	acg	caa	gcc	tta	aac	agc	tac	act	tcg	cct	tta	ttg	aga	gat	1584
Leu	Ser	Thr	Gln	Ala	Leu	Asn	Ser	Tyr	Thr	Ser	Pro	Leu	Leu	Arg	Asp	
		515					520					525				
tat	gat	tat	caa	ggg	cgt	ttg	tat	gac	tcc	gtg	tgg	aat	cct	agc	agc	1632
Tyr	Asp	Tyr	Gln	Gly	Arg	Leu	Tyr	Asp	Ser	Val	Trp	Asn	Pro	Ser	Ser	
	530					535					540					

att tta cct agc gat gcg agc aat aaa acg gtg aat tta acc cta acg	1680
Ile Leu Pro Ser Asp Ala Ser Asn Lys Thr Val Asn Leu Thr Leu Thr	
545 550 555 560	
caa tac ctt tat ggc tta gga ggg caa gag ttg ttg tat ttt aaa ata	1728
Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile	
565 570 575	
tcg caa ctc atc aat ctt gac gat aaa gtt tcg ccc ttt aaa atg ccc	1776
Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Lys Met Pro	
580 585 590	
cta gaa agc aag atc ggg ttt tcg ccc tta acg gga ttg aat atc ttt	1824
Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe	
595 600 605	
ggg aat gtc ttt tat tcg ttt tat caa aac cgc cta gaa gaa atc tct	1872
Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser	
610 615 620	
gtg aac gcc aat tac caa cgc aag ttt tta agc ttt aac ctc tct tat	1920
Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr	
625 630 635 640	
ttt tta agg aac aat ttt agc agt ggg att aat agc att gta gaa aat	1968
Phe Leu Arg Asn Asn Phe Ser Ser Gly Ile Asn Ser Ile Val Glu Asn	
645 650 655	
ctg cgg att att taa	1983
Leu Arg Ile Ile	
660	

<210> 130  
 <211> 660  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <221> misc\_feature  
 <222> (403)..(403)  
 <223> The 'Xaa' at location 403 stands for Glu, or Asp.

<220>  
 <221> misc\_feature  
 <222> (500)..(500)  
 <223> The 'Xaa' at location 500 stands for Thr, or Pro.

<400> 130

Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Gly Ala Leu
1 5 10 15

Asp	Ala	Lys	Glu	Ile	Ala	Met	Gln	Arg	Phe	Asp	Lys	Gln	Asn	His	Lys	
			20					25					30			
Ile	Phe	Glu	Ile	Leu	Ala	Asp	Lys	Val	Ser	Ala	Lys	Asp	Asn	Val	Ile	
		35					40					45				
Thr	Ala	Ser	Gly	Asn	Ala	Ile	Leu	Leu	Asn	Tyr	Asp	Val	Tyr	Ile	Leu	
	50					55					60					
Ala	Asp	Lys	Val	Arg	Tyr	Asp	Thr	Lys	Thr	Lys	Glu	Ala	Leu	Leu	Glu	
65					70					75					80	
Gly	Asn	Ile	Lys	Val	Tyr	Arg	Gly	Glu	Gly	Leu	Leu	Val	Lys	Thr	Asp	
				85					90					95		
Tyr	Val	Lys	Leu	Ser	Leu	Asn	Glu	Lys	Tyr	Glu	Ile	Ile	Phe	Pro	Phe	
			100					105					110			
Tyr	Val	Gln	Asp	Ser	Val	Ser	Gly	Ile	Trp	Val	Ser	Ala	Asp	Ile	Ala	
		115					120					125				
Ser	Gly	Lys	Asp	Gln	Lys	Tyr	Lys	Val	Lys	Asn	Met	Ser	Ala	Ser	Gly	
	130					135					140					
Cys	Ser	Ile	Asp	Asn	Pro	Ile	Trp	His	Val	Asn	Ala	Thr	Ser	Gly	Ser	
145					150					155					160	
Phe	Asn	Met	Gln	Lys	Ser	His	Leu	Ser	Met	Trp	Asn	Pro	Lys	Ile	Tyr	
				165					170					175		
Val	Gly	Asp	Ile	Pro	Val	Leu	Tyr	Leu	Pro	Tyr	Ile	Phe	Met	Ser	Thr	
			180					185					190			
Ser	Asn	Lys	Arg	Thr	Thr	Gly	Phe	Leu	Tyr	Pro	Glu	Phe	Gly	Thr	Ser	
		195					200					205				
Asn	Leu	Asp	Gly	Phe	Ile	Tyr	Leu	Gln	Pro	Phe	Tyr	Leu	Ala	Pro	Lys	
	210					215					220					
Asn	Ser	Trp	Asp	Met	Thr	Phe	Thr	Pro	Gln	Ile	Arg	Tyr	Lys	Arg	Gly	

225		230		235		240
Phe Gly Leu Asn	Phe Glu Ala Arg Tyr Ile Asn Ser Lys Asp Asp Arg	245		250		255
Phe Leu Phe Asn	Ala Arg Tyr Phe Arg Asn Tyr Thr Gln Tyr Val Lys	260		265		270
Arg Tyr Asp Leu	Arg Asn Gln Asn Ile Tyr Gly Phe Glu Phe Leu Ser	275		280		285
Ser Ser Arg Asp Thr	Leu Gln Lys Tyr Phe His Leu Lys Ser Asn Ile	290		295		300
Asp Asn Gly His Tyr	Ile Asp Phe Leu Tyr Met Asn Asp Leu Asp Tyr	305		310		315
Val Arg Phe Glu Lys	Val Asn Lys Arg Ile Thr Asp Ala Thr His Met	325		330		335
Ser Arg Ala Asn Tyr Tyr	Leu Gln Thr Glu Asn Asn Tyr Tyr Gly Leu	340		345		350
Asn Ile Lys Tyr Phe	Leu Asn Leu Asn Lys Ile Asn Asn Asn Arg Thr	355		360		365
Phe Gln Ser Val Pro	Asn Leu Gln Tyr His Lys Tyr Leu Asn Ser Leu	370		375		380
Tyr Phe Arg Asn Leu	Leu Tyr Ser Val Asp Tyr Gln Phe Arg Asn Thr	385		390		395
Ala Arg Xaa Ile Gly Tyr	Gly Tyr Val Gln Asn Ala Leu Asn Val Pro	405		410		415
Val Gly Leu Gln Phe Ser	Leu Phe Lys Lys Tyr Leu Ser Leu Gly Leu	420		425		430
Trp Asn Asp Leu Gln	Leu Ser Asn Val Ala Leu Met Gln Ser Asn Asn	435		440		445

Ser Phe Val Pro Thr Ile Pro Asn Glu Ser Arg Glu Phe Gly Asn Phe  
 450 455 460

Val Ser Ser Asn Phe Ser Met Tyr Val Asn Met Asp Leu Ala Arg Glu  
 465 470 475 480

Tyr Asn Lys Leu Phe His Thr Ile Gln Leu Glu Ala Ile Phe Asn Ile  
 485 490 495

Pro Tyr Tyr Xaa Phe Lys Asn Gly Leu Phe Ser Gln Asn Met Tyr Ala  
 500 505 510

Leu Ser Thr Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp  
 515 520 525

Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser  
 530 535 540

Ile Leu Pro Ser Asp Ala Ser Asn Lys Thr Val Asn Leu Thr Leu Thr  
 545 550 555 560

Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile  
 565 570 575

Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Lys Met Pro  
 580 585 590

Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe  
 595 600 605

Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser  
 610 615 620

Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr  
 625 630 635 640

Phe Leu Arg Asn Asn Phe Ser Ser Gly Ile Asn Ser Ile Val Glu Asn  
 645 650 655

Leu Arg Ile Ile  
 660

<210> 131  
 <211> 768  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(768)

<220>  
 <221> misc\_feature  
 <222> (310)..(310)  
 <223> n = any nucleotide

<400> 131  
 atg gat att tat gcg tta tac ata gcg ata ggg ctt ttt act ggc att 48  
 Met Asp Ile Tyr Ala Leu Tyr Ile Ala Ile Gly Leu Phe Thr Gly Ile  
 1 5 10 15  
 cta tca ggg att ttt ggc att ggt ggg ggg ttg atc att gtc cct atc 96  
 Leu Ser Gly Ile Phe Gly Ile Gly Gly Gly Leu Ile Ile Val Pro Ile  
 20 25 30  
 atg ctc gca acc ggg cat tct ttt gaa gaa tcc atc ggc att tcc att 144  
 Met Leu Ala Thr Gly His Ser Phe Glu Glu Ser Ile Gly Ile Ser Ile  
 35 40 45  
 ttg caa atg gtg ctt tca tcg ttc gtg gga tct gtt ttg aat ttc aaa 192  
 Leu Gln Met Val Leu Ser Ser Phe Val Gly Ser Val Leu Asn Phe Lys  
 50 55 60  
 aaa aaa tcg ctt gat ttt tct tta ggc ttg ttg ata ggg gca ggg ggg 240  
 Lys Lys Ser Leu Asp Phe Ser Leu Gly Leu Leu Ile Gly Ala Gly Gly  
 65 70 75 80  
 ctg ata ggg gca agt ttt agc gga ttt gtt tta aaa atc gtt tcc agt 288  
 Leu Ile Gly Ala Ser Phe Ser Gly Phe Val Leu Lys Ile Val Ser Ser  
 85 90 95  
 aaa att tta atg gtt att ttc ncg ctt tta gtc gtg tat tct atg atc 336  
 Lys Ile Leu Met Val Ile Phe Xaa Leu Leu Val Val Tyr Ser Met Ile  
 100 105 110  
 caa ttt gtc tta aaa ccc aaa aaa gat ttt ata gcg gat aat aaa 384  
 Gln Phe Val Leu Lys Pro Lys Lys Lys Asp Phe Ile Ala Asp Asn Lys  
 115 120 125  
 cgc tac cct ttg caa ggt tta aaa tta ttt tta att ggc gcg ctc aca 432  
 Arg Tyr Pro Leu Gln Gly Leu Lys Leu Phe Leu Ile Gly Ala Leu Thr  
 130 135 140  
 ggg ttt ttt gcc atc act tta ggg att ggt ggg ggg atg ctc atg gtg 480

Gly	Phe	Phe	Ala	Ile	Thr	Leu	Gly	Ile	Gly	Gly	Gly	Met	Leu	Met	Val	
145					150				155						160	
cct	ttg	atg	cat	tat	ttt	tta	ggg	tat	gat	tct	aaa	aaa	tgc	gtg	gcg	528
Pro	Leu	Met	His	Tyr	Phe	Leu	Gly	Tyr	Asp	Ser	Lys	Lys	Cys	Val	Ala	
			165					170					175			
cta	ggg	tta	ttt	ttc	atc	ttg	ttt	tct	tct	att	tca	gga	gct	ttt	tct	576
Leu	Gly	Leu	Phe	Phe	Ile	Leu	Phe	Ser	Ser	Ile	Ser	Gly	Ala	Phe	Ser	
			180					185					190			
tta	atg	tat	cac	cac	atc	atc	aat	aaa	gaa	gtt	ctc	tta	gca	ggg	gcg	624
Leu	Met	Tyr	His	His	Ile	Ile	Asn	Lys	Glu	Val	Leu	Leu	Ala	Gly	Ala	
		195					200					205				
att	gtg	ggc	tta	ggc	tca	gtt	atg	ggc	gtg	agc	att	ggg	att	aaa	tgg	672
Ile	Val	Gly	Leu	Gly	Ser	Val	Met	Gly	Val	Ser	Ile	Gly	Ile	Lys	Trp	
	210					215					220					
atc	atg	ggg	ctt	ttg	aat	gaa	aaa	atg	cat	aaa	att	ttg	att	tta	ggg	720
Ile	Met	Gly	Leu	Leu	Asn	Glu	Lys	Met	His	Lys	Ile	Leu	Ile	Leu	Gly	
225					230					235					240	
gtg	tat	ggt	ttg	tcg	tta	ttg	att	att	tta	tac	aaa	ctc	ttt	ttt	taa	768
Val	Tyr	Gly	Leu	Ser	Leu	Leu	Ile	Ile	Leu	Tyr	Lys	Leu	Phe	Phe		
			245						250					255		

<210> 132  
 <211> 255  
 <212> PRT  
 <213> Helicobacter pylori  
  
 <220>  
 <221> misc\_feature  
 <222> (104)..(104)  
 <223> The 'Xaa' at location 104 stands for Thr, Ala, Pro, or Ser.  
  
 <400> 132

Met	Asp	Ile	Tyr	Ala	Leu	Tyr	Ile	Ala	Ile	Gly	Leu	Phe	Thr	Gly	Ile	
1				5				10						15		
Leu	Ser	Gly	Ile	Phe	Gly	Ile	Gly	Gly	Gly	Leu	Ile	Ile	Val	Pro	Ile	
			20				25						30			
Met	Leu	Ala	Thr	Gly	His	Ser	Phe	Glu	Glu	Ser	Ile	Gly	Ile	Ser	Ile	
		35					40					45				
Leu	Gln	Met	Val	Leu	Ser	Ser	Phe	Val	Gly	Ser	Val	Leu	Asn	Phe	Lys	
	50					55					60					

Lys Lys Ser Leu Asp Phe Ser Leu Gly Leu Leu Ile Gly Ala Gly Gly  
65 70 75 80

Leu Ile Gly Ala Ser Phe Ser Gly Phe Val Leu Lys Ile Val Ser Ser  
85 90 95

Lys Ile Leu Met Val Ile Phe Xaa Leu Leu Val Val Tyr Ser Met Ile  
100 105 110

Gln Phe Val Leu Lys Pro Lys Lys Lys Asp Phe Ile Ala Asp Asn Lys  
115 120 125

Arg Tyr Pro Leu Gln Gly Leu Lys Leu Phe Leu Ile Gly Ala Leu Thr  
130 135 140

Gly Phe Phe Ala Ile Thr Leu Gly Ile Gly Gly Gly Met Leu Met Val  
145 150 155 160

Pro Leu Met His Tyr Phe Leu Gly Tyr Asp Ser Lys Lys Cys Val Ala  
165 170 175

Leu Gly Leu Phe Phe Ile Leu Phe Ser Ser Ile Ser Gly Ala Phe Ser  
180 185 190

Leu Met Tyr His His Ile Ile Asn Lys Glu Val Leu Leu Ala Gly Ala  
195 200 205

Ile Val Gly Leu Gly Ser Val Met Gly Val Ser Ile Gly Ile Lys Trp  
210 215 220

Ile Met Gly Leu Leu Asn Glu Lys Met His Lys Ile Leu Ile Leu Gly  
225 230 235 240

Val Tyr Gly Leu Ser Leu Leu Ile Ile Leu Tyr Lys Leu Phe Phe  
245 250 255

<210> 133  
<211> 1510  
<212> DNA  
<213> Helicobacter pylori



<220>

<221> CDS

<222> (1)..(1509)

<400> 133

atg	aaa	tgt	tcg	cat	tgc	cag	ttg	gag	ttt	aaa	gaa	agt	gag	ctt	ttt	48
Met	Lys	Cys	Ser	His	Cys	Gln	Leu	Glu	Phe	Lys	Glu	Ser	Glu	Leu	Phe	
1				5				10						15		

aaa	gaa	gtg	atc	cat	cat	aag	gaa	ttg	tat	ttt	tgc	tgc	acg	ggg	tgt	96
Lys	Glu	Val	Ile	His	His	Lys	Glu	Leu	Tyr	Phe	Cys	Cys	Thr	Gly	Cys	
			20					25					30			

gct	aga	gtg	tat	gcg	tta	tta	ttg	gat	ttg	aat	tta	gag	agc	ttt	tat	144
Ala	Arg	Val	Tyr	Ala	Leu	Leu	Leu	Asp	Leu	Asn	Leu	Glu	Ser	Phe	Tyr	
		35					40					45				

gac	aaa	tta	aac	gat	tcc	act	tta	gcc	ccc	gta	acg	ccc	caa	gat	tca	192
Asp	Lys	Leu	Asn	Asp	Ser	Thr	Leu	Ala	Pro	Val	Thr	Pro	Gln	Asp	Ser	
	50					55					60					

atg	agc	gct	ttg	gaa	tta	gaa	caa	gcc	ctt	gaa	gaa	aac	aat	aaa	agc	240
Met	Ser	Ala	Leu	Glu	Leu	Glu	Gln	Ala	Leu	Glu	Glu	Asn	Asn	Lys	Ser	
65					70					75					80	

gat	ttt	atc	ctt	aat	ctt	ttg	cta	gaa	aaa	acg	cat	tgt	aac	gct	tgc	288
Asp	Phe	Ile	Leu	Asn	Leu	Leu	Leu	Glu	Lys	Thr	His	Cys	Asn	Ala	Cys	
				85					90					95		

ttg	tgg	ctc	aat	caa	aag	gtt	tta	gag	cgc	tta	aag	ggg	gtt	aaa	aaa	336
Leu	Trp	Leu	Asn	Gln	Lys	Val	Leu	Glu	Arg	Leu	Lys	Gly	Val	Lys	Lys	
			100					105					110			

gtg	agc	gtg	aat	ttc	acc	acc	cac	cat	tta	caa	atc	gtg	ttt	gac	aag	384
Val	Ser	Val	Asn	Phe	Thr	Thr	His	His	Leu	Gln	Ile	Val	Phe	Asp	Lys	
		115					120					125				

tcc	tta	aac	cct	aaa	gag	att	att	caa	aaa	att	gag	agt	ttg	ggg	tat	432
Ser	Leu	Asn	Pro	Lys	Glu	Ile	Ile	Gln	Lys	Ile	Glu	Ser	Leu	Gly	Tyr	
	130					135					140					

ggg	gct	aaa	att	tat	aac	gca	aaa	aat	tac	gcc	cta	aaa	gcc	caa	aaa	480
Gly	Ala	Lys	Ile	Tyr	Asn	Ala	Lys	Asn	Tyr	Ala	Leu	Lys	Ala	Gln	Lys	
145					150					155					160	

gag	cag	cgc	tcc	tat	ttg	ctc	act	tta	agc	gtg	ggg	ttt	ttt	gcc	acc	528
Glu	Gln	Arg	Ser	Tyr	Leu	Leu	Thr	Leu	Ser	Val	Gly	Phe	Phe	Ala	Thr	
			165					170						175		

atg	aat	ttg	atg	ttt	att	gca	att	gcc	aaa	tac	gca	agt	tat	ggc	ggg	576
Met	Asn	Leu	Met	Phe	Ile	Ala	Ile	Ala	Lys	Tyr	Ala	Ser	Tyr	Gly	Gly	
			180					185					190			

gcg	agt	tat	ggc	act	ggc	atg	gat	aag	ctt	atg	caa	agg	aat	ttg	gat	624
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Ala	Ser	Tyr	Gly	Thr	Gly	Met	Asp	Lys	Leu	Met	Gln	Arg	Asn	Leu	Asp	
		195					200					205				
ctc	gta	tcg	ctc	ttt	tta	agc	ttg	ttg	gtg	tta	gtg	gtt	gtg	ggg	cgt	672
Leu	Val	Ser	Leu	Phe	Leu	Ser	Leu	Leu	Val	Leu	Val	Val	Val	Gly	Arg	
	210					215					220					
ttt	ttc	att	aag	ggg	gcg	ttt	tat	ggg	ata	aaa	aat	ggc	ggt	ttg	ggc	720
Phe	Phe	Ile	Lys	Gly	Ala	Phe	Tyr	Gly	Ile	Lys	Asn	Gly	Val	Leu	Gly	
225					230					235					240	
atg	gat	ttg	agc	gtg	tct	ttt	gga	gcg	tta	tcg	gca	ttt	ggt	tat	tcc	768
Met	Asp	Leu	Ser	Val	Ser	Phe	Gly	Ala	Leu	Ser	Ala	Phe	Val	Tyr	Ser	
				245					250					255		
ctt	tat	gcc	atg	ctg	gtg	tcc	caa	gag	act	tat	ttt	gaa	gcg	agc	agc	816
Leu	Tyr	Ala	Met	Leu	Val	Ser	Gln	Glu	Thr	Tyr	Phe	Glu	Ala	Ser	Ser	
			260					265					270			
acg	att	tta	acg	ctt	ggt	ttt	ggc	tct	aag	ttt	ttg	gaa	tta	aaa	gcc	864
Thr	Ile	Leu	Thr	Leu	Val	Phe	Gly	Ser	Lys	Phe	Leu	Glu	Leu	Lys	Ala	
		275					280					285				
agg	ctg	ttt	gcg	aat	gaa	aaa	tgt	ctg	gcc	cta	gaa	tcg	cat	gaa	atc	912
Arg	Leu	Phe	Ala	Asn	Glu	Lys	Cys	Leu	Ala	Leu	Glu	Ser	His	Glu	Ile	
	290					295					300					
cat	agc	gtg	atc	ggt	gta	gaa	aag	gac	aag	cag	ata	gaa	aaa	cac	cct	960
His	Ser	Val	Ile	Val	Val	Glu	Lys	Asp	Lys	Gln	Ile	Glu	Lys	His	Pro	
305					310					315					320	
aaa	gat	gtg	gcg	ata	ggc	tct	ggt	ggt	tgg	gtg	cca	agc	ggg	gct	aaa	1008
Lys	Asp	Val	Ala	Ile	Gly	Ser	Val	Val	Trp	Val	Pro	Ser	Gly	Ala	Lys	
				325					330					335		
atc	gca	cta	gat	gga	gtg	ctt	tta	aat	aac	gcg	agc	gtg	gat	gcg	tct	1056
Ile	Ala	Leu	Asp	Gly	Val	Leu	Leu	Asn	Asn	Ala	Ser	Val	Asp	Ala	Ser	
			340					345					350			
ttg	atc	agc	ggg	gag	ttt	aag	cct	ttg	gaa	ttg	ggg	ggt	aat	gat	cta	1104
Leu	Ile	Ser	Gly	Glu	Phe	Lys	Pro	Leu	Glu	Leu	Gly	Val	Asn	Asp	Leu	
		355					360					365				
att	tta	ggg	ggt	tat	gtg	aat	gtg	ggc	gtg	cct	ttt	agc	tat	caa	gtg	1152
Ile	Leu	Gly	Gly	Tyr	Val	Asn	Val	Gly	Val	Pro	Phe	Ser	Tyr	Gln	Val	
	370					375					380					
agc	gcg	act	ttt	caa	aac	tca	cgc	ctt	tct	agt	ttg	tta	gaa	act	tta	1200
Ser	Ala	Thr	Phe	Gln	Asn	Ser	Arg	Leu	Ser	Ser	Leu	Leu	Glu	Thr	Leu	
385					390					395					400	
aaa	aag	agt	ttt	tta	gaa	aag	ccc	tta	att	gag	agt	agc	gcg	aat	aaa	1248
Lys	Lys	Ser	Phe	Leu	Glu	Lys	Pro	Leu	Ile	Glu	Ser	Ser	Ala	Asn	Lys	
				405					410					415		

att gcg gat att ttt tct aaa gcg gtg ttg ttt tta gcc ttt gta agc	1296
Ile Ala Asp Ile Phe Ser Lys Ala Val Leu Phe Leu Ala Phe Val Ser	
420 425 430	
ttt tta tta tgg caa ttt ggt ttg ggg ggt aat ttt gaa aaa gcc tta	1344
Phe Leu Leu Trp Gln Phe Gly Leu Gly Gly Asn Phe Glu Lys Ala Leu	
435 440 445	
atg gtg tgt att agc gtg tta gtc atc agc tgc cct tgc gca ttc gcc	1392
Met Val Cys Ile Ser Val Leu Val Ile Ser Cys Pro Cys Ala Phe Ala	
450 455 460	
tta gct acg ccc att gcg tta gtg ata ggg gtg ttt aaa aac cct ttg	1440
Leu Ala Thr Pro Ile Ala Leu Val Ile Gly Val Phe Lys Asn Pro Leu	
465 470 475 480	
atc gtg ttt aaa gaa gcg tta ttt tta gaa act ctg gct aaa gtg gaa	1488
Ile Val Phe Lys Glu Ala Leu Phe Leu Glu Thr Leu Ala Lys Val Glu	
485 490 495	
aaa atc ttt ata gac aaa acc g	1510
Lys Ile Phe Ile Asp Lys Thr	
500	

<210> 134  
 <211> 503  
 <212> PRT  
 <213> Helicobacter pylori

<400> 134

Met Lys Cys Ser His Cys Gln Leu Glu Phe Lys Glu Ser Glu Leu Phe	
1 5 10 15	
Lys Glu Val Ile His His Lys Glu Leu Tyr Phe Cys Cys Thr Gly Cys	
20 25 30	
Ala Arg Val Tyr Ala Leu Leu Leu Asp Leu Asn Leu Glu Ser Phe Tyr	
35 40 45	
Asp Lys Leu Asn Asp Ser Thr Leu Ala Pro Val Thr Pro Gln Asp Ser	
50 55 60	
Met Ser Ala Leu Glu Leu Glu Gln Ala Leu Glu Glu Asn Asn Lys Ser	
65 70 75 80	
Asp Phe Ile Leu Asn Leu Leu Leu Glu Lys Thr His Cys Asn Ala Cys	
85 90 95	

Leu Trp Leu Asn Gln Lys Val Leu Glu Arg Leu Lys Gly Val Lys Lys  
 100 105 110

Val Ser Val Asn Phe Thr Thr His His Leu Gln Ile Val Phe Asp Lys  
 115 120 125

Ser Leu Asn Pro Lys Glu Ile Ile Gln Lys Ile Glu Ser Leu Gly Tyr  
 130 135 140

Gly Ala Lys Ile Tyr Asn Ala Lys Asn Tyr Ala Leu Lys Ala Gln Lys  
 145 150 155 160

Glu Gln Arg Ser Tyr Leu Leu Thr Leu Ser Val Gly Phe Phe Ala Thr  
 165 170 175

Met Asn Leu Met Phe Ile Ala Ile Ala Lys Tyr Ala Ser Tyr Gly Gly  
 180 185 190

Ala Ser Tyr Gly Thr Gly Met Asp Lys Leu Met Gln Arg Asn Leu Asp  
 195 200 205

Leu Val Ser Leu Phe Leu Ser Leu Leu Val Leu Val Val Val Gly Arg  
 210 215 220

Phe Phe Ile Lys Gly Ala Phe Tyr Gly Ile Lys Asn Gly Val Leu Gly  
 225 230 235 240

Met Asp Leu Ser Val Ser Phe Gly Ala Leu Ser Ala Phe Val Tyr Ser  
 245 250 255

Leu Tyr Ala Met Leu Val Ser Gln Glu Thr Tyr Phe Glu Ala Ser Ser  
 260 265 270

Thr Ile Leu Thr Leu Val Phe Gly Ser Lys Phe Leu Glu Leu Lys Ala  
 275 280 285

Arg Leu Phe Ala Asn Glu Lys Cys Leu Ala Leu Glu Ser His Glu Ile  
 290 295 300

His Ser Val Ile Val Val Glu Lys Asp Lys Gln Ile Glu Lys His Pro  
 305 310 315 320

Lys Asp Val Ala Ile Gly Ser Val Val Trp Val Pro Ser Gly Ala Lys  
325 330 335

Ile Ala Leu Asp Gly Val Leu Leu Asn Asn Ala Ser Val Asp Ala Ser  
340 345 350

Leu Ile Ser Gly Glu Phe Lys Pro Leu Glu Leu Gly Val Asn Asp Leu  
355 360 365

Ile Leu Gly Gly Tyr Val Asn Val Gly Val Pro Phe Ser Tyr Gln Val  
370 375 380

Ser Ala Thr Phe Gln Asn Ser Arg Leu Ser Ser Leu Leu Glu Thr Leu  
385 390 395 400

Lys Lys Ser Phe Leu Glu Lys Pro Leu Ile Glu Ser Ser Ala Asn Lys  
405 410 415

Ile Ala Asp Ile Phe Ser Lys Ala Val Leu Phe Leu Ala Phe Val Ser  
420 425 430

Phe Leu Leu Trp Gln Phe Gly Leu Gly Gly Asn Phe Glu Lys Ala Leu  
435 440 445

Met Val Cys Ile Ser Val Leu Val Ile Ser Cys Pro Cys Ala Phe Ala  
450 455 460

Leu Ala Thr Pro Ile Ala Leu Val Ile Gly Val Phe Lys Asn Pro Leu  
465 470 475 480

Ile Val Phe Lys Glu Ala Leu Phe Leu Glu Thr Leu Ala Lys Val Glu  
485 490 495

Lys Ile Phe Ile Asp Lys Thr  
500

<210> 135

<211> 1017

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1017)

<400> 135

atg	cta	cta	aca	aca	ctc	aag	cta	aaa	tct	att	aag	gaa	atc	agt	att	48
Met	Leu	Leu	Thr	Thr	Leu	Lys	Leu	Lys	Ser	Ile	Lys	Glu	Ile	Ser	Ile	
1				5					10					15		

aaa	aaa	ttt	att	cta	tct	tct	ctt	gtt	ttc	gca	tgt	atc	aat	acc	agc	96
Lys	Lys	Phe	Ile	Leu	Ser	Ser	Leu	Val	Phe	Ala	Cys	Ile	Asn	Thr	Ser	
			20					25					30			

gtt	gaa	gct	tta	gaa	aat	gac	ggc	tct	aaa	cca	aac	gat	ttg	acc	tct	144
Val	Glu	Ala	Leu	Glu	Asn	Asp	Gly	Ser	Lys	Pro	Asn	Asp	Leu	Thr	Ser	
		35					40					45				

cca	aaa	gaa	gtc	tct	caa	gaa	gct	caa	aga	aat	gag	act	caa	aga	aat	192
Pro	Lys	Glu	Val	Ser	Gln	Glu	Ala	Gln	Arg	Asn	Glu	Thr	Gln	Arg	Asn	
	50					55					60					

gaa	gct	caa	aga	aat	gaa	gct	caa	aac	gaa	act	tct	caa	tcc	aat	caa	240
Glu	Ala	Gln	Arg	Asn	Glu	Ala	Gln	Asn	Glu	Thr	Ser	Gln	Ser	Asn	Gln	
65					70					75					80	

acg	cct	aaa	gaa	atg	aaa	gtc	aaa	tcc	att	tcg	tat	atc	ggg	ctt	tct	288
Thr	Pro	Lys	Glu	Met	Lys	Val	Lys	Ser	Ile	Ser	Tyr	Ile	Gly	Leu	Ser	
				85					90					95		

tac	atg	tct	gac	atg	ctt	gct	aat	gag	att	gta	aag	att	cgt	gtg	ggc	336
Tyr	Met	Ser	Asp	Met	Leu	Ala	Asn	Glu	Ile	Val	Lys	Ile	Arg	Val	Gly	
			100					105					110			

gat	att	gtg	gat	tct	aaa	aaa	ata	gac	acc	gct	gtt	ttg	gct	ttg	ttc	384
Asp	Ile	Val	Asp	Ser	Lys	Lys	Ile	Asp	Thr	Ala	Val	Leu	Ala	Leu	Phe	
		115					120					125				

aat	caa	ggg	tat	ttt	aaa	gac	gtt	tat	gcc	act	ttt	gaa	ggc	ggc	ata	432
Asn	Gln	Gly	Tyr	Phe	Lys	Asp	Val	Tyr	Ala	Thr	Phe	Glu	Gly	Gly	Ile	
	130					135					140					

tta	gag	ttt	cat	ttt	gat	gaa	aaa	gcc	aga	att	gcc	ggg	gta	gaa	atc	480
Leu	Glu	Phe	His	Phe	Asp	Glu	Lys	Ala	Arg	Ile	Ala	Gly	Val	Glu	Ile	
145					150					155					160	

aag	ggt	tat	ggg	act	gaa	aag	gaa	aaa	ggc	gac	tta	aaa	tcc	caa	atg	528
Lys	Gly	Tyr	Gly	Thr	Glu	Lys	Glu	Lys	Gly	Asp	Leu	Lys	Ser	Gln	Met	
				165					170					175		

ggg	atc	aaa	aag	ggc	gac	acc	ttt	gat	gag	caa	aaa	tta	gag	cat	gct	576
Gly	Ile	Lys	Lys	Gly	Asp	Thr	Phe	Asp	Glu	Gln	Lys	Leu	Glu	His	Ala	
			180					185					190			

aaa	acg	gct	tta	aaa	aca	gct	tta	gag	ggg	cag	ggc	tat	tat	ggg	agc	624
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Lys	Thr	Ala	Leu	Lys	Thr	Ala	Leu	Glu	Gly	Gln	Gly	Tyr	Tyr	Gly	Ser		
		195					200					205					
gtg	gtg	gag	gtg	cgc	aca	gaa	aag	gtc	agt	gag	ggc	gcg	tta	tta	att		672
Val	Val	Glu	Val	Arg	Thr	Glu	Lys	Val	Ser	Glu	Gly	Ala	Leu	Leu	Ile		
	210					215					220						
gtg	ttt	gat	gtg	aat	agg	ggg	gat	agt	att	tat	atc	aaa	caa	tcc	att		720
Val	Phe	Asp	Val	Asn	Arg	Gly	Asp	Ser	Ile	Tyr	Ile	Lys	Gln	Ser	Ile		
225					230					235					240		
tat	gag	ggg	agt	gcg	aaa	tta	aaa	cgc	cgc	atg	att	gaa	tct	ttg	agt		768
Tyr	Glu	Gly	Ser	Ala	Lys	Leu	Lys	Arg	Arg	Met	Ile	Glu	Ser	Leu	Ser		
				245					250					255			
gcg	aac	aag	caa	aga	gat	ttc	atg	ggc	tgg	atg	tgg	ggc	ttg	aat	gac		816
Ala	Asn	Lys	Gln	Arg	Asp	Phe	Met	Gly	Trp	Met	Trp	Gly	Leu	Asn	Asp		
			260					265					270				
ggg	aaa	ttg	cgt	tta	gat	caa	tta	gaa	tac	gat	tct	ttg	cgt	atc	caa		864
Gly	Lys	Leu	Arg	Leu	Asp	Gln	Leu	Glu	Tyr	Asp	Ser	Leu	Arg	Ile	Gln		
		275					280					285					
gat	gtg	tat	atg	cgt	agg	ggt	tac	tta	gac	gct	cat	att	tct	tcg	cct		912
Asp	Val	Tyr	Met	Arg	Arg	Gly	Tyr	Leu	Asp	Ala	His	Ile	Ser	Ser	Pro		
	290					295					300						
ttt	ttg	aaa	acg	gat	ttt	tct	acc	cat	gac	gct	aag	ctc	cat	tat	aaa		960
Phe	Leu	Lys	Thr	Asp	Phe	Ser	Thr	His	Asp	Ala	Lys	Leu	His	Tyr	Lys		
305					310				315						320		
gtc	aaa	gag	ggg	atc	caa	tac	agg	att	tca	gac	att	tta	ata	gag	att		1008
Val	Lys	Glu	Gly	Ile	Gln	Tyr	Arg	Ile	Ser	Asp	Ile	Leu	Ile	Glu	Ile		
				325					330					335			
gac	aac	ccg															1017
Asp	Asn	Pro															

<210> 136  
 <211> 339  
 <212> PRT  
 <213> Helicobacter pylori

<400> 136

Met	Leu	Leu	Thr	Thr	Leu	Lys	Leu	Lys	Ser	Ile	Lys	Glu	Ile	Ser	Ile		
1				5					10					15			
Lys	Lys	Phe	Ile	Leu	Ser	Ser	Leu	Val	Phe	Ala	Cys	Ile	Asn	Thr	Ser		
			20					25					30				

Val	Glu	Ala	Leu	Glu	Asn	Asp	Gly	Ser	Lys	Pro	Asn	Asp	Leu	Thr	Ser	
		35					40					45				
Pro	Lys	Glu	Val	Ser	Gln	Glu	Ala	Gln	Arg	Asn	Glu	Thr	Gln	Arg	Asn	
	50					55					60					
Glu	Ala	Gln	Arg	Asn	Glu	Ala	Gln	Asn	Glu	Thr	Ser	Gln	Ser	Asn	Gln	
65					70					75					80	
Thr	Pro	Lys	Glu	Met	Lys	Val	Lys	Ser	Ile	Ser	Tyr	Ile	Gly	Leu	Ser	
				85					90					95		
Tyr	Met	Ser	Asp	Met	Leu	Ala	Asn	Glu	Ile	Val	Lys	Ile	Arg	Val	Gly	
			100					105					110			
Asp	Ile	Val	Asp	Ser	Lys	Lys	Ile	Asp	Thr	Ala	Val	Leu	Ala	Leu	Phe	
		115					120					125				
Asn	Gln	Gly	Tyr	Phe	Lys	Asp	Val	Tyr	Ala	Thr	Phe	Glu	Gly	Gly	Ile	
	130					135					140					
Leu	Glu	Phe	His	Phe	Asp	Glu	Lys	Ala	Arg	Ile	Ala	Gly	Val	Glu	Ile	
145					150					155					160	
Lys	Gly	Tyr	Gly	Thr	Glu	Lys	Glu	Lys	Gly	Asp	Leu	Lys	Ser	Gln	Met	
				165					170					175		
Gly	Ile	Lys	Lys	Gly	Asp	Thr	Phe	Asp	Glu	Gln	Lys	Leu	Glu	His	Ala	
			180					185					190			
Lys	Thr	Ala	Leu	Lys	Thr	Ala	Leu	Glu	Gly	Gln	Gly	Tyr	Tyr	Gly	Ser	
		195					200					205				
Val	Val	Glu	Val	Arg	Thr	Glu	Lys	Val	Ser	Glu	Gly	Ala	Leu	Leu	Ile	
	210					215					220					
Val	Phe	Asp	Val	Asn	Arg	Gly	Asp	Ser	Ile	Tyr	Ile	Lys	Gln	Ser	Ile	
225					230					235					240	
Tyr	Glu	Gly	Ser	Ala	Lys	Leu	Lys	Arg	Arg	Met	Ile	Glu	Ser	Leu	Ser	
				245					250					255		



Ala Asn Lys Gln Arg Asp Phe Met Gly Trp Met Trp Gly Leu Asn Asp  
260 265 270

Gly Lys Leu Arg Leu Asp Gln Leu Glu Tyr Asp Ser Leu Arg Ile Gln  
275 280 285

Asp Val Tyr Met Arg Arg Gly Tyr Leu Asp Ala His Ile Ser Ser Pro  
290 295 300

Phe Leu Lys Thr Asp Phe Ser Thr His Asp Ala Lys Leu His Tyr Lys  
305 310 315 320

Val Lys Glu Gly Ile Gln Tyr Arg Ile Ser Asp Ile Leu Ile Glu Ile  
325 330 335

Asp Asn Pro

<210> 137  
<211> 193  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(192)

<400> 137  
atg aaa aga ttt gtt ttg ttt tta tca ctc atg ggt gtt tgc gtt tgc 48  
Met Lys Arg Phe Val Leu Phe Leu Ser Leu Met Gly Val Cys Val Cys  
1 5 10 15  
gtt caa gct tac gcc gag caa gat tac ttt ttt agg gat ttt aaa tct 96  
Val Gln Ala Tyr Ala Glu Gln Asp Tyr Phe Phe Arg Asp Phe Lys Ser  
20 25 30  
aaa gac ttg ccc caa aaa ctc cat ctt gat aaa aag ctt tcc caa aca 144  
Lys Asp Leu Pro Gln Lys Leu His Leu Asp Lys Lys Leu Ser Gln Thr  
35 40 45  
ata cag cca tgc gcg caa ctt aac gca tca aaa cac tac act gct acc g 193  
Ile Gln Pro Cys Ala Gln Leu Asn Ala Ser Lys His Tyr Thr Ala Thr  
50 55 60

<210> 138  
<211> 64

<212> PRT  
 <213> Helicobacter pylori

<400> 138

Met	Lys	Arg	Phe	Val	Leu	Phe	Leu	Ser	Leu	Met	Gly	Val	Cys	Val	Cys
1				5					10					15	

Val	Gln	Ala	Tyr	Ala	Glu	Gln	Asp	Tyr	Phe	Phe	Arg	Asp	Phe	Lys	Ser
			20					25					30		

Lys	Asp	Leu	Pro	Gln	Lys	Leu	His	Leu	Asp	Lys	Lys	Leu	Ser	Gln	Thr
		35					40					45			

Ile	Gln	Pro	Cys	Ala	Gln	Leu	Asn	Ala	Ser	Lys	His	Tyr	Thr	Ala	Thr
	50					55					60				

<210> 139  
 <211> 530  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(528)

<400> 139

atg	caa	agt	ctt	agt	tgg	ctg	aat	tta	gcg	ttc	cgt	tgg	ctc	ttt	ata	48
Met	Gln	Ser	Leu	Ser	Trp	Leu	Asn	Leu	Ala	Phe	Arg	Trp	Leu	Phe	Ile	
1				5					10					15		

aca	ggg	ctt	ggc	tat	tat	ata	atg	act	tta	ttg	caa	tgg	tat	cat	tac	96
Thr	Gly	Leu	Gly	Tyr	Tyr	Ile	Met	Thr	Leu	Leu	Gln	Trp	Tyr	His	Tyr	
			20					25					30			

agc	gtg	ttc	agg	att	tta	act	aag	cat	cat	aaa	atg	cgt	tgg	cat	ggg	144
Ser	Val	Phe	Arg	Ile	Leu	Thr	Lys	His	His	Lys	Met	Arg	Trp	His	Gly	
			35				40					45				

att	tat	ttt	tta	ttg	cct	tta	ggg	gtg	ttt	atc	cta	tcg	tat	gct	ttc	192
Ile	Tyr	Phe	Leu	Leu	Pro	Leu	Gly	Val	Phe	Ile	Leu	Ser	Tyr	Ala	Phe	
			50			55					60					

aaa	atg	cgc	ttt	gtt	ttt	gat	ttc	ttt	tgc	ggc	gtt	att	caa	atg	ccc	240
Lys	Met	Pro	Phe	Val	Phe	Asp	Phe	Phe	Cys	Gly	Val	Ile	Gln	Met	Pro	
65					70				75					80		

atg	ctt	att	atc	tgg	gcc	aaa	cgc	aac	gac	aaa	cct	tta	gtt	ttc	acg	288
Met	Leu	Ile	Ile	Trp	Ala	Lys	Arg	Asn	Asp	Lys	Pro	Leu	Val	Phe	Thr	
				85					90					95		

cca	agg	gtg	aag	cgc	ttt	ttt	att	ttc	ttg	tta	ctc	ttt	tta	atc	ttg	336
Pro	Arg	Val	Lys	Arg	Phe	Phe	Ile	Phe	Leu	Leu	Leu	Phe	Leu	Ile	Leu	
			100					105					110			

cat	gaa	atc	tta	aat	aca	gaa	tta	gtc	cct	ttg	aat	ggg	att	tcg	ctc	384
His	Glu	Ile	Leu	Asn	Thr	Glu	Leu	Val	Pro	Leu	Asn	Gly	Ile	Ser	Leu	
		115					120					125				

gcg	ctt	ggc	tat	ttg	tgt	tta	ttt	ata	ttc	ggt	tta	agc	gct	tct	tta	432
Ala	Leu	Gly	Tyr	Leu	Cys	Leu	Phe	Ile	Phe	Val	Leu	Ser	Ala	Ser	Leu	
	130					135					140					

atc	ttt	gaa	aaa	gcc	tta	tcc	aag	cag	tat	tta	caa	acc	gct	aaa	gat	480
Ile	Phe	Glu	Lys	Ala	Leu	Ser	Lys	Gln	Tyr	Leu	Gln	Thr	Ala	Lys	Asp	
145					150					155					160	

aaa	atc	gcc	tct	tta	aag	aat	tta	aaa	gtc	atc	gcc	att	acc	gga	agc	528
Lys	Ile	Ala	Ser	Leu	Lys	Asn	Leu	Lys	Val	Ile	Ala	Ile	Thr	Gly	Ser	
				165					170					175		

tt																530
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<210> 140  
 <211> 176  
 <212> PRT  
 <213> Helicobacter pylori  
  
 <400> 140

Met	Gln	Ser	Leu	Ser	Trp	Leu	Asn	Leu	Ala	Phe	Arg	Trp	Leu	Phe	Ile
1				5					10					15	

Thr	Gly	Leu	Gly	Tyr	Tyr	Ile	Met	Thr	Leu	Leu	Gln	Trp	Tyr	His	Tyr
		20					25						30		

Ser	Val	Phe	Arg	Ile	Leu	Thr	Lys	His	His	Lys	Met	Arg	Trp	His	Gly
		35					40					45			

Ile	Tyr	Phe	Leu	Leu	Pro	Leu	Gly	Val	Phe	Ile	Leu	Ser	Tyr	Ala	Phe
	50					55					60				

Lys	Met	Pro	Phe	Val	Phe	Asp	Phe	Phe	Cys	Gly	Val	Ile	Gln	Met	Pro
65					70					75				80	

Met	Leu	Ile	Ile	Trp	Ala	Lys	Arg	Asn	Asp	Lys	Pro	Leu	Val	Phe	Thr
				85					90					95	

Pro Arg Val Lys Arg Phe Phe Ile Phe Leu Leu Leu Phe Leu Ile Leu  
100 105 110

His Glu Ile Leu Asn Thr Glu Leu Val Pro Leu Asn Gly Ile Ser Leu  
115 120 125

Ala Leu Gly Tyr Leu Cys Leu Phe Ile Phe Val Leu Ser Ala Ser Leu  
130 135 140

Ile Phe Glu Lys Ala Leu Ser Lys Gln Tyr Leu Gln Thr Ala Lys Asp  
145 150 155 160

Lys Ile Ala Ser Leu Lys Asn Leu Lys Val Ile Ala Ile Thr Gly Ser  
165 170 175

<210> 141  
<211> 1536  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(1536)

<400> 141  
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Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu Leu Leu Ile Gly Leu  
1 5 10 15  
tta aca acc tat atc atc ctt ttt aca gaa tgg ggg aac aaa atc atc 96  
Leu Thr Thr Tyr Ile Ile Leu Phe Thr Glu Trp Gly Asn Lys Ile Ile  
20 25 30  
gct tcg tat ata gag aaa aaa atc aac ccg aac gag cgc tac ttg agc 144  
Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn Glu Arg Tyr Leu Ser  
35 40 45  
gtt aaa acc ttt aaa ttg aga ttc aac tct ttg gat ttt aaa gct caa 192  
Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu Asp Phe Lys Ala Gln  
50 55 60  
gcc aac gat gat tcc acg ctc att ctt aag ggg gat ttt tca ctt tta 240  
Ala Asn Asp Asp Ser Thr Leu Ile Leu Lys Gly Asp Phe Ser Leu Leu  
65 70 75 80  
aag caa agc gtg gat ttg aat tac cac ata gat att aaa gat tta cgc 288  
Lys Gln Ser Val Asp Leu Asn Tyr His Ile Asp Ile Lys Asp Leu Arg  
85 90 95

tct ttc aaa gaa tgg ata ccc tac cct tta aga ggg gct att att act	336
Ser Phe Lys Glu Trp Ile Pro Tyr Pro Leu Arg Gly Ala Ile Ile Thr	
100 105 110	
tct ggg aat atc aaa ggg cat aga aaa gcc ctt gtg att caa ggc gtc	384
Ser Gly Asn Ile Lys Gly His Arg Lys Ala Leu Val Ile Gln Gly Val	
115 120 125	
tct aat gtc gct caa tcc cac act gcc tac aac gcc ctt tta gat gat	432
Ser Asn Val Ala Gln Ser His Thr Ala Tyr Asn Ala Leu Leu Asp Asp	
130 135 140	
ttc aag ctt tct cac tta agc ttg aac gca aaa gac gcc aat tta gaa	480
Phe Lys Leu Ser His Leu Ser Leu Asn Ala Lys Asp Ala Asn Leu Glu	
145 150 155 160	
gat ttg ctt tat tta atc aat cgc ccc gct tat gcg aac gca aaa gtg	528
Asp Leu Leu Tyr Leu Ile Asn Arg Pro Ala Tyr Ala Asn Ala Lys Val	
165 170 175	
tcc tta caa gcg gat ttt aac tct cta aag cct tta gaa ggg cat ttg	576
Ser Leu Gln Ala Asp Phe Asn Ser Leu Lys Pro Leu Glu Gly His Leu	
180 185 190	
att cta aca gcc aat aac gct tta atc aat aac gcc cta atc aat caa	624
Ile Leu Thr Ala Asn Asn Ala Leu Ile Asn Asn Ala Leu Ile Asn Gln	
195 200 205	
atg ttt cat tta aac ctt aaa gac acg ctt atc ttc aac ctc tcg cac	672
Met Phe His Leu Asn Leu Lys Asp Thr Leu Ile Phe Asn Leu Ser His	
210 215 220	
tca agc gac ttt aaa gag aac aaa gcc atc agc gat acc acc ctg act	720
Ser Ser Asp Phe Lys Glu Asn Lys Ala Ile Ser Asp Thr Thr Leu Thr	
225 230 235 240	
agc cct tta gcc aat ttt aca gcc cta aaa agc gaa tac ctt ttc tct	768
Ser Pro Leu Ala Asn Phe Thr Ala Leu Lys Ser Glu Tyr Leu Phe Ser	
245 250 255	
att tta aaa ctc aat gcc ccc tac act tta gaa ata ccc aat ctg gcc	816
Ile Leu Lys Leu Asn Ala Pro Tyr Thr Leu Glu Ile Pro Asn Leu Ala	
260 265 270	
aaa ctc caa aac atg act aac cac ccc cta aaa ggg agt ttg act tta	864
Lys Leu Gln Asn Met Thr Asn His Pro Leu Lys Gly Ser Leu Thr Leu	
275 280 285	
aaa ggc gct ata gag caa agc ccc aaa ctc tta aaa gtc agc ggc cat	912
Lys Gly Ala Ile Glu Gln Ser Pro Lys Leu Leu Lys Val Ser Gly His	
290 295 300	

tca aat tta ctg gat ggc acg ctc gat ttc acg ctt tta aat aaa gat	960
Ser Asn Leu Leu Asp Gly Thr Leu Asp Phe Thr Leu Leu Asn Lys Asp	
305 310 315 320	
ttg aaa gcc cgt ttt tca aat att tcc act tta aaa gcc tta gat tta	1008
Leu Lys Ala Arg Phe Ser Asn Ile Ser Thr Leu Lys Ala Leu Asp Leu	
325 330 335	
ttc aat tac ccc aag ttt ttc caa tcc att gca gac gct aac ttg gat	1056
Phe Asn Tyr Pro Lys Phe Phe Gln Ser Ile Ala Asp Ala Asn Leu Asp	
340 345 350	
tat gac ctt agc gct aag caa ggc aca ttg aaa gcc cgc cta aaa aac	1104
Tyr Asp Leu Ser Ala Lys Gln Gly Thr Leu Lys Ala Arg Leu Lys Asn	
355 360 365	
gca aga ttc ctc aaa aat gca ttc agc gat ttc ctc tac tcc att tct	1152
Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe Leu Tyr Ser Ile Ser	
370 375 380	
caa ttt gat att act aaa gaa atc tat aac gat gcc aat cta gta agc	1200
Gln Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp Ala Asn Leu Val Ser	
385 390 395 400	
caa atc aac cag caa cgc ctg ctc tct agt ctc agc tta aaa agc ccc	1248
Gln Ile Asn Gln Gln Arg Leu Leu Ser Ser Leu Ser Leu Lys Ser Pro	
405 410 415	
aaa acc caa ttg aaa atc cat aac ggg ctt gtg gat tta aac acc aaa	1296
Lys Thr Gln Leu Lys Ile His Asn Gly Leu Val Asp Leu Asn Thr Lys	
420 425 430	
caa atg gac atg ctc ata gat gcg gaa atc tta aaa ttc gtt ttt aaa	1344
Gln Met Asp Met Leu Ile Asp Ala Glu Ile Leu Lys Phe Val Phe Lys	
435 440 445	
atg aaa ctt caa ggc aac ata cac cag cca aaa ttt tcc ctc att tta	1392
Met Lys Leu Gln Gly Asn Ile His Gln Pro Lys Phe Ser Leu Ile Leu	
450 455 460	
aac gaa aaa gcc atc caa caa aac ctg caa caa ggc ttg aaa gaa atc	1440
Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln Gly Leu Lys Glu Ile	
465 470 475 480	
cta aaa aac gac acc ctt aaa aaa ggt tta gat cat ttg ctt aaa gat	1488
Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp His Leu Leu Lys Asp	
485 490 495	
gat aag ctc aaa gaa aag ctt gaa aaa ggg ctt aag ggg ctt ttt taa	1536
Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu Lys Gly Leu Phe	
500 505 510	

<210> 142

<211> 511  
 <212> PRT  
 <213> Helicobacter pylori  
 <400> 142

Met	Lys	Lys	Leu	Leu	Tyr	Thr	Ile	Leu	Ala	Leu	Leu	Leu	Ile	Gly	Leu
1			5					10					15		
Leu	Thr	Thr	Tyr	Ile	Ile	Leu	Phe	Thr	Glu	Trp	Gly	Asn	Lys	Ile	Ile
			20					25					30		
Ala	Ser	Tyr	Ile	Glu	Lys	Lys	Ile	Asn	Pro	Asn	Glu	Arg	Tyr	Leu	Ser
		35					40					45			
Val	Lys	Thr	Phe	Lys	Leu	Arg	Phe	Asn	Ser	Leu	Asp	Phe	Lys	Ala	Gln
	50					55					60				
Ala	Asn	Asp	Asp	Ser	Thr	Leu	Ile	Leu	Lys	Gly	Asp	Phe	Ser	Leu	Leu
65					70					75					80
Lys	Gln	Ser	Val	Asp	Leu	Asn	Tyr	His	Ile	Asp	Ile	Lys	Asp	Leu	Arg
			85						90					95	
Ser	Phe	Lys	Glu	Trp	Ile	Pro	Tyr	Pro	Leu	Arg	Gly	Ala	Ile	Ile	Thr
			100					105					110		
Ser	Gly	Asn	Ile	Lys	Gly	His	Arg	Lys	Ala	Leu	Val	Ile	Gln	Gly	Val
		115					120					125			
Ser	Asn	Val	Ala	Gln	Ser	His	Thr	Ala	Tyr	Asn	Ala	Leu	Leu	Asp	Asp
	130					135					140				
Phe	Lys	Leu	Ser	His	Leu	Ser	Leu	Asn	Ala	Lys	Asp	Ala	Asn	Leu	Glu
145					150					155					160
Asp	Leu	Leu	Tyr	Leu	Ile	Asn	Arg	Pro	Ala	Tyr	Ala	Asn	Ala	Lys	Val
				165					170					175	
Ser	Leu	Gln	Ala	Asp	Phe	Asn	Ser	Leu	Lys	Pro	Leu	Glu	Gly	His	Leu
		180						185					190		

Ile Leu Thr Ala Asn Asn Ala Leu Ile Asn Asn Ala Leu Ile Asn Gln  
 195 200 205

Met Phe His Leu Asn Leu Lys Asp Thr Leu Ile Phe Asn Leu Ser His  
 210 215 220

Ser Ser Asp Phe Lys Glu Asn Lys Ala Ile Ser Asp Thr Thr Leu Thr  
 225 230 235 240

Ser Pro Leu Ala Asn Phe Thr Ala Leu Lys Ser Glu Tyr Leu Phe Ser  
 245 250 255

Ile Leu Lys Leu Asn Ala Pro Tyr Thr Leu Glu Ile Pro Asn Leu Ala  
 260 265 270

Lys Leu Gln Asn Met Thr Asn His Pro Leu Lys Gly Ser Leu Thr Leu  
 275 280 285

Lys Gly Ala Ile Glu Gln Ser Pro Lys Leu Leu Lys Val Ser Gly His  
 290 295 300

Ser Asn Leu Leu Asp Gly Thr Leu Asp Phe Thr Leu Leu Asn Lys Asp  
 305 310 315 320

Leu Lys Ala Arg Phe Ser Asn Ile Ser Thr Leu Lys Ala Leu Asp Leu  
 325 330 335

Phe Asn Tyr Pro Lys Phe Phe Gln Ser Ile Ala Asp Ala Asn Leu Asp  
 340 345 350

Tyr Asp Leu Ser Ala Lys Gln Gly Thr Leu Lys Ala Arg Leu Lys Asn  
 355 360 365

Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe Leu Tyr Ser Ile Ser  
 370 375 380

Gln Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp Ala Asn Leu Val Ser  
 385 390 395 400

Gln Ile Asn Gln Gln Arg Leu Leu Ser Ser Leu Ser Leu Lys Ser Pro  
 405 410 415



Lys Thr Gln Leu Lys Ile His Asn Gly Leu Val Asp Leu Asn Thr Lys  
420 425 430

Gln Met Asp Met Leu Ile Asp Ala Glu Ile Leu Lys Phe Val Phe Lys  
435 440 445

Met Lys Leu Gln Gly Asn Ile His Gln Pro Lys Phe Ser Leu Ile Leu  
450 455 460

Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln Gly Leu Lys Glu Ile  
465 470 475 480

Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp His Leu Leu Lys Asp  
485 490 495

Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu Lys Gly Leu Phe  
500 505 510

<210> 143  
<211> 88  
<212> DNA  
<213> Helicobacter pylori

<220>

<221> CDS  
<222> (1)..(87)

<400> 143  
atg aag aga tct tct gta ttt agt ttc ttg gta gct ttt tta ttg gta 48  
Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val  
1 5 10 15  
act ggc tgt agt cat aaa atg gat aat aag act gtg gcc g 88  
Thr Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala  
20 25

<210> 144  
<211> 29  
<212> PRT  
<213> Helicobacter pylori

<400> 144

Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val  
1 5 10 15

Thr Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala  
 20 25

<210> 145  
 <211> 1080  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1080)

<400> 145  
 ttg aaa cat ttg acc cca ctc act cac acc ctt ttt aaa gcc tta tgg 48  
 Leu Lys His Leu Thr Pro Leu Thr His Thr Leu Phe Lys Ala Leu Trp  
 1 5 10 15  
 cta ggc acg gtc tta agc gca tct tta agc tta gtt gca gca gaa agc 96  
 Leu Gly Thr Val Leu Ser Ala Ser Leu Ser Leu Val Ala Ala Glu Ser  
 20 25 30  
 ccc act aga aca gag cct aaa ccc gct aag ggg gtt aaa aat aaa ccc 144  
 Pro Thr Arg Thr Glu Pro Lys Pro Ala Lys Gly Val Lys Asn Lys Pro  
 35 40 45  
 aaa tcg ccc gtt act aaa gtc atg atg acc aat tgc gac aac ctt aaa 192  
 Lys Ser Pro Val Thr Lys Val Met Met Thr Asn Cys Asp Asn Leu Lys  
 50 55 60  
 gac ttt aac gct aat caa aaa gaa gtt cta aaa gcc gcc tat caa ttc 240  
 Asp Phe Asn Ala Asn Gln Lys Glu Val Leu Lys Ala Ala Tyr Gln Phe  
 65 70 75 80  
 ggc tct aaa gaa aat tta ggc tat gaa atg gca ggc att gca tgg aaa 288  
 Gly Ser Lys Glu Asn Leu Gly Tyr Glu Met Ala Gly Ile Ala Trp Lys  
 85 90 95  
 gaa tca tgt gca ggg gtt tat aaa atc aat ttt tcc gat ccg agt gcg 336  
 Glu Ser Cys Ala Gly Val Tyr Lys Ile Asn Phe Ser Asp Pro Ser Ala  
 100 105 110  
 ggc gtg tat cat tct tat atc cca agc gtt cta aaa agc tat ggg cat 384  
 Gly Val Tyr His Ser Tyr Ile Pro Ser Val Leu Lys Ser Tyr Gly His  
 115 120 125  
 aat gat agc ccc ttt ttg cgt aat gtg atg ggg gaa ttg ctc att aaa 432  
 Asn Asp Ser Pro Phe Leu Arg Asn Val Met Gly Glu Leu Leu Ile Lys  
 130 135 140  
 gac gat gcg ttt gct tct gaa gtg gct tta aaa gag ttg ctc tat tgg 480  
 Asp Asp Ala Phe Ala Ser Glu Val Ala Leu Lys Glu Leu Leu Tyr Trp

145		150		155		160	
aaa aca cgc tac cat gac aat cta aaa gac atg att aaa tct tac aac							528
Lys Thr Arg Tyr His Asp Asn Leu Lys Asp Met Ile Lys Ser Tyr Asn							
		165		170		175	
aag ggc agt cgt tgg gaa aaa aac gag aag tct aac gcc gaa gct gaa							576
Lys Gly Ser Arg Trp Glu Lys Asn Glu Lys Ser Asn Ala Glu Ala Glu							
		180		185		190	
aaa tat tat gaa gag ata caa gac agg atc agg cgt ttg aaa gaa tct							624
Lys Tyr Tyr Glu Glu Ile Gln Asp Arg Ile Arg Arg Leu Lys Glu Ser							
		195		200		205	
aaa atc ttt gat tcg cag tct agt aat gac caa gaa ttg caa aaa agc							672
Lys Ile Phe Asp Ser Gln Ser Ser Asn Asp Gln Glu Leu Gln Lys Ser							
		210		215		220	
gct aat agc aac ctg gat tta gac cct atc ggc agc acc atg ccc caa							720
Ala Asn Ser Asn Leu Asp Leu Asp Pro Ile Gly Ser Thr Met Pro Gln							
		225		230		235	240
act tta gcc acc caa aaa tct caa ata gaa aaa tct caa ata gag gaa							768
Thr Leu Ala Thr Gln Lys Ser Gln Ile Glu Lys Ser Gln Ile Glu Glu							
		245		250		255	
acc caa gca gaa aaa ccc caa gaa atg aaa gag aca act agc gag caa							816
Thr Gln Ala Glu Lys Pro Gln Glu Met Lys Glu Thr Thr Ser Glu Gln							
		260		265		270	
ata acc aac aag cca gaa aaa gca aaa gat aaa ccc atg tat ttg gct							864
Ile Thr Asn Lys Pro Glu Lys Ala Lys Asp Lys Pro Met Tyr Leu Ala							
		275		280		285	
caa atc aat agc act gat ttc aca ccc gct aaa aaa cgc tct caa aaa							912
Gln Ile Asn Ser Thr Asp Phe Thr Pro Ala Lys Lys Arg Ser Gln Lys							
		290		295		300	
ccg gct aga gtg agc caa aaa cgc tcc tct aaa aat aat atc agc gtt							960
Pro Ala Arg Val Ser Gln Lys Arg Ser Ser Lys Asn Asn Ile Ser Val							
		305		310		315	320
aaa aac aac acc aaa acc gct tcc aaa aat tcc aaa aat aaa gaa atg							1008
Lys Asn Asn Thr Lys Thr Ala Ser Lys Asn Ser Lys Asn Lys Glu Met							
		325		330		335	
tgc aaa aat tgc tct cca ggg caa agg aat gcg att tta gct aac cac							1056
Cys Lys Asn Cys Ser Pro Gly Gln Arg Asn Ala Ile Leu Ala Asn His							
		340		345		350	
atc act ctc atg caa gag ctt taa							1080
Ile Thr Leu Met Gln Glu Leu							
		355					

<210> 146  
 <211> 359  
 <212> PRT  
 <213> Helicobacter pylori

<400> 146

Leu Lys His Leu Thr Pro Leu Thr His Thr Leu Phe Lys Ala Leu Trp  
 1 5 10 15

Leu Gly Thr Val Leu Ser Ala Ser Leu Ser Leu Val Ala Ala Glu Ser  
 20 25 30

Pro Thr Arg Thr Glu Pro Lys Pro Ala Lys Gly Val Lys Asn Lys Pro  
 35 40 45

Lys Ser Pro Val Thr Lys Val Met Met Thr Asn Cys Asp Asn Leu Lys  
 50 55 60

Asp Phe Asn Ala Asn Gln Lys Glu Val Leu Lys Ala Ala Tyr Gln Phe  
 65 70 75 80

Gly Ser Lys Glu Asn Leu Gly Tyr Glu Met Ala Gly Ile Ala Trp Lys  
 85 90 95

Glu Ser Cys Ala Gly Val Tyr Lys Ile Asn Phe Ser Asp Pro Ser Ala  
 100 105 110

Gly Val Tyr His Ser Tyr Ile Pro Ser Val Leu Lys Ser Tyr Gly His  
 115 120 125

Asn Asp Ser Pro Phe Leu Arg Asn Val Met Gly Glu Leu Leu Ile Lys  
 130 135 140

Asp Asp Ala Phe Ala Ser Glu Val Ala Leu Lys Glu Leu Leu Tyr Trp  
 145 150 155 160

Lys Thr Arg Tyr His Asp Asn Leu Lys Asp Met Ile Lys Ser Tyr Asn  
 165 170 175

Lys Gly Ser Arg Trp Glu Lys Asn Glu Lys Ser Asn Ala Glu Ala Glu  
 180 185 190

Lys Tyr Tyr Glu Glu Ile Gln Asp Arg Ile Arg Arg Leu Lys Glu Ser  
195 200 205

Lys Ile Phe Asp Ser Gln Ser Ser Asn Asp Gln Glu Leu Gln Lys Ser  
210 215 220

Ala Asn Ser Asn Leu Asp Leu Asp Pro Ile Gly Ser Thr Met Pro Gln  
225 230 235 240

Thr Leu Ala Thr Gln Lys Ser Gln Ile Glu Lys Ser Gln Ile Glu Glu  
245 250 255

Thr Gln Ala Glu Lys Pro Gln Glu Met Lys Glu Thr Thr Ser Glu Gln  
260 265 270

Ile Thr Asn Lys Pro Glu Lys Ala Lys Asp Lys Pro Met Tyr Leu Ala  
275 280 285

Gln Ile Asn Ser Thr Asp Phe Thr Pro Ala Lys Lys Arg Ser Gln Lys  
290 295 300

Pro Ala Arg Val Ser Gln Lys Arg Ser Ser Lys Asn Asn Ile Ser Val  
305 310 315 320

Lys Asn Asn Thr Lys Thr Ala Ser Lys Asn Ser Lys Asn Lys Glu Met  
325 330 335

Cys Lys Asn Cys Ser Pro Gly Gln Arg Asn Ala Ile Leu Ala Asn His  
340 345 350

Ile Thr Leu Met Gln Glu Leu  
355

<210> 147  
<211> 695  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (2)..(694)  
  
<400> 147

g atc att atc gtg ccg tta ccg cct ttt gtg ttg gat ttt tha ctc acg	49
Ile Ile Ile Val Pro Leu Pro Pro Phe Val Leu Asp Phe Xaa Leu Thr	
1 5 10 15	
att tct att gcg cta tcg gtg ttg att att tta atc ggg ctt tat att	97
Ile Ser Ile Ala Leu Ser Val Leu Ile Ile Leu Ile Gly Leu Tyr Ile	
20 25 30	
gac aag ccg act gat ttt agc gct ttc ccc act cta tta ctc att gta	145
Asp Lys Pro Thr Asp Phe Ser Ala Phe Pro Thr Leu Leu Leu Ile Val	
35 40 45	
acc cta tac cgc ttg gct tta aat gtc gcc acc act aga atg att tta	193
Thr Leu Tyr Arg Leu Ala Leu Asn Val Ala Thr Thr Arg Met Ile Leu	
50 55 60	
acg caa ggc tat aaa ggg cct agc acg gtg agc gat att atc acg gcg	241
Thr Gln Gly Tyr Lys Gly Pro Ser Thr Val Ser Asp Ile Ile Thr Ala	
65 70 75 80	
ttt ggg gaa ttt agc gtg agc ggg aat tat gtg att ggt gcg att atc	289
Phe Gly Glu Phe Ser Val Ser Gly Asn Tyr Val Ile Gly Ala Ile Ile	
85 90 95	
ttt agt att tta gtg ctg gtg aat cta tta gtg gtt act aat ggc tct	337
Phe Ser Ile Leu Val Leu Val Asn Leu Leu Val Val Thr Asn Gly Ser	
100 105 110	
act agg gtt act gaa gtg aga gcg cga ttc gct cta gac gct atg cca	385
Thr Arg Val Thr Glu Val Arg Ala Arg Phe Ala Leu Asp Ala Met Pro	
115 120 125	
gga aag caa atg gcg att gat gcg gat tta aat tca ggg ctt att gat	433
Gly Lys Gln Met Ala Ile Asp Ala Asp Leu Asn Ser Gly Leu Ile Asp	
130 135 140	
gat aag gaa gcc aaa aaa cgg cgc gcc gct cta agc caa gaa gcg gat	481
Asp Lys Glu Ala Lys Lys Arg Arg Ala Ala Leu Ser Gln Glu Ala Asp	
145 150 155 160	
ttt tat ggc gcg atg gat ggc gcg tct aaa ttc gtc aaa ggc gat gcg	529
Phe Tyr Gly Ala Met Asp Gly Ala Ser Lys Phe Val Lys Gly Asp Ala	
165 170 175	
atc gct tct att atc atc acg ctt atc aat atc att gga ggg ttt tta	577
Ile Ala Ser Ile Ile Ile Thr Leu Ile Asn Ile Ile Gly Gly Phe Leu	
180 185 190	
gtg ggc gtg ttc caa agg gat atg agt ttg agc ttt agc gct agc act	625
Val Gly Val Phe Gln Arg Asp Met Ser Leu Ser Phe Ser Ala Ser Thr	
195 200 205	
ttc act atc tta acc att ggc gat ggg ctt gta ggg caa atc cct gct	673
Phe Thr Ile Leu Thr Ile Gly Asp Gly Leu Val Gly Gln Ile Pro Ala	
210 215 220	

tta atc att gcg aca gcg acc g  
 Leu Ile Ile Ala Thr Ala Thr  
 225 230

<210> 148  
 <211> 231  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <221> misc\_feature  
 <222> (14)..(14)  
 <223> The 'Xaa' at location 14 stands for Ser, or Leu.

<400> 148

Ile Ile Ile Val Pro Leu Pro Pro Phe Val Leu Asp Phe Xaa Leu Thr  
 1 5 10 15

Ile Ser Ile Ala Leu Ser Val Leu Ile Ile Leu Ile Gly Leu Tyr Ile  
 20 25 30

Asp Lys Pro Thr Asp Phe Ser Ala Phe Pro Thr Leu Leu Leu Ile Val  
 35 40 45

Thr Leu Tyr Arg Leu Ala Leu Asn Val Ala Thr Thr Arg Met Ile Leu  
 50 55 60

Thr Gln Gly Tyr Lys Gly Pro Ser Thr Val Ser Asp Ile Ile Thr Ala  
 65 70 75 80

Phe Gly Glu Phe Ser Val Ser Gly Asn Tyr Val Ile Gly Ala Ile Ile  
 85 90 95

Phe Ser Ile Leu Val Leu Val Asn Leu Leu Val Val Thr Asn Gly Ser  
 100 105 110

Thr Arg Val Thr Glu Val Arg Ala Arg Phe Ala Leu Asp Ala Met Pro  
 115 120 125

Gly Lys Gln Met Ala Ile Asp Ala Asp Leu Asn Ser Gly Leu Ile Asp  
 130 135 140

Asp Lys Glu Ala Lys Lys Arg Arg Ala Ala Leu Ser Gln Glu Ala Asp

145		150		155		160
Phe Tyr Gly Ala Met Asp Gly Ala Ser Lys Phe Val Lys Gly Asp Ala						
		165		170		175
Ile Ala Ser Ile Ile Ile Thr Leu Ile Asn Ile Ile Gly Gly Phe Leu						
		180		185		190
Val Gly Val Phe Gln Arg Asp Met Ser Leu Ser Phe Ser Ala Ser Thr						
		195		200		205
Phe Thr Ile Leu Thr Ile Gly Asp Gly Leu Val Gly Gln Ile Pro Ala						
		210		215		220
Leu Ile Ile Ala Thr Ala Thr						
225				230		

<210> 149  
 <211> 384  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(384)

<400> 149	
atg aaa aag ttt aaa aag aaa cca aaa agt atc aaa cga ttg cat caa	48
Met Lys Lys Phe Lys Lys Lys Pro Lys Ser Ile Lys Arg Leu His Gln	
1 5 10 15	
aat caa aaa aca atc tta aag cgt cct tta tgg ctc gca cct tta ctc	96
Asn Gln Lys Thr Ile Leu Lys Arg Pro Leu Trp Leu Ala Pro Leu Leu	
20 25 30	
atc agc ggg ttt gtt agt ggg gtg tat gct gat gga aca gac att ttg	144
Ile Ser Gly Phe Val Ser Gly Val Tyr Ala Asp Gly Thr Asp Ile Leu	
35 40 45	
ggg ctt agt tgg ggt gaa aaa agc caa aag gta tgc gtg cat cat cca	192
Gly Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His His Pro	
50 55 60	
tgg tat gct ata tgg agt tgc gat aaa tgg gag gaa aaa aca caa caa	240
Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln	
65 70 75 80	
ttc aca gga aac caa ctc atc aca aaa act tgg gca ggg ggt aat gcg	288



Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala  
85 90 95

gct aat tac tac cac act caa aac aac caa aat att aca gcc aat tta 336  
Ala Asn Tyr Tyr His Thr Gln Asn Asn Gln Asn Ile Thr Ala Asn Leu  
100 105 110

aaa aat gat aac ggc act tat ttt tta agc ggt ctg tat aac tac acc 384  
Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr  
115 120 125

<210> 150

<211> 128

<212> PRT

<213> Helicobacter pylori

<400> 150

Met Lys Lys Phe Lys Lys Lys Pro Lys Ser Ile Lys Arg Leu His Gln  
1 5 10 15

Asn Gln Lys Thr Ile Leu Lys Arg Pro Leu Trp Leu Ala Pro Leu Leu  
20 25 30

Ile Ser Gly Phe Val Ser Gly Val Tyr Ala Asp Gly Thr Asp Ile Leu  
35 40 45

Gly Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His His Pro  
50 55 60

Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln  
65 70 75 80

Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala  
85 90 95

Ala Asn Tyr Tyr His Thr Gln Asn Asn Gln Asn Ile Thr Ala Asn Leu  
100 105 110

Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr  
115 120 125

<210> 151

<211> 1008

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1008)

<400> 151

atg	tta	ggt	act	cgc	ttt	aaa	aaa	gct	ttg	atc	tct	tat	tct	tta	ggt	48
Met	Leu	Val	Thr	Arg	Phe	Lys	Lys	Ala	Leu	Ile	Ser	Tyr	Ser	Leu	Gly	
1				5					10					15		

gcg	ctc	att	ggt	tca	tcg	tta	ttg	ggc	gtg	gct	aac	gct	tca	gca	caa	96
Ala	Leu	Ile	Val	Ser	Ser	Leu	Leu	Gly	Val	Ala	Asn	Ala	Ser	Ala	Gln	
			20					25					30			

gag	ggt	aaa	gtc	aag	gat	tat	ttc	ggg	gag	caa	act	gta	aag	ctt	cct	144
Glu	Val	Lys	Val	Lys	Asp	Tyr	Phe	Gly	Glu	Gln	Thr	Val	Lys	Leu	Pro	
		35					40					45				

ggt	tct	aaa	ata	gcc	tat	ata	ggg	agc	tat	gta	gaa	gtg	cct	gcc	atg	192
Val	Ser	Lys	Ile	Ala	Tyr	Ile	Gly	Ser	Tyr	Val	Glu	Val	Pro	Ala	Met	
	50					55					60					

ctt	aat	ggt	tgg	aat	agg	ggt	gta	ggc	ggt	tcg	gat	tac	gct	ttt	aaa	240
Leu	Asn	Val	Trp	Asn	Arg	Val	Val	Gly	Val	Ser	Asp	Tyr	Ala	Phe	Lys	
65					70					75					80	

gat	gac	att	ggt	aaa	gcc	act	ctc	aaa	ggc	gaa	gat	ctt	aaa	cgc	gtc	288
Asp	Asp	Ile	Val	Lys	Ala	Thr	Leu	Lys	Gly	Glu	Asp	Leu	Lys	Arg	Val	
				85					90					95		

aaa	cac	atg	agc	act	gat	cat	aca	gcc	gca	cta	aat	gta	gag	ctt	tta	336
Lys	His	Met	Ser	Thr	Asp	His	Thr	Ala	Ala	Leu	Asn	Val	Glu	Leu	Leu	
			100					105					110			

aaa	aag	ctc	agc	cct	gat	ctt	gtg	gta	acc	ttt	gtg	ggc	aac	cct	aaa	384
Lys	Lys	Leu	Ser	Pro	Asp	Leu	Val	Val	Thr	Phe	Val	Gly	Asn	Pro	Lys	
		115					120					125				

gcg	gta	gag	cat	gcg	aaa	aaa	ttt	ggg	ata	tca	ttt	ctt	tct	ttc	caa	432
Ala	Val	Glu	His	Ala	Lys	Lys	Phe	Gly	Ile	Ser	Phe	Leu	Ser	Phe	Gln	
	130					135					140					

gag	aca	acg	atc	gca	gag	gcc	atg	cag	gct	atg	caa	gct	caa	gct	gcg	480
Glu	Thr	Thr	Ile	Ala	Glu	Ala	Met	Gln	Ala	Met	Gln	Ala	Gln	Ala	Ala	
145					150				155						160	

gtc	tta	gaa	att	gac	gct	tct	aaa	aaa	ttc	gcc	aaa	atg	caa	gaa	act	528
Val	Leu	Glu	Ile	Asp	Ala	Ser	Lys	Lys	Phe	Ala	Lys	Met	Gln	Glu	Thr	
				165					170					175		

ttg	gat	ttt	atc	gct	gag	cgt	ttg	aaa	gat	gtc	aaa	aag	aaa	aag	ggg	576
Leu	Asp	Phe	Ile	Ala	Glu	Arg	Leu	Lys	Asp	Val	Lys	Lys	Lys	Lys	Gly	
			180					185					190			

gtg gag ctt ttc cat aaa gcc aat aaa att agc ggc cat caa gcc att	624
Val Glu Leu Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Ile	
195 200 205	
agc tca gac att tta gaa aaa ggg ggc ata gac aat ttt ggc ttg aaa	672
Ser Ser Asp Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys	
210 215 220	
tac gtc aaa ttt ggg cgc gct gat att agc gtg gaa aaa atc gtt aaa	720
Tyr Val Lys Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys	
225 230 235 240	
gaa aac cct gaa atc att ttc atc tgg tgg gta agc cca ctc acg cct	768
Glu Asn Pro Glu Ile Ile Phe Ile Trp Trp Val Ser Pro Leu Thr Pro	
245 250 255	
gaa gat gtg tta aac aac cct aag ttt tcc act att aaa gcc att aaa	816
Glu Asp Val Leu Asn Asn Pro Lys Phe Ser Thr Ile Lys Ala Ile Lys	
260 265 270	
aac aag caa gtt tat aaa ctc ccc aca atg gat att ggc ggc cct aga	864
Asn Lys Gln Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro Arg	
275 280 285	
gcc cca ctc ata agc tta ttt atc gct tta aaa gcc cac cct gaa gcc	912
Ala Pro Leu Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala	
290 295 300	
ttt aag ggc gtg gat att aat gcg att gtt aaa gac tac tat aaa gtg	960
Phe Lys Gly Val Asp Ile Asn Ala Ile Val Lys Asp Tyr Tyr Lys Val	
305 310 315 320	
gtt ttt gat ttg aac gat gca gag gtt gaa ccc ttt tta tgg cat taa	1008
Val Phe Asp Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His	
325 330 335	

<210> 152  
 <211> 335  
 <212> PRT  
 <213> Helicobacter pylori

<400> 152

Met Leu Val Thr Arg Phe Lys Lys Ala Leu Ile Ser Tyr Ser Leu Gly	
1 5 10 15	
Ala Leu Ile Val Ser Ser Leu Leu Gly Val Ala Asn Ala Ser Ala Gln	
20 25 30	
Glu Val Lys Val Lys Asp Tyr Phe Gly Glu Gln Thr Val Lys Leu Pro	
35 40 45	

Val	Ser	Lys	Ile	Ala	Tyr	Ile	Gly	Ser	Tyr	Val	Glu	Val	Pro	Ala	Met	
50						55					60					
Leu	Asn	Val	Trp	Asn	Arg	Val	Val	Gly	Val	Ser	Asp	Tyr	Ala	Phe	Lys	
65					70					75					80	
Asp	Asp	Ile	Val	Lys	Ala	Thr	Leu	Lys	Gly	Glu	Asp	Leu	Lys	Arg	Val	
				85					90					95		
Lys	His	Met	Ser	Thr	Asp	His	Thr	Ala	Ala	Leu	Asn	Val	Glu	Leu	Leu	
			100					105					110			
Lys	Lys	Leu	Ser	Pro	Asp	Leu	Val	Val	Thr	Phe	Val	Gly	Asn	Pro	Lys	
		115					120					125				
Ala	Val	Glu	His	Ala	Lys	Lys	Phe	Gly	Ile	Ser	Phe	Leu	Ser	Phe	Gln	
	130					135					140					
Glu	Thr	Thr	Ile	Ala	Glu	Ala	Met	Gln	Ala	Met	Gln	Ala	Gln	Ala	Ala	
145					150					155					160	
Val	Leu	Glu	Ile	Asp	Ala	Ser	Lys	Lys	Phe	Ala	Lys	Met	Gln	Glu	Thr	
				165					170					175		
Leu	Asp	Phe	Ile	Ala	Glu	Arg	Leu	Lys	Asp	Val	Lys	Lys	Lys	Lys	Gly	
			180					185					190			
Val	Glu	Leu	Phe	His	Lys	Ala	Asn	Lys	Ile	Ser	Gly	His	Gln	Ala	Ile	
		195					200					205				
Ser	Ser	Asp	Ile	Leu	Glu	Lys	Gly	Gly	Ile	Asp	Asn	Phe	Gly	Leu	Lys	
	210					215					220					
Tyr	Val	Lys	Phe	Gly	Arg	Ala	Asp	Ile	Ser	Val	Glu	Lys	Ile	Val	Lys	
225					230					235					240	
Glu	Asn	Pro	Glu	Ile	Ile	Phe	Ile	Trp	Trp	Val	Ser	Pro	Leu	Thr	Pro	
				245					250					255		
Glu	Asp	Val	Leu	Asn	Asn	Pro	Lys	Phe	Ser	Thr	Ile	Lys	Ala	Ile	Lys	
			260					265					270			

Asn Lys Gln Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro Arg  
 275 280 285

Ala Pro Leu Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala  
 290 295 300

Phe Lys Gly Val Asp Ile Asn Ala Ile Val Lys Asp Tyr Tyr Lys Val  
 305 310 315 320

Val Phe Asp Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His  
 325 330 335

<210> 153  
 <211> 240  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(240)

<400> 153  
 atg ggc gga ttc aca agc ata tgg cat tgg gtc att gtt tta tta gtg 48  
 Met Gly Gly Phe Thr Ser Ile Trp His Trp Val Ile Val Leu Leu Val  
 1 5 10 15  
 att gtg ttg ttg ttt ggg gct aaa aag atc cca gaa ttg gct aag ggt 96  
 Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Glu Leu Ala Lys Gly  
 20 25 30  
 tta ggc agt ggg att aag aat ttc aaa aaa gcc gtg aaa gac gat gaa 144  
 Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp Glu  
 35 40 45  
 gaa gag gct aaa aac gag cca aaa acc cta gac gct caa gca acg caa 192  
 Glu Glu Ala Lys Asn Glu Pro Lys Thr Leu Asp Ala Gln Ala Thr Gln  
 50 55 60  
 acc aaa gtg cat gag agt agc gag att aaa agc aaa caa gaa agt taa 240  
 Thr Lys Val His Glu Ser Ser Glu Ile Lys Ser Lys Gln Glu Ser  
 65 70 75

<210> 154  
 <211> 79  
 <212> PRT  
 <213> Helicobacter pylori

<400> 154

Met Gly Gly Phe Thr Ser Ile Trp His Trp Val Ile Val Leu Leu Val  
1 5 10 15

Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Glu Leu Ala Lys Gly  
20 25 30

Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp Glu  
35 40 45

Glu Glu Ala Lys Asn Glu Pro Lys Thr Leu Asp Ala Gln Ala Thr Gln  
50 55 60

Thr Lys Val His Glu Ser Ser Glu Ile Lys Ser Lys Gln Glu Ser  
65 70 75

<210> 155

<211> 264

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS .

<222> (1)..(264)

<400> 155

atg aaa aac ttt tcc cca ctt tgt tgt ttt aaa aag ctc aaa aaa cgc 48  
Met Lys Asn Phe Ser Pro Leu Cys Cys Phe Lys Lys Leu Lys Lys Arg  
1 5 10 15

cat tta atc gct ttg agc ctg ccc ttg ctt tct tat gcc aat ggc ttt 96  
His Leu Ile Ala Leu Ser Leu Pro Leu Leu Ser Tyr Ala Asn Gly Phe  
20 25 30

aaa atc caa gag caa agc cta aat ggc acg gct tta ggc tcg gcg tat 144  
Lys Ile Gln Glu Gln Ser Leu Asn Gly Thr Ala Leu Gly Ser Ala Tyr  
35 40 45

gtc gct ggg gct agg ggt gct gat gct tcc ttt tat aac ccg gcg aat 192  
Val Ala Gly Ala Arg Gly Ala Asp Ala Ser Phe Tyr Asn Pro Ala Asn  
50 55 60

atg ggc ttt act aac gat tgg ggt gaa aac aga agc gaa ttt gaa atg 240  
Met Gly Phe Thr Asn Asp Trp Gly Glu Asn Arg Ser Glu Phe Glu Met  
65 70 75 80

acc acc acc gtg att aac att ccg 264

Thr Thr Thr Val Ile Asn Ile Pro  
85

<210> 156  
<211> 88  
<212> PRT  
<213> Helicobacter pylori

<400> 156

Met Lys Asn Phe Ser Pro Leu Cys Cys Phe Lys Lys Leu Lys Lys Arg  
1 5 10 15

His Leu Ile Ala Leu Ser Leu Pro Leu Leu Ser Tyr Ala Asn Gly Phe  
20 25 30

Lys Ile Gln Glu Gln Ser Leu Asn Gly Thr Ala Leu Gly Ser Ala Tyr  
35 40 45

Val Ala Gly Ala Arg Gly Ala Asp Ala Ser Phe Tyr Asn Pro Ala Asn  
50 55 60

Met Gly Phe Thr Asn Asp Trp Gly Glu Asn Arg Ser Glu Phe Glu Met  
65 70 75 80

Thr Thr Thr Val Ile Asn Ile Pro  
85

<210> 157  
<211> 1443  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(1443)

<400> 157

ttg gaa ttg aaa aaa atc gcc ctt att tta gat ggc att gta gca aaa 48  
Leu Glu Leu Lys Lys Ile Ala Leu Ile Leu Asp Gly Ile Val Ala Lys  
1 5 10 15

aat ttt tta gac ttg gtg cta agg cat tat tct aat cat aat ttt tat 96  
Asn Phe Leu Asp Leu Val Leu Arg His Tyr Ser Asn His Asn Phe Tyr  
20 25 30

ata gtg gtt gtc aaa aat gag agc ctt atc cct aaa aat tac ccg agc 144

Ile	Val	Val	Val	Lys	Asn	Glu	Ser	Leu	Ile	Pro	Lys	Asn	Tyr	Pro	Ser	
		35					40					45				
act	ttc	gct	ttt	tat	tgt	ttt	gat	gcg	act	tct	agt	ttc	agg	ctt	ttg	192
Thr	Phe	Ala	Phe	Tyr	Cys	Phe	Asp	Ala	Thr	Ser	Ser	Phe	Arg	Leu	Leu	
	50					55					60					
caa	gtg	tta	aac	gat	gag	gtg	agc	gat	gcg	ttt	tta	atc	ata	caa	gat	240
Gln	Val	Leu	Asn	Asp	Glu	Val	Ser	Asp	Ala	Phe	Leu	Ile	Ile	Gln	Asp	
65					70					75					80	
ttt	aaa	gaa	cag	cgc	atc	att	cat	aaa	atc	att	caa	acc	cat	ttc	aaa	288
Phe	Lys	Glu	Gln	Arg	Ile	Ile	His	Lys	Ile	Ile	Gln	Thr	His	Phe	Lys	
			85						90					95		
cgc	atg	cgc	gtg	gtt	ttg	agc	gtg	aaa	aaa	gat	ggg	gaa	aaa	act	tta	336
Arg	Met	Arg	Val	Val	Leu	Ser	Val	Lys	Lys	Asp	Gly	Glu	Lys	Thr	Leu	
			100					105					110			
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Glu	Asn	Asn	Glu	Glu	Asn	Lys	Asp	Glu	Lys	Leu	Ile	Leu	Ile	Asp	Glu	
		115					120					125				
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Phe	Glu	Val	Leu	Ala	Asn	Lys	Phe	Ile	Ser	Arg	Leu	Pro	Asn	Ile	Pro	
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agc	acc	cct	aga	gaa	ttt	ggg	tta	ggc	aaa	ggc	gag	atc	atg	gag	att	480
Ser	Thr	Pro	Arg	Glu	Phe	Gly	Leu	Gly	Lys	Gly	Glu	Ile	Met	Glu	Ile	
145					150					155					160	
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Asp	Val	Pro	Phe	Gly	Ser	Ile	Phe	Ala	Tyr	Arg	His	Ile	Gly	Ser	Ile	
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agg	caa	aaa	gaa	tac	agg	att	gta	ggg	ctt	tat	cg	aac	gat	gtt	ttg	576
Arg	Gln	Lys	Glu	Tyr	Arg	Ile	Val	Gly	Leu	Tyr	Arg	Asn	Asp	Val	Leu	
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ttg	ctc	tcc	act	aaa	tct	tta	gtt	atc	cag	cca	cga	gac	att	ctt	tta	624
Leu	Leu	Ser	Thr	Lys	Ser	Leu	Val	Ile	Gln	Pro	Arg	Asp	Ile	Leu	Leu	
		195					200					205				
gtg	gcg	ggg	aat	ccg	gaa	att	tta	aac	gcg	gtg	tat	ctt	cag	gtc	aaa	672
Val	Ala	Gly	Asn	Pro	Glu	Ile	Leu	Asn	Ala	Val	Tyr	Leu	Gln	Val	Lys	
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Ser	Asn	Val	Gly	Gln	Phe	Pro	Ala	Pro	Phe	Gly	Lys	Ser	Ile	Tyr	Leu	
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Tyr	Ile	Asp	Met	Arg	Leu	Gln	Ser	Arg	Lys	Ala	Met	Met	Arg	Asp	Val	
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tat	caa	gcc	ttg	ttt	ttg	cac	aaa	cat	tta	aag	agc	tac	aag	ctc	tac	816
Tyr	Gln	Ala	Leu	Phe	Leu	His	Lys	His	Leu	Lys	Ser	Tyr	Lys	Leu	Tyr	
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att	cag	gtt	tta	cac	ccc	act	agc	cct	aag	ttt	tac	cat	aaa	ttt	tta	864
Ile	Gln	Val	Leu	His	Pro	Thr	Ser	Pro	Lys	Phe	Tyr	His	Lys	Phe	Leu	
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tcg	cta	gaa	acc	gaa	agc	att	gaa	gtg	aat	ttt	gat	ttt	tat	ggg	aaa	912
Ser	Leu	Glu	Thr	Glu	Ser	Ile	Glu	Val	Asn	Phe	Asp	Phe	Tyr	Gly	Lys	
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Ser	Phe	Ile	Gln	Lys	Leu	His	Glu	Asp	His	Gln	Lys	Lys	Met	Gly	Leu	
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Ile	Val	Val	Gly	Arg	Glu	Leu	Phe	Leu	Ser	Lys	Lys	His	Arg	Lys	Ala	
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cta	tat	aaa	aca	gcc	acc	ccg	gtt	tat	aaa	acc	aac	act	tcc	ggc	ttg	1056
Leu	Tyr	Lys	Thr	Ala	Thr	Pro	Val	Tyr	Lys	Thr	Asn	Thr	Ser	Gly	Leu	
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tct	aaa	acc	tct	caa	agc	gtg	gtg	gtg	ttg	aat	gaa	agc	ttg	gat	atc	1104
Ser	Lys	Thr	Ser	Gln	Ser	Val	Val	Val	Leu	Asn	Glu	Ser	Leu	Asp	Ile	
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aat	gag	gac	atg	tct	tca	gtg	atc	ttt	gat	gtg	tct	atg	caa	atg	gat	1152
Asn	Glu	Asp	Met	Ser	Ser	Val	Ile	Phe	Asp	Val	Ser	Met	Gln	Met	Asp	
	370					375					380					
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Leu	Gly	Leu	Leu	Leu	Tyr	Asp	Phe	Asp	Pro	Asn	Lys	Arg	Tyr	Lys	Asn	
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gag	att	gtc	aat	cat	tat	gaa	aat	tta	gcc	aac	acg	ctc	aac	cgc	aag	1248
Glu	Ile	Val	Asn	His	Tyr	Glu	Asn	Leu	Ala	Asn	Thr	Leu	Asn	Arg	Lys	
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Ile	Glu	Ile	Phe	Gln	Thr	Asp	Ile	Arg	Asn	Pro	Ile	Met	Tyr	Leu	Asn	
			420					425					430			
tct	tta	aga	aat	ccc	att	ttg	cat	ttc	atg	cct	ttt	gaa	gag	tgc	atc	1344
Ser	Leu	Arg	Asn	Pro	Ile	Leu	His	Phe	Met	Pro	Phe	Glu	Glu	Cys	Ile	
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Thr	His	Thr	Arg	Phe	Trp	Trp	Phe	Leu	Ser	Thr	Lys	Val	Glu	Lys	Leu	
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gcg	ttt	tta	aac	gat	gat	aac	cct	caa	att	ttt	atc	cct	gta	gcg	gag	1440
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1443

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<213> Helicobacter pylori

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Ile Val Val Val Lys Asn Glu Ser Leu Ile Pro Lys Asn Tyr Pro Ser  
35 40 45

Thr Phe Ala Phe Tyr Cys Phe Asp Ala Thr Ser Ser Phe Arg Leu Leu  
50 55 60

Gln Val Leu Asn Asp Glu Val Ser Asp Ala Phe Leu Ile Ile Gln Asp  
65 70 75 80

Phe Lys Glu Gln Arg Ile Ile His Lys Ile Ile Gln Thr His Phe Lys  
85 90 95

Arg Met Arg Val Val Leu Ser Val Lys Lys Asp Gly Glu Lys Thr Leu  
100 105 110

Glu Asn Asn Glu Glu Asn Lys Asp Glu Lys Leu Ile Leu Ile Asp Glu  
115 120 125

Phe Glu Val Leu Ala Asn Lys Phe Ile Ser Arg Leu Pro Asn Ile Pro  
130 135 140

Ser Thr Pro Arg Glu Phe Gly Leu Gly Lys Gly Glu Ile Met Glu Ile  
145 150 155 160

Asp Val Pro Phe Gly Ser Ile Phe Ala Tyr Arg His Ile Gly Ser Ile  
165 170 175

Arg	Gln	Lys	Glu	Tyr	Arg	Ile	Val	Gly	Leu	Tyr	Arg	Asn	Asp	Val	Leu	
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Leu	Leu	Ser	Thr	Lys	Ser	Leu	Val	Ile	Gln	Pro	Arg	Asp	Ile	Leu	Leu	
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Val	Ala	Gly	Asn	Pro	Glu	Ile	Leu	Asn	Ala	Val	Tyr	Leu	Gln	Val	Lys	
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Ser	Asn	Val	Gly	Gln	Phe	Pro	Ala	Pro	Phe	Gly	Lys	Ser	Ile	Tyr	Leu	
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Tyr	Ile	Asp	Met	Arg	Leu	Gln	Ser	Arg	Lys	Ala	Met	Met	Arg	Asp	Val	
				245					250					255		
Tyr	Gln	Ala	Leu	Phe	Leu	His	Lys	His	Leu	Lys	Ser	Tyr	Lys	Leu	Tyr	
			260					265					270			
Ile	Gln	Val	Leu	His	Pro	Thr	Ser	Pro	Lys	Phe	Tyr	His	Lys	Phe	Leu	
		275					280						285			
Ser	Leu	Glu	Thr	Glu	Ser	Ile	Glu	Val	Asn	Phe	Asp	Phe	Tyr	Gly	Lys	
	290					295					300					
Ser	Phe	Ile	Gln	Lys	Leu	His	Glu	Asp	His	Gln	Lys	Lys	Met	Gly	Leu	
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Leu	Tyr	Lys	Thr	Ala	Thr	Pro	Val	Tyr	Lys	Thr	Asn	Thr	Ser	Gly	Leu	
			340					345					350			
Ser	Lys	Thr	Ser	Gln	Ser	Val	Val	Val	Leu	Asn	Glu	Ser	Leu	Asp	Ile	
		355					360					365				
Asn	Glu	Asp	Met	Ser	Ser	Val	Ile	Phe	Asp	Val	Ser	Met	Gln	Met	Asp	
	370					375					380					
Leu	Gly	Leu	Leu	Leu	Tyr	Asp	Phe	Asp	Pro	Asn	Lys	Arg	Tyr	Lys	Asn	
385					390					395					400	

Glu Ile Val Asn His Tyr Glu Asn Leu Ala Asn Thr Leu Asn Arg Lys  
405 410 415

Ile Glu Ile Phe Gln Thr Asp Ile Arg Asn Pro Ile Met Tyr Leu Asn  
420 425 430

Ser Leu Arg Asn Pro Ile Leu His Phe Met Pro Phe Glu Glu Cys Ile  
435 440 445

Thr His Thr Arg Phe Trp Trp Phe Leu Ser Thr Lys Val Glu Lys Leu  
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gca att gcc tta aac cac tta aac gct gtg gct atg att gtg gat aat 96  
Ala Ile Ala Leu Asn His Leu Asn Ala Val Ala Met Ile Val Asp Asn  
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cct acg cag aac gct tgg aat ggt gct aaa aga gca tgg gat gaa agc 144  
Pro Thr Gln Asn Ala Trp Asn Gly Ala Lys Arg Ala Trp Asp Glu Ser  
35 40 45  
aag tgg gct aaa cat tta gcc act att act gaa agg atc aag ctc gct 192  
Lys Trp Ala Lys His Leu Ala Thr Ile Thr Glu Arg Ile Lys Leu Ala  
50 55 60  
caa gac aca tta gat agg gct aat cag acg ctt aat tcc atc aac aaa 240  
Gln Asp Thr Leu Asp Arg Ala Asn Gln Thr Leu Asn Ser Ile Asn Lys  
65 70 75 80  
gtg aat gat gtt ttg aac aaa acc aat caa ttt cta aca ggc agt att 288  
Val Asn Asp Val Leu Asn Lys Thr Asn Gln Phe Leu Thr Gly Ser Ile  
85 90 95

tta agc atc ccc aat ccc atg cag tat gta gaa aaa atc caa agt ttt	336
Leu Ser Ile Pro Asn Pro Met Gln Tyr Val Glu Lys Ile Gln Ser Phe	
100 105 110	
gcc aag caa gtt caa gcc aat act gaa agg atc aaa gaa aat gca caa	384
Ala Lys Gln Val Gln Ala Asn Thr Glu Arg Ile Lys Glu Asn Ala Gln	
115 120 125	
aac tat gat ata cgc aat caa att gca gcc aaa cgc atc tct gaa aaa	432
Asn Tyr Asp Ile Arg Asn Gln Ile Ala Ala Lys Arg Ile Ser Glu Lys	
130 135 140	
tgc cct gaa ctc aat tgg gat gtc agt caa gac gcg agc cct aca gag	480
Cys Pro Glu Leu Asn Trp Asp Val Ser Gln Asp Ala Ser Pro Thr Glu	
145 150 155 160	
aaa aac tta cac caa ttt ttc acg agc aag ggg aaa gaa agc gct aac	528
Lys Asn Leu His Gln Phe Phe Thr Ser Lys Gly Lys Glu Ser Ala Asn	
165 170 175	
aca aag gct cta aag gat ttt gct aac gcc ata ggt aac act caa atc	576
Thr Lys Ala Leu Lys Asp Phe Ala Asn Ala Ile Gly Asn Thr Gln Ile	
180 185 190	
agc acg gcg aac gat tta gga gct gga ctt aga ggc aga gcc tta tta	624
Ser Thr Ala Asn Asp Leu Gly Ala Gly Leu Arg Gly Arg Ala Leu Leu	
195 200 205	
gaa tac att tgc att caa aaa ggc aat tta gaa gcg gct aaa aaa atc	672
Glu Tyr Ile Cys Ile Gln Lys Gly Asn Leu Glu Ala Ala Lys Lys Ile	
210 215 220	
caa tta tta gac agc caa atg act tta gct cta ctc aat aac gac tat	720
Gln Leu Leu Asp Ser Gln Met Thr Leu Ala Leu Leu Asn Asn Asp Tyr	
225 230 235 240	
acg gct tat gaa aaa ctt aga gct gaa aaa gaa gaa tta aaa aga caa	768
Thr Ala Tyr Glu Lys Leu Arg Ala Glu Lys Glu Glu Leu Lys Arg Gln	
245 250 255	
atc gct tca aat gtg tat gcg aaa gtc aaa cag ctt gtt gta gct tcc	816
Ile Ala Ser Asn Val Tyr Ala Lys Val Lys Gln Leu Val Val Ala Ser	
260 265 270	
caa gat aga gcg ttt agt caa atg gat aat gag ttg ggc gtt aaa act	864
Gln Asp Arg Ala Phe Ser Gln Met Asp Asn Glu Leu Gly Val Lys Thr	
275 280 285	
ttt ggg ttc aac gat gag aat gtt aaa aaa ggt tat tgc aag aaa gaa	912
Phe Gly Phe Asn Asp Glu Asn Val Lys Lys Gly Tyr Cys Lys Lys Glu	
290 295 300	
aac aga aat ggc aaa agc gag tgc atc cct aac atg ctc aat gtt aat	960
Asn Arg Asn Gly Lys Ser Glu Cys Ile Pro Asn Met Leu Asn Val Asn	

305	310	315	320	
cgc tta aaa gcg caa ttt gat gag ctt aat tta gat tat agt agg gat				1008
Arg Leu Lys Ala Gln Phe Asp Glu Leu Asn Leu Asp Tyr Ser Arg Asp	325	330	335	
att gct ggt aaa aaa ggt gaa gca gcc gct aaa gtg ttc aat gac tac				1056
Ile Ala Gly Lys Lys Gly Glu Ala Ala Lys Val Phe Asn Asp Tyr	340	345	350	
aaa cac cga ttc caa caa tta agc gta gaa act gct tta gaa atc gct				1104
Lys His Arg Phe Gln Gln Leu Ser Val Glu Thr Ala Leu Glu Ile Ala	355	360	365	
caa aat tta agt ttt atg aat aag acg cta ggt tta atg gtg caa atg				1152
Gln Asn Leu Ser Phe Met Asn Lys Thr Leu Gly Leu Met Val Gln Met	370	375	380	
caa agc tat gca ttc aag caa caa atg ggc tat ttt gaa gat att att				1200
Gln Ser Tyr Ala Phe Lys Gln Gln Met Gly Tyr Phe Glu Asp Ile Ile	385	390	395	400
cct gct gac gcc cta aaa gat gac aaa gag cat caa gaa aat ctt gaa				1248
Pro Ala Asp Ala Leu Lys Asp Asp Lys Glu His Gln Glu Asn Leu Glu	405	410	415	
caa aaa caa caa gaa ata gag aaa gtc tat agg gct aaa tta gac gct				1296
Gln Lys Gln Gln Glu Ile Glu Lys Val Tyr Arg Ala Lys Leu Asp Ala	420	425	430	
tat ggt ttc cct aat ggt agt gta gga aag gca agt ggc gtg aat tca				1344
Tyr Gly Phe Pro Asn Gly Ser Val Gly Lys Ala Ser Gly Val Asn Ser	435	440	445	
aat agt aat aat gaa gcc cca agc tct gat aat atc cag tcg ttt aat				1392
Asn Ser Asn Asn Glu Ala Pro Ser Ser Asp Asn Ile Gln Ser Phe Asn	450	455	460	
ccg tat tga				1401
Pro Tyr				
465				

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 <213> Helicobacter pylori

<400> 160

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20

25

30

Pro Thr Gln Asn Ala Trp Asn Gly Ala Lys Arg Ala Trp Asp Glu Ser  
35 40 45

Lys Trp Ala Lys His Leu Ala Thr Ile Thr Glu Arg Ile Lys Leu Ala  
50 55 60

Gln Asp Thr Leu Asp Arg Ala Asn Gln Thr Leu Asn Ser Ile Asn Lys  
65 70 75 80

Val Asn Asp Val Leu Asn Lys Thr Asn Gln Phe Leu Thr Gly Ser Ile  
85 90 95

Leu Ser Ile Pro Asn Pro Met Gln Tyr Val Glu Lys Ile Gln Ser Phe  
100 105 110

Ala Lys Gln Val Gln Ala Asn Thr Glu Arg Ile Lys Glu Asn Ala Gln  
115 120 125

Asn Tyr Asp Ile Arg Asn Gln Ile Ala Ala Lys Arg Ile Ser Glu Lys  
130 135 140

Cys Pro Glu Leu Asn Trp Asp Val Ser Gln Asp Ala Ser Pro Thr Glu  
145 150 155 160

Lys Asn Leu His Gln Phe Phe Thr Ser Lys Gly Lys Glu Ser Ala Asn  
165 170 175

Thr Lys Ala Leu Lys Asp Phe Ala Asn Ala Ile Gly Asn Thr Gln Ile  
180 185 190

Ser Thr Ala Asn Asp Leu Gly Ala Gly Leu Arg Gly Arg Ala Leu Leu  
195 200 205

Glu Tyr Ile Cys Ile Gln Lys Gly Asn Leu Glu Ala Ala Lys Lys Ile  
210 215 220

Gln Leu Leu Asp Ser Gln Met Thr Leu Ala Leu Leu Asn Asn Asp Tyr  
225 230 235 240

Thr	Ala	Tyr	Glu	Lys	Leu	Arg	Ala	Glu	Lys	Glu	Glu	Leu	Lys	Arg	Gln	
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Ile	Ala	Ser	Asn	Val	Tyr	Ala	Lys	Val	Lys	Gln	Leu	Val	Val	Ala	Ser	
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Gln	Asp	Arg	Ala	Phe	Ser	Gln	Met	Asp	Asn	Glu	Leu	Gly	Val	Lys	Thr	
		275					280					285				
Phe	Gly	Phe	Asn	Asp	Glu	Asn	Val	Lys	Lys	Gly	Tyr	Cys	Lys	Lys	Glu	
	290					295					300					
Asn	Arg	Asn	Gly	Lys	Ser	Glu	Cys	Ile	Pro	Asn	Met	Leu	Asn	Val	Asn	
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Arg	Leu	Lys	Ala	Gln	Phe	Asp	Glu	Leu	Asn	Leu	Asp	Tyr	Ser	Arg	Asp	
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Ile	Ala	Gly	Lys	Lys	Gly	Glu	Ala	Ala	Ala	Lys	Val	Phe	Asn	Asp	Tyr	
			340					345					350			
Lys	His	Arg	Phe	Gln	Gln	Leu	Ser	Val	Glu	Thr	Ala	Leu	Glu	Ile	Ala	
		355					360					365				
Gln	Asn	Leu	Ser	Phe	Met	Asn	Lys	Thr	Leu	Gly	Leu	Met	Val	Gln	Met	
	370					375					380					
Gln	Ser	Tyr	Ala	Phe	Lys	Gln	Gln	Met	Gly	Tyr	Phe	Glu	Asp	Ile	Ile	
385					390					395					400	
Pro	Ala	Asp	Ala	Leu	Lys	Asp	Asp	Lys	Glu	His	Gln	Glu	Asn	Leu	Glu	
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Gln	Lys	Gln	Gln	Glu	Ile	Glu	Lys	Val	Tyr	Arg	Ala	Lys	Leu	Asp	Ala	
			420					425					430			
Tyr	Gly	Phe	Pro	Asn	Gly	Ser	Val	Gly	Lys	Ala	Ser	Gly	Val	Asn	Ser	
		435					440					445				
Asn	Ser	Asn	Asn	Glu	Ala	Pro	Ser	Ser	Asp	Asn	Ile	Gln	Ser	Phe	Asn	
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Pro Tyr  
465

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ggt tta tta gcg ttt tta acc cta tct tca tgg ctg ggt aat agc ggt      96
Val Leu Leu Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn Ser Gly
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tta gtg ggg cgt ttt ggg gtg tgg ttt gcc gca ctc aat aaa aaa tat      144
Leu Val Gly Arg Phe Gly Val Trp Phe Ala Ala Leu Asn Lys Lys Tyr
                35                               40          45

ttt ggg cat ctt tca ttc att aat tta ccc tat tta gca tgg gtt tta      192
Phe Gly His Leu Ser Phe Ile Asn Leu Pro Tyr Leu Ala Trp Val Leu
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ttc ctt tta tac aag act aaa aac cct ttt aca gaa atc gtt tta gaa      240
Phe Leu Leu Tyr Lys Thr Lys Asn Pro Phe Thr Glu Ile Val Leu Glu
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aaa act tta ggg cat cta tta ggc att tta tct ttg ctc ttt tta caa      288
Lys Thr Leu Gly His Leu Leu Gly Ile Leu Ser Leu Leu Phe Leu Gln
                85                               90          95

tct agc cta tta aat caa ggg gaa atc ggc aac agc gcg cgt ttg ttt      336
Ser Ser Leu Leu Asn Gln Gly Glu Ile Gly Asn Ser Ala Arg Leu Phe
                100                              105          110

tta cgc cct ttt ata ggg gat ttt ggg ctt tat gcg ctg ata acg ctt      384
Leu Arg Pro Phe Ile Gly Asp Phe Gly Leu Tyr Ala Leu Ile Thr Leu
                115                              120          125

atg gta gtt att tct tat ttg att cta ttc aaa cta ccc cct aaa agc      432
Met Val Val Ile Ser Tyr Leu Ile Leu Phe Lys Leu Pro Pro Lys Ser
                130                              135          140

ggt ttt tat cct tat atg aac aaa aca caa aac ctt tta aaa gag att      480
Val Phe Tyr Pro Tyr Met Asn Lys Thr Gln Asn Leu Leu Lys Glu Ile
145                              150          155          160

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			165						170					175		
gag	ggt	ttt	gaa	aac	acc	cca	tca	gat	att	caa	aaa	aaa	gaa	acc	aaa	576
Glu	Gly	Phe	Glu	Asn	Thr	Pro	Ser	Asp	Ile	Gln	Lys	Lys	Glu	Thr	Lys	
			180					185					190			
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Asn	Asp	Lys	Glu	Lys	Glu	Asn	Arg	Lys	Glu	Asn	Pro	Ile	Asn	Glu	Asn	
		195					200					205				
cac	aaa	acc	cct	aac	gaa	gaa	ccg	ttt	tta	gcg	atc	cct	acc	ccc	tat	672
His	Lys	Thr	Pro	Asn	Glu	Glu	Pro	Phe	Leu	Ala	Ile	Pro	Thr	Pro	Tyr	
	210					215					220					
aac	acg	act	tta	aat	gat	tca	gag	ccg	caa	gaa	ggc	tta	gtc	caa	att	720
Asn	Thr	Thr	Leu	Asn	Asp	Ser	Glu	Pro	Gln	Glu	Gly	Leu	Val	Gln	Ile	
225					230					235					240	
tcc	tcc	cac	ccc	cct	acc	cat	tac	acc	att	tac	cct	aaa	aga	aac	cga	768
Ser	Ser	His	Pro	Pro	Thr	His	Tyr	Thr	Ile	Tyr	Pro	Lys	Arg	Asn	Arg	
			245						250					255		
ttt	gat	gat	ttg	act	aac	ccc	act	aac	ccc	cct	tta	aaa	gaa	att	aaa	816
Phe	Asp	Asp	Leu	Thr	Asn	Pro	Thr	Asn	Pro	Pro	Leu	Lys	Glu	Ile	Lys	
			260					265					270			
caa	gaa	act	aaa	gaa	aga	gaa	ccc	acg	cct	aca	aaa	gaa	act	ctt	acg	864
Gln	Glu	Thr	Lys	Glu	Arg	Glu	Pro	Thr	Pro	Thr	Lys	Glu	Thr	Leu	Thr	
		275					280					285				
ccc	acc	acg	ccc	aaa	cct	atc	atg	ccc	aca	ctt	gca	ccc	ata	ata	gaa	912
Pro	Thr	Thr	Pro	Lys	Pro	Ile	Met	Pro	Thr	Leu	Ala	Pro	Ile	Ile	Glu	
	290					295					300					
aat	gac	aac	aaa	aca	gaa	aac	caa	aaa	acc	ccc	aac	cac	cct	aaa	aaa	960
Asn	Asp	Asn	Lys	Thr	Glu	Asn	Gln	Lys	Thr	Pro	Asn	His	Pro	Lys	Lys	
305					310					315					320	
gaa	gaa	aac	cca	caa	gaa	aac	acg	caa	gaa	gaa	atg	ata	gaa	gga	agg	1008
Glu	Glu	Asn	Pro	Gln	Glu	Asn	Thr	Gln	Glu	Glu	Met	Ile	Glu	Gly	Arg	
			325						330					335		
ata	gaa	gaa	atg	ata	aag	gaa	aat	cta	aaa	aaa	gaa	gaa	aaa	gaa	gtg	1056
Ile	Glu	Glu	Met	Ile	Lys	Glu	Asn	Leu	Lys	Lys	Glu	Glu	Lys	Glu	Val	
			340					345					350			
caa	aac	gct	cca	aac	ttt	agc	cca	gta	acc	ccc	aca	agc	gct	aaa	aaa	1104
Gln	Asn	Ala	Pro	Asn	Phe	Ser	Pro	Val	Thr	Pro	Thr	Ser	Ala	Lys	Lys	
		355					360					365				
ccc	gtt	atg	gtt	aaa	gaa	ttg	agc	gaa	aat	aaa	gag	ata	tta	gac	gga	1152
Pro	Val	Met	Val	Lys	Glu	Leu	Ser	Glu	Asn	Lys	Glu	Ile	Leu	Asp	Gly	

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acg caa tta ttg aat gcg gtt tgt ttg aaa gac act tct tta gac gaa Thr Gln Leu Leu Asn Ala Val Cys Leu Lys Asp Thr Ser Leu Asp Glu 405 410 415			1248
aac gag att gac caa aaa atc cag gat cta ttg agc aaa ctg cgc acc Asn Glu Ile Asp Gln Lys Ile Gln Asp Leu Leu Ser Lys Leu Arg Thr 420 425 430			1296
ttt aaa att gat ggc gat att atc cgc act tat tca ggc cct att gta Phe Lys Ile Asp Gly Asp Ile Ile Arg Thr Tyr Ser Gly Pro Ile Val 435 440 445			1344
acc act ttt gaa ttc cgc cca gcc cct aac gtt aag gtg agt cgt att Thr Thr Phe Glu Phe Arg Pro Ala Pro Asn Val Lys Val Ser Arg Ile 450 455 460			1392
tta ggc ttg agc gat gat tta gcg atg act tta tgc gct gaa tcc atc Leu Gly Leu Ser Asp Asp Leu Ala Met Thr Leu Cys Ala Glu Ser Ile 465 470 475 480			1440
cgc att caa gcc cct att aag ggt aaa gat gtc gtt ggc att gaa atc Arg Ile Gln Ala Pro Ile Lys Gly Lys Asp Val Val Gly Ile Glu Ile 485 490 495			1488
cct aac agc caa agc caa att att tat tta aga gaa att cta gag agc Pro Asn Ser Gln Ser Gln Ile Ile Tyr Leu Arg Glu Ile Leu Glu Ser 500 505 510			1536
gaa ttg ttt caa aaa tcc agc tcg ccc tta act cta gct tta ggc aaa Glu Leu Phe Gln Lys Ser Ser Ser Pro Leu Thr Leu Ala Leu Gly Lys 515 520 525			1584
gac att gtg ggt aac cct ttc atc acg gat tta aaa aag ctc ccc cat Asp Ile Val Gly Asn Pro Phe Ile Thr Asp Leu Lys Lys Leu Pro His 530 535 540			1632
ttg ctc atc gct ggc acg aca gga agc ggt aag agc gtg ggc gtg aat Leu Leu Ile Ala Gly Thr Thr Gly Ser Gly Lys Ser Val Gly Val Asn 545 550 555 560			1680
gcg atg att tta tcc tta ctt tat aaa aac cct ccc gat caa ctc aaa Ala Met Ile Leu Ser Leu Leu Tyr Lys Asn Pro Pro Asp Gln Leu Lys 565 570 575			1728
tta gtg atg atc gat ccc aaa atg gta gaa ttt agt att tat gcg gat Leu Val Met Ile Asp Pro Lys Met Val Glu Phe Ser Ile Tyr Ala Asp 580 585 590			1776
atc cct cat ttg ctc acg ccc att atc acc gac cct aaa aaa gct att			1824

Ile	Pro	His	Leu	Leu	Thr	Pro	Ile	Ile	Thr	Asp	Pro	Lys	Lys	Ala	Ile	
		595					600					605				
ggg	gct	ttg	caa	agc	gtg	gct	aaa	gaa	atg	gaa	cgc	cgg	tat	tct	tta	1872
Gly	Ala	Leu	Gln	Ser	Val	Ala	Lys	Glu	Met	Glu	Arg	Arg	Tyr	Ser	Leu	
	610					615				620						
atg	agc	gaa	tac	aag	ggt	aaa	acc	att	gat	tct	tat	aat	gaa	caa	gcc	1920
Met	Ser	Glu	Tyr	Lys	Val	Lys	Thr	Ile	Asp	Ser	Tyr	Asn	Glu	Gln	Ala	
625					630				635						640	
cca	agt	aac	ggc	ggt	gaa	gcg	ttc	ccc	tat	ttg	att	gtg	gtg	att	gat	1968
Pro	Ser	Asn	Gly	Val	Glu	Ala	Phe	Pro	Tyr	Leu	Ile	Val	Val	Ile	Asp	
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gaa	tta	gcg	gat	tta	atg	atg	aca	ggg	ggc	aaa	gaa	gcg	gag	ttt	cct	2016
Glu	Leu	Ala	Asp	Leu	Met	Met	Thr	Gly	Gly	Lys	Glu	Ala	Glu	Phe	Pro	
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Ile	Ala	Arg	Ile	Ala	Gln	Met	Gly	Arg	Ala	Ser	Gly	Leu	His	Leu	Ile	
		675					680					685				
gta	gcg	acc	caa	cgc	cca	agc	gtg	gat	gtc	gta	acc	ggc	ttg	att	aaa	2112
Val	Ala	Thr	Gln	Arg	Pro	Ser	Val	Asp	Val	Val	Thr	Gly	Leu	Ile	Lys	
	690					695					700					
acc	aac	ttg	cct	tca	agg	gtg	agt	ttt	agg	gta	ggc	act	aag	att	gat	2160
Thr	Asn	Leu	Pro	Ser	Arg	Val	Ser	Phe	Arg	Val	Gly	Thr	Lys	Ile	Asp	
705					710				715						720	
tct	aaa	gtg	att	tta	gac	act	gat	ggg	gcg	caa	agc	ttg	tta	gga	aga	2208
Ser	Lys	Val	Ile	Leu	Asp	Thr	Asp	Gly	Ala	Gln	Ser	Leu	Leu	Gly	Arg	
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ggc	gat	atg	ctc	ttt	acc	ccc	cca	gga	gcg	aac	ggg	tta	gtg	cgc	ttg	2256
Gly	Asp	Met	Leu	Phe	Thr	Pro	Pro	Gly	Ala	Asn	Gly	Leu	Val	Arg	Leu	
			740					745				750				
cat	gcc	ccc	ttt	gcc	act	gaa	gat	gaa	atc	aaa	aaa	atc	gtg	gat	ttt	2304
His	Ala	Pro	Phe	Ala	Thr	Glu	Asp	Glu	Ile	Lys	Lys	Ile	Val	Asp	Phe	
		755					760					765				
att	aaa	gcc	caa	aaa	gaa	gta	caa	tac	gat	aaa	gat	ttc	ttg	cta	gaa	2352
Ile	Lys	Ala	Gln	Lys	Glu	Val	Gln	Tyr	Asp	Lys	Asp	Phe	Leu	Leu	Glu	
	770					775					780					
gaa	tca	cgc	atg	cct	tta	gac	acc	cct	aat	tat	caa	ggc	gat	gac	att	2400
Glu	Ser	Arg	Met	Pro	Leu	Asp	Thr	Pro	Asn	Tyr	Gln	Gly	Asp	Asp	Ile	
785					790				795						800	
tta	gaa	agg	gct	aaa	gcg	gtg	att	tta	gaa	aaa	aag	atc	act	tct	acg	2448
Leu	Glu	Arg	Ala	Lys	Ala	Val	Ile	Leu	Glu	Lys	Lys	Ile	Thr	Ser	Thr	
				805					810					815		

agc ttt tta caa cgc caa tta aaa atc ggc tac aac caa gcc gct acc 2496  
 Ser Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala Ala Thr  
 820 825 830

att act gac gaa tta gaa gct caa ggc ttt tta tcc cca aga aac gct 2544  
 Ile Thr Asp Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg Asn Ala  
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 <213> Helicobacter pylori

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Leu Val Gly Arg Phe Gly Val Trp Phe Ala Ala Leu Asn Lys Lys Tyr  
 35 40 45

Phe Gly His Leu Ser Phe Ile Asn Leu Pro Tyr Leu Ala Trp Val Leu  
 50 55 60

Phe Leu Leu Tyr Lys Thr Lys Asn Pro Phe Thr Glu Ile Val Leu Glu  
 65 70 75 80

Lys Thr Leu Gly His Leu Leu Gly Ile Leu Ser Leu Leu Phe Leu Gln  
 85 90 95

Ser Ser Leu Leu Asn Gln Gly Glu Ile Gly Asn Ser Ala Arg Leu Phe  
 100 105 110

Leu Arg Pro Phe Ile Gly Asp Phe Gly Leu Tyr Ala Leu Ile Thr Leu  
 115 120 125

Met Val Val Ile Ser Tyr Leu Ile Leu Phe Lys Leu Pro Pro Lys Ser  
 130 135 140

Val Phe Tyr Pro Tyr Met Asn Lys Thr Gln Asn Leu Leu Lys Glu Ile  
145 150 155 160

Tyr Lys Gln Cys Leu Gln Ala Phe Ser Pro Asn Phe Ser Pro Lys Lys  
165 170 175

Glu Gly Phe Glu Asn Thr Pro Ser Asp Ile Gln Lys Lys Glu Thr Lys  
180 185 190

Asn Asp Lys Glu Lys Glu Asn Arg Lys Glu Asn Pro Ile Asn Glu Asn  
195 200 205

His Lys Thr Pro Asn Glu Glu Pro Phe Leu Ala Ile Pro Thr Pro Tyr  
210 215 220

Asn Thr Thr Leu Asn Asp Ser Glu Pro Gln Glu Gly Leu Val Gln Ile  
225 230 235 240

Ser Ser His Pro Pro Thr His Tyr Thr Ile Tyr Pro Lys Arg Asn Arg  
245 250 255

Phe Asp Asp Leu Thr Asn Pro Thr Asn Pro Pro Leu Lys Glu Ile Lys  
260 265 270

Gln Glu Thr Lys Glu Arg Glu Pro Thr Pro Thr Lys Glu Thr Leu Thr  
275 280 285

Pro Thr Thr Pro Lys Pro Ile Met Pro Thr Leu Ala Pro Ile Ile Glu  
290 295 300

Asn Asp Asn Lys Thr Glu Asn Gln Lys Thr Pro Asn His Pro Lys Lys  
305 310 315 320

Glu Glu Asn Pro Gln Glu Asn Thr Gln Glu Glu Met Ile Glu Gly Arg  
325 330 335

Ile Glu Glu Met Ile Lys Glu Asn Leu Lys Lys Glu Glu Lys Glu Val  
340 345 350

Gln Asn Ala Pro Asn Phe Ser Pro Val Thr Pro Thr Ser Ala Lys Lys  
355 360 365

Pro Val Met Val Lys Glu Leu Ser Glu Asn Lys Glu Ile Leu Asp Gly  
 370 375 380

Leu Asp Tyr Gly Glu Val Gln Lys Pro Lys Asp Tyr Glu Leu Pro Thr  
 385 390 395 400

Thr Gln Leu Leu Asn Ala Val Cys Leu Lys Asp Thr Ser Leu Asp Glu  
 405 410 415

Asn Glu Ile Asp Gln Lys Ile Gln Asp Leu Leu Ser Lys Leu Arg Thr  
 420 425 430

Phe Lys Ile Asp Gly Asp Ile Ile Arg Thr Tyr Ser Gly Pro Ile Val  
 435 440 445

Thr Thr Phe Glu Phe Arg Pro Ala Pro Asn Val Lys Val Ser Arg Ile  
 450 455 460

Leu Gly Leu Ser Asp Asp Leu Ala Met Thr Leu Cys Ala Glu Ser Ile  
 465 470 475 480

Arg Ile Gln Ala Pro Ile Lys Gly Lys Asp Val Val Gly Ile Glu Ile  
 485 490 495

Pro Asn Ser Gln Ser Gln Ile Ile Tyr Leu Arg Glu Ile Leu Glu Ser  
 500 505 510

Glu Leu Phe Gln Lys Ser Ser Ser Pro Leu Thr Leu Ala Leu Gly Lys  
 515 520 525

Asp Ile Val Gly Asn Pro Phe Ile Thr Asp Leu Lys Lys Leu Pro His  
 530 535 540

Leu Leu Ile Ala Gly Thr Thr Gly Ser Gly Lys Ser Val Gly Val Asn  
 545 550 555 560

Ala Met Ile Leu Ser Leu Leu Tyr Lys Asn Pro Pro Asp Gln Leu Lys  
 565 570 575

Leu Val Met Ile Asp Pro Lys Met Val Glu Phe Ser Ile Tyr Ala Asp

580		585		590											
Ile	Pro	His	Leu	Leu	Thr	Pro	Ile	Ile	Thr	Asp	Pro	Lys	Lys	Ala	Ile
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Gly	Ala	Leu	Gln	Ser	Val	Ala	Lys	Glu	Met	Glu	Arg	Arg	Tyr	Ser	Leu
	610					615					620				
Met	Ser	Glu	Tyr	Lys	Val	Lys	Thr	Ile	Asp	Ser	Tyr	Asn	Glu	Gln	Ala
625					630					635					640
Pro	Ser	Asn	Gly	Val	Glu	Ala	Phe	Pro	Tyr	Leu	Ile	Val	Val	Ile	Asp
				645					650					655	
Glu	Leu	Ala	Asp	Leu	Met	Met	Thr	Gly	Gly	Lys	Glu	Ala	Glu	Phe	Pro
			660					665					670		
Ile	Ala	Arg	Ile	Ala	Gln	Met	Gly	Arg	Ala	Ser	Gly	Leu	His	Leu	Ile
		675					680					685			
Val	Ala	Thr	Gln	Arg	Pro	Ser	Val	Asp	Val	Val	Thr	Gly	Leu	Ile	Lys
	690					695					700				
Thr	Asn	Leu	Pro	Ser	Arg	Val	Ser	Phe	Arg	Val	Gly	Thr	Lys	Ile	Asp
705					710					715					720
Ser	Lys	Val	Ile	Leu	Asp	Thr	Asp	Gly	Ala	Gln	Ser	Leu	Leu	Gly	Arg
				725					730					735	
Gly	Asp	Met	Leu	Phe	Thr	Pro	Pro	Gly	Ala	Asn	Gly	Leu	Val	Arg	Leu
			740					745					750		
His	Ala	Pro	Phe	Ala	Thr	Glu	Asp	Glu	Ile	Lys	Lys	Ile	Val	Asp	Phe
		755					760					765			
Ile	Lys	Ala	Gln	Lys	Glu	Val	Gln	Tyr	Asp	Lys	Asp	Phe	Leu	Leu	Glu
	770					775					780				
Glu	Ser	Arg	Met	Pro	Leu	Asp	Thr	Pro	Asn	Tyr	Gln	Gly	Asp	Asp	Ile
785					790					795					800



Leu Glu Arg Ala Lys Ala Val Ile Leu Glu Lys Lys Ile Thr Ser Thr  
805 810 815

Ser Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala Ala Thr  
820 825 830

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agc gcg ata ggt tta ggg cat atc tgg cgt ttc ccc tac atg act ggg 96  
Ser Ala Ile Gly Leu Gly His Ile Trp Arg Phe Pro Tyr Met Thr Gly  
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Val Ser Gly Gly Gly Ala Phe Val Leu Leu Phe Leu Phe Leu Ser Leu  
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Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu Gly Gln Ser  
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Thr Gln Lys Asn Val Thr Glu Ala Phe Lys Glu Leu Asp Ile Asn Pro  
65 70 75 80  
aaa aaa cgc tgg aaa tac gca ggg ctt ttg ctt gtt tct ggg cca tta 288  
Lys Lys Arg Trp Lys Tyr Ala Gly Leu Leu Leu Val Ser Gly Pro Leu  
85 90 95  
ata ctg act ttt tac ggc acg att tta ggt tgg gtg ctt tat tat ttg 336  
Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu Tyr Tyr Leu  
100 105 110

gtg	agt	gtt	agt	ttt	aat	ttg	cct	aac	aat	atc	caa	gaa	tct	gaa	caa	384
Val	Ser	Val	Ser	Phe	Asn	Leu	Pro	Asn	Asn	Ile	Gln	Glu	Ser	Glu	Gln	
		115					120					125				
att	ttt	act	caa	act	ttg	cag	tct	ata	ggg	cta	caa	tcc	ata	ggg	ctt	432
Ile	Phe	Thr	Gln	Thr	Leu	Gln	Ser	Ile	Gly	Leu	Gln	Ser	Ile	Gly	Leu	
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Phe	Ser	Val	Leu	Leu	Ile	Thr	Gly	Trp	Ile	Val	Ser	Arg	Gly	Ile	Lys	
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gaa	ggc	att	gaa	aag	ctc	aat	ttg	gtt	tta	atg	ccc	tta	ctc	ttt	gct	528
Glu	Gly	Ile	Glu	Lys	Leu	Asn	Leu	Val	Leu	Met	Pro	Leu	Leu	Phe	Ala	
				165				170						175		
act	ttt	ttt	ggg	ttg	ctt	ttc	tat	gcg	atg	agc	atg	gat	tct	ttt	tct	576
Thr	Phe	Phe	Gly	Leu	Leu	Phe	Tyr	Ala	Met	Ser	Met	Asp	Ser	Phe	Ser	
			180					185					190			
aaa	gct	ttt	cat	ttc	atg	ttt	gat	ttc	aaa	cca	aaa	gat	ttg	acc	tct	624
Lys	Ala	Phe	His	Phe	Met	Phe	Asp	Phe	Lys	Pro	Lys	Asp	Leu	Thr	Ser	
		195					200					205				
caa	gtg	ttc	act	tat	tcc	ttg	ggg	cag	gtt	ttc	ttt	tcc	tta	agc	atc	672
Gln	Val	Phe	Thr	Tyr	Ser	Leu	Gly	Gln	Val	Phe	Phe	Ser	Leu	Ser	Ile	
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Gly	Leu	Gly	Ile	Asn	Ile	Thr	Tyr	Ala	Ala	Val	Thr	Asp	Lys	Thr	Gln	
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Asn	Leu	Leu	Lys	Ser	Thr	Ile	Trp	Val	Val	Leu	Ser	Gly	Ile	Leu	Ile	
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tct	ctt	gtg	gca	gga	ctt	atg	att	ttc	act	ttt	gtg	ttt	gaa	tat	ggg	816
Ser	Leu	Val	Ala	Gly	Leu	Met	Ile	Phe	Thr	Phe	Val	Phe	Glu	Tyr	Gly	
			260					265					270			
gcg	aat	gtc	tca	caa	ggc	aca	ggg	tta	atc	ttc	act	tct	tta	ccg	gtg	864
Ala	Asn	Val	Ser	Gln	Gly	Thr	Gly	Leu	Ile	Phe	Thr	Ser	Leu	Pro	Val	
		275					280					285				
gtt	ttt	ggc	caa	atg	gga	gcg	ata	ggc	att	ctt	gtt	tcg	att	ctt	ttc	912
Val	Phe	Gly	Gln	Met	Gly	Ala	Ile	Gly	Ile	Leu	Val	Ser	Ile	Leu	Phe	
	290					295					300					
ttg	ctc	gcg	ctc	gct	ttt	gct	ggc	atc	act	tct	acg	gtg	gct	tta	ttg	960
Leu	Leu	Ala	Leu	Ala	Phe	Ala	Gly	Ile	Thr	Ser	Thr	Val	Ala	Leu	Leu	
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gag	cca	agc	gtg	atg	tat	ctt	acc	gaa	agg	tat	caa	tac	tct	cgt	ttt	1008
Glu	Pro	Ser	Val	Met	Tyr	Leu	Thr	Glu	Arg	Tyr	Gln	Tyr	Ser	Arg	Phe	
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Lys Val Thr Trp Gly Leu Val Ala Leu Ile Phe Val Val Gly Val Val	
340 345 350	
ttg att ttc tcg ctc cat aag gat tat aaa gat tat ctc act ttc ttt	1104
Leu Ile Phe Ser Leu His Lys Asp Tyr Lys Asp Tyr Leu Thr Phe Phe	
355 360 365	
gaa aaa agt ctt ttt gat tgg ttg gat ttt gca tca agc acc att atc	1152
Glu Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser Ser Thr Ile Ile	
370 375 380	
atg cct tta ggc ggg atg gca acc ttt att ttt atg ggt tgg gtt ttg	1200
Met Pro Leu Gly Gly Met Ala Thr Phe Ile Phe Met Gly Trp Val Leu	
385 390 395 400	
aaa aaa gaa aaa ttg cgt ctt ttg agc gtg cac ttt tta ggc cct aaa	1248
Lys Lys Glu Lys Leu Arg Leu Leu Ser Val His Phe Leu Gly Pro Lys	
405 410 415	
ttg ttt gca act tgg tat ttc ttg ctt aaa tat atc acc cct tta att	1296
Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile Thr Pro Leu Ile	
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Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr	
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Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu Gly Gln Ser	
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Thr Gln Lys Asn Val Thr Glu Ala Phe Lys Glu Leu Asp Ile Asn Pro	
65 70 75 80	

Lys Lys Arg Trp Lys Tyr Ala Gly Leu Leu Leu Val Ser Gly Pro Leu  
85 90 95

Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu Tyr Tyr Leu  
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Val Ser Val Ser Phe Asn Leu Pro Asn Asn Ile Gln Glu Ser Glu Gln  
115 120 125

Ile Phe Thr Gln Thr Leu Gln Ser Ile Gly Leu Gln Ser Ile Gly Leu  
130 135 140

Phe Ser Val Leu Leu Ile Thr Gly Trp Ile Val Ser Arg Gly Ile Lys  
145 150 155 160

Glu Gly Ile Glu Lys Leu Asn Leu Val Leu Met Pro Leu Leu Phe Ala  
165 170 175

Thr Phe Phe Gly Leu Leu Phe Tyr Ala Met Ser Met Asp Ser Phe Ser  
180 185 190

Lys Ala Phe His Phe Met Phe Asp Phe Lys Pro Lys Asp Leu Thr Ser  
195 200 205

Gln Val Phe Thr Tyr Ser Leu Gly Gln Val Phe Phe Ser Leu Ser Ile  
210 215 220

Gly Leu Gly Ile Asn Ile Thr Tyr Ala Ala Val Thr Asp Lys Thr Gln  
225 230 235 240

Asn Leu Leu Lys Ser Thr Ile Trp Val Val Leu Ser Gly Ile Leu Ile  
245 250 255

Ser Leu Val Ala Gly Leu Met Ile Phe Thr Phe Val Phe Glu Tyr Gly  
260 265 270

Ala Asn Val Ser Gln Gly Thr Gly Leu Ile Phe Thr Ser Leu Pro Val  
275 280 285

Val Phe Gly Gln Met Gly Ala Ile Gly Ile Leu Val Ser Ile Leu Phe

290	295	300	
Leu Leu Ala Leu Ala Phe Ala Gly Ile Thr Ser Thr Val Ala Leu Leu			
305	310	315	320
Glu Pro Ser Val Met Tyr Leu Thr Glu Arg Tyr Gln Tyr Ser Arg Phe			
	325	330	335
Lys Val Thr Trp Gly Leu Val Ala Leu Ile Phe Val Val Gly Val Val			
	340	345	350
Leu Ile Phe Ser Leu His Lys Asp Tyr Lys Asp Tyr Leu Thr Phe Phe			
	355	360	365
Glu Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser Ser Thr Ile Ile			
	370	375	380
Met Pro Leu Gly Gly Met Ala Thr Phe Ile Phe Met Gly Trp Val Leu			
385	390	395	400
Lys Lys Glu Lys Leu Arg Leu Leu Ser Val His Phe Leu Gly Pro Lys			
	405	410	415
Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile Thr Pro Leu Ile			
	420	425	430
Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr			
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<210> 165  
 <211> 1785  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1785)

<400> 165		
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Val Val Phe Lys Ile Leu Gly Leu Trp Leu Gly Val Phe Cys Phe Leu		
1 5 10 15		
gag gct acg cct tat tta tac ttg ggc gaa gag cct aaa tat aaa gac		96

Glu	Ala	Thr	Pro	Tyr	Leu	Tyr	Leu	Gly	Glu	Glu	Pro	Lys	Tyr	Lys	Asp	
			20					25					30			
aat	ttc	acg	cat	ttt	gaa	tac	gct	aac	cct	aac	gct	aaa	aag	ggc	ggc	144
Asn	Phe	Thr	His	Phe	Glu	Tyr	Ala	Asn	Pro	Asn	Ala	Lys	Lys	Gly	Gly	
		35					40					45				
ggt	tta	agg	aat	gac	gcc	ata	ggg	act	ttt	gat	agc	ctt	aac	cct	ttc	192
Val	Leu	Arg	Asn	Asp	Ala	Ile	Gly	Thr	Phe	Asp	Ser	Leu	Asn	Pro	Phe	
	50					55					60					
gcg	ctt	aaa	ggc	act	aaa	gct	gaa	ggc	ttg	gat	ctg	att	tat	gac	act	240
Ala	Leu	Lys	Gly	Thr	Lys	Ala	Glu	Gly	Leu	Asp	Leu	Ile	Tyr	Asp	Thr	
65					70					75					80	
tta	atg	gtg	caa	agt	tta	gac	gaa	cct	ttt	gcc	gaa	tac	ccc	ttg	atc	288
Leu	Met	Val	Gln	Ser	Leu	Asp	Glu	Pro	Phe	Ala	Glu	Tyr	Pro	Leu	Ile	
				85					90					95		
gct	aaa	gac	gca	gaa	gtg	gct	aag	gat	aac	agc	tat	gtg	att	ttt	acg	336
Ala	Lys	Asp	Ala	Glu	Val	Ala	Lys	Asp	Asn	Ser	Tyr	Val	Ile	Phe	Thr	
			100					105					110			
ata	gat	aaa	aga	gcg	aga	ttt	agc	aac	aac	gct	ccc	att	tta	gcg	agc	384
Ile	Asp	Lys	Arg	Ala	Arg	Phe	Ser	Asn	Asn	Ala	Pro	Ile	Leu	Ala	Ser	
		115					120					125				
gac	gtg	aag	ttt	agt	ttt	gat	acg	atc	atg	aaa	tta	gga	tcg	cct	att	432
Asp	Val	Lys	Phe	Ser	Phe	Asp	Thr	Ile	Met	Lys	Leu	Gly	Ser	Pro	Ile	
	130					135					140					
tat	agg	cag	tat	tac	caa	gat	gtt	aaa	aag	gcg	gtt	gtt	tta	gac	aaa	480
Tyr	Arg	Gln	Tyr	Tyr	Gln	Asp	Val	Lys	Lys	Ala	Val	Val	Leu	Asp	Lys	
145					150					155					160	
cac	cat	gtt	aaa	ttc	att	ttc	aaa	acc	act	gaa	aat	aaa	gag	ttg	cct	528
His	His	Val	Lys	Phe	Ile	Phe	Lys	Thr	Thr	Glu	Asn	Lys	Glu	Leu	Pro	
				165				170						175		
ctc	att	tta	ggg	cag	ttg	cag	atc	ttt	tcc	aaa	aaa	gcg	ttt	caa	gag	576
Leu	Ile	Leu	Gly	Gln	Leu	Gln	Ile	Phe	Ser	Lys	Lys	Ala	Phe	Gln	Glu	
			180					185					190			
gat	tat	ttt	gaa	aaa	aac	ccc	tta	ctc	att	cct	gtt	tct	agc	ggc	cct	624
Asp	Tyr	Phe	Glu	Lys	Asn	Pro	Leu	Leu	Ile	Pro	Val	Ser	Ser	Gly	Pro	
		195					200					205				
tat	gtg	atc	gct	tct	ttt	gat	gtg	ggc	aag	aaa	atc	acc	tac	caa	aga	672
Tyr	Val	Ile	Ala	Ser	Phe	Asp	Val	Gly	Lys	Lys	Ile	Thr	Tyr	Gln	Arg	
	210					215					220					
aac	cct	aat	tat	tgg	gcg	agg	aat	ttg	cct	agc	aga	aag	ggg	caa	ttc	720
Asn	Pro	Asn	Tyr	Trp	Ala	Arg	Asn	Leu	Pro	Ser	Arg	Lys	Gly	Gln	Phe	
225					230					235					240	

aat ttt gat caa atc aaa ttt gag tat tac aaa gac gaa acc atc gcc Asn Phe Asp Gln Ile Lys Phe Glu Tyr Tyr Lys Asp Glu Thr Ile Ala 245 250 255	768
tta cag gct ttt tta agt ggg gcg tat gat tgg cgt ctt gaa agc acg Leu Gln Ala Phe Leu Ser Gly Ala Tyr Asp Trp Arg Leu Glu Ser Thr 260 265 270	816
gct aag gtt tgg gct agg ggc tat gtg ggg aaa gct atg gac aat aaa Ala Lys Val Trp Ala Arg Gly Tyr Val Gly Lys Ala Met Asp Asn Lys 275 280 285	864
gag att acg aaa tat ttg ata gcc cac aaa atg cca agc ggc atg caa Glu Ile Thr Lys Tyr Leu Ile Ala His Lys Met Pro Ser Gly Met Gln 290 295 300	912
ggg ttt ttc ttc aac acg cgc cga gaa att ttc aag gat aaa agg gtg Gly Phe Phe Phe Asn Thr Arg Arg Glu Ile Phe Lys Asp Lys Arg Val 305 310 315 320	960
cgt gaa gcc tta ttt tat gcg ttt gat ttt gaa tgg gcg aat aaa aat Arg Glu Ala Leu Phe Tyr Ala Phe Asp Phe Glu Trp Ala Asn Lys Asn 325 330 335	1008
ttg ttt ttt tcg caa tac aag cgc acc acc agt ttt ttc agt aac tct Leu Phe Phe Ser Gln Tyr Lys Arg Thr Thr Ser Phe Phe Ser Asn Ser 340 345 350	1056
atc tat gcg tcc cct ccc ctc cca agc cct gaa gaa aaa gcc ttg cta Ile Tyr Ala Ser Pro Pro Leu Pro Ser Pro Glu Glu Lys Ala Leu Leu 355 360 365	1104
gcc cct tat gaa aag agt ttg gat gaa agg gtt ttt aaa gag cct tat Ala Pro Tyr Glu Lys Ser Leu Asp Glu Arg Val Phe Lys Glu Pro Tyr 370 375 380	1152
gtc gtg cct aga acc gat gga gtt gat gtt tta ggc tat aat ttg agg Val Val Pro Arg Thr Asp Gly Val Asp Val Leu Gly Tyr Asn Leu Arg 385 390 395 400	1200
gaa aat tta aaa tac gcc caa aag ctt tta gag agc acg ggc ttt tct Glu Asn Leu Lys Tyr Ala Gln Lys Leu Leu Glu Ser Thr Gly Phe Ser 405 410 415	1248
tac aaa aac atg cgt ttg gtg gat aag aat aac aag cct ttc agt ttc Tyr Lys Asn Met Arg Leu Val Asp Lys Asn Asn Lys Pro Phe Ser Phe 420 425 430	1296
act ttg ctt tta aat agc ccg gca ttt gaa aga ctg gcc cta gct ttt Thr Leu Leu Leu Asn Ser Pro Ala Phe Glu Arg Leu Ala Leu Ala Phe 435 440 445	1344
gct aaa aac tta agg gtg tta ggg att gaa atg aaa atc caa aga gtg Ala Lys Asn Leu Arg Val Leu Gly Ile Glu Met Lys Ile Gln Arg Val 450 455 460	1392

gat tta agc cag tat gtc aat cgg atc aaa agc tat gat ttt gac atg Asp Leu Ser Gln Tyr Val Asn Arg Ile Lys Ser Tyr Asp Phe Asp Met 465 470 475 480	1440
att gta gga gtg att ggc caa tcg tct ttc cca ggt aat gag cag cgc Ile Val Gly Val Ile Gly Gln Ser Ser Phe Pro Gly Asn Glu Gln Arg 485 490 495	1488
ttt tat ttt ggt tct ttg agt gcg aaa gaa aaa ggc aca agg aat tat Phe Tyr Phe Gly Ser Leu Ser Ala Lys Glu Lys Gly Thr Arg Asn Tyr 500 505 510	1536
gcg gga atc tct agt aaa gcg gta gat gat ttg att gaa aaa atc att Ala Gly Ile Ser Ser Lys Ala Val Asp Asp Leu Ile Glu Lys Ile Ile 515 520 525	1584
aac gct aaa gat tac aag gaa caa ttg gcc gcc att caa gcg atg gat Asn Ala Lys Asp Tyr Lys Glu Gln Leu Ala Ala Ile Gln Ala Met Asp 530 535 540	1632
agg gta ttg ttg tgg ggg ttt tat gtg ata ccg cat ttt tat ttg cct Arg Val Leu Leu Trp Gly Phe Tyr Val Ile Pro His Phe Tyr Leu Pro 545 550 555 560	1680
aat tac agg atc gca gcg tat aat tac att ggc atg cct gaa atc agc Asn Tyr Arg Ile Ala Ala Tyr Asn Tyr Ile Gly Met Pro Glu Ile Ser 565 570 575	1728
cct agc tat gga ttt tcg ccg tat ttg tgg tgg ata aaa gaa aag gat Pro Ser Tyr Gly Phe Ser Pro Tyr Leu Trp Trp Ile Lys Glu Lys Asp 580 585 590	1776
ctt caa tga Leu Gln	1785

<210> 166  
 <211> 594  
 <212> PRT  
 <213> Helicobacter pylori

<400> 166

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Glu Ala Thr Pro Tyr Leu Tyr Leu Gly Glu Glu Pro Lys Tyr Lys Asp 20 25 30
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Asn Phe Thr His Phe Glu Tyr Ala Asn Pro Asn Ala Lys Lys Gly Gly 35 40 45
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Val Leu Arg Asn Asp Ala Ile Gly Thr Phe Asp Ser Leu Asn Pro Phe  
50 55 60

Ala Leu Lys Gly Thr Lys Ala Glu Gly Leu Asp Leu Ile Tyr Asp Thr  
65 70 75 80

Leu Met Val Gln Ser Leu Asp Glu Pro Phe Ala Glu Tyr Pro Leu Ile  
85 90 95

Ala Lys Asp Ala Glu Val Ala Lys Asp Asn Ser Tyr Val Ile Phe Thr  
100 105 110

Ile Asp Lys Arg Ala Arg Phe Ser Asn Asn Ala Pro Ile Leu Ala Ser  
115 120 125

Asp Val Lys Phe Ser Phe Asp Thr Ile Met Lys Leu Gly Ser Pro Ile  
130 135 140

Tyr Arg Gln Tyr Tyr Gln Asp Val Lys Lys Ala Val Val Leu Asp Lys  
145 150 155 160

His His Val Lys Phe Ile Phe Lys Thr Thr Glu Asn Lys Glu Leu Pro  
165 170 175

Leu Ile Leu Gly Gln Leu Gln Ile Phe Ser Lys Lys Ala Phe Gln Glu  
180 185 190

Asp Tyr Phe Glu Lys Asn Pro Leu Leu Ile Pro Val Ser Ser Gly Pro  
195 200 205

Tyr Val Ile Ala Ser Phe Asp Val Gly Lys Lys Ile Thr Tyr Gln Arg  
210 215 220

Asn Pro Asn Tyr Trp Ala Arg Asn Leu Pro Ser Arg Lys Gly Gln Phe  
225 230 235 240

Asn Phe Asp Gln Ile Lys Phe Glu Tyr Tyr Lys Asp Glu Thr Ile Ala  
245 250 255

Leu Gln Ala Phe Leu Ser Gly Ala Tyr Asp Trp Arg Leu Glu Ser Thr

260					265					270					
Ala	Lys	Val	Trp	Ala	Arg	Gly	Tyr	Val	Gly	Lys	Ala	Met	Asp	Asn	Lys
		275					280					285			
Glu	Ile	Thr	Lys	Tyr	Leu	Ile	Ala	His	Lys	Met	Pro	Ser	Gly	Met	Gln
	290					295					300				
Gly	Phe	Phe	Phe	Asn	Thr	Arg	Arg	Glu	Ile	Phe	Lys	Asp	Lys	Arg	Val
305						310					315				320
Arg	Glu	Ala	Leu	Phe	Tyr	Ala	Phe	Asp	Phe	Glu	Trp	Ala	Asn	Lys	Asn
				325					330					335	
Leu	Phe	Phe	Ser	Gln	Tyr	Lys	Arg	Thr	Thr	Ser	Phe	Phe	Ser	Asn	Ser
			340					345					350		
Ile	Tyr	Ala	Ser	Pro	Pro	Leu	Pro	Ser	Pro	Glu	Glu	Lys	Ala	Leu	Leu
		355					360					365			
Ala	Pro	Tyr	Glu	Lys	Ser	Leu	Asp	Glu	Arg	Val	Phe	Lys	Glu	Pro	Tyr
	370					375					380				
Val	Val	Pro	Arg	Thr	Asp	Gly	Val	Asp	Val	Leu	Gly	Tyr	Asn	Leu	Arg
385						390					395				400
Glu	Asn	Leu	Lys	Tyr	Ala	Gln	Lys	Leu	Leu	Glu	Ser	Thr	Gly	Phe	Ser
				405					410					415	
Tyr	Lys	Asn	Met	Arg	Leu	Val	Asp	Lys	Asn	Asn	Lys	Pro	Phe	Ser	Phe
			420					425					430		
Thr	Leu	Leu	Leu	Asn	Ser	Pro	Ala	Phe	Glu	Arg	Leu	Ala	Leu	Ala	Phe
			435				440					445			
Ala	Lys	Asn	Leu	Arg	Val	Leu	Gly	Ile	Glu	Met	Lys	Ile	Gln	Arg	Val
	450					455					460				
Asp	Leu	Ser	Gln	Tyr	Val	Asn	Arg	Ile	Lys	Ser	Tyr	Asp	Phe	Asp	Met
465						470					475				480

Ile Val Gly Val Ile Gly Gln Ser Ser Phe Pro Gly Asn Glu Gln Arg  
485 490 495

Phe Tyr Phe Gly Ser Leu Ser Ala Lys Glu Lys Gly Thr Arg Asn Tyr  
500 505 510

Ala Gly Ile Ser Ser Lys Ala Val Asp Asp Leu Ile Glu Lys Ile Ile  
515 520 525

Asn Ala Lys Asp Tyr Lys Glu Gln Leu Ala Ala Ile Gln Ala Met Asp  
530 535 540

Arg Val Leu Leu Trp Gly Phe Tyr Val Ile Pro His Phe Tyr Leu Pro  
545 550 555 560

Asn Tyr Arg Ile Ala Ala Tyr Asn Tyr Ile Gly Met Pro Glu Ile Ser  
565 570 575

Pro Ser Tyr Gly Phe Ser Pro Tyr Leu Trp Trp Ile Lys Glu Lys Asp  
580 585 590

Leu Gln

<210> 167  
<211> 2007  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(2007)

<400> 167  
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Met Lys Asn Gln His Lys Asn Pro Leu Thr Lys Ala Leu Met Lys Thr  
1 5 10 15  
tat cca tat aac cat ttt tta ttt ttc tgc ttt att cta gga gcg ttt 96  
Tyr Pro Tyr Asn His Phe Leu Phe Phe Cys Phe Ile Leu Gly Ala Phe  
20 25 30  
tta tta ggt ttg ctc agt cca gct tat gct tta agt att atc acc act 144  
Leu Leu Gly Leu Leu Ser Pro Ala Tyr Ala Leu Ser Ile Ile Thr Thr  
35 40 45

aaa gaa att gac gct aat ttg ctt aat gga gcg ata gaa agc agg gtg Lys Glu Ile Asp Ala Asn Leu Leu Asn Gly Ala Ile Glu Ser Arg Val 50 55 60	192
gtg tta ggc aag agg gtg ttt aaa gta gaa gct cat ggg ttt tat ttt Val Leu Gly Lys Arg Val Phe Lys Val Glu Ala His Gly Phe Tyr Phe 65 70 75 80	240
aga aac aat gcg act aac agc ata gat ata gaa atc acc agt ctt tta Arg Asn Asn Ala Thr Asn Ser Ile Asp Ile Glu Ile Thr Ser Leu Leu 85 90 95	288
aga gac aat caa tcg ttt cct ttg act agc agt gct aaa acc agt tta Arg Asp Asn Gln Ser Phe Pro Leu Thr Ser Ser Ala Lys Thr Ser Leu 100 105 110	336
aaa ata cct cct aac gcc aag att aaa aaa tcc act atc ctt gtt ttg Lys Ile Pro Pro Asn Ala Lys Ile Lys Lys Ser Thr Ile Leu Val Leu 115 120 125	384
aaa ggc gag aac gct gaa gaa gtg gct aag att tta ggc gtt agc aaa Lys Gly Glu Asn Ala Glu Glu Val Ala Lys Ile Leu Gly Val Ser Lys 130 135 140	432
gaa gaa tac caa aag cta gaa aac atc gct caa acc aaa gcg gct aat Glu Glu Tyr Gln Lys Leu Glu Asn Ile Ala Gln Thr Lys Ala Ala Asn 145 150 155 160	480
gac cct atg tat gct aac acg cct ttt agt aat ggt tct gat agt tcc Asp Pro Met Tyr Ala Asn Thr Pro Phe Ser Asn Gly Ser Asp Ser Ser 165 170 175	528
ttt tac gat aac aat cct aat agc cct agc aat aac gct atc aat ggc Phe Tyr Asp Asn Asn Pro Asn Ser Pro Ser Asn Asn Ala Ile Asn Gly 180 185 190	576
aaa gat ggc gca aat ggg agt aac ggc tat ggg gca aat ggc aat gat Lys Asp Gly Ala Asn Gly Ser Asn Gly Tyr Gly Ala Asn Gly Asn Asp 195 200 205	624
ggg gta aat ggg atc agt ggg agt aat ggt gca aat ggg agt cat tca Gly Val Asn Gly Ile Ser Gly Ser Asn Gly Ala Asn Gly Ser His Ser 210 215 220	672
aat aat aat gca ata ggc agt ggt att gat aca gat ggc gtg tta ggg Asn Asn Asn Ala Ile Gly Ser Gly Ile Asp Thr Asp Gly Val Leu Gly 225 230 235 240	720
gtg gat ggg gtg aat ggc tct agt tct tca agt ggc ggc tct gta ggg Val Asp Gly Val Asn Gly Ser Ser Ser Ser Ser Gly Gly Ser Val Gly 245 250 255	768
ggt tat gag aat aat ttc act aat cat ggc tct act aac aat aac aca Gly Tyr Glu Asn Asn Phe Thr Asn His Gly Ser Thr Asn Asn Asn Thr 260 265 270	816

gga ggg tat gac aat ttt aat aat ggc agc tca agt ggt ggg agt tta	864
Gly Gly Tyr Asp Asn Phe Asn Asn Gly Ser Ser Ser Gly Gly Ser Leu	
275 280 285	
ggg aat ggg ggg ctt ttc cct att cct ttt ggt aat gga gac aca aac	912
Gly Asn Gly Gly Leu Phe Pro Ile Pro Phe Gly Asn Gly Asp Thr Asn	
290 295 300	
aat tcc aat aat tcc act aac acc act agc cca act aat ggc agt agt	960
Asn Ser Asn Asn Ser Thr Asn Thr Thr Ser Pro Thr Asn Gly Ser Ser	
305 310 315 320	
tct aat aac gcc act aat cct agt tcg caa gaa aac aat tac tcc agc	1008
Ser Asn Asn Ala Thr Asn Pro Ser Ser Gln Glu Asn Asn Tyr Ser Ser	
325 330 335	
cag tat tgt aaa gtg cca gag tta agc ccc aac aac acg atg aaa cta	1056
Gln Tyr Cys Lys Val Pro Glu Leu Ser Pro Asn Asn Thr Met Lys Leu	
340 345 350	
gat gtt atc gct aaa gat ggc tct tgt att tct atg aac gct tta aga	1104
Asp Val Ile Ala Lys Asp Gly Ser Cys Ile Ser Met Asn Ala Leu Arg	
355 360 365	
gat gac act aaa tgc gct tat aga tac gat ttt gaa gcc ggt aaa gcc	1152
Asp Asp Thr Lys Cys Ala Tyr Arg Tyr Asp Phe Glu Ala Gly Lys Ala	
370 375 380	
atc aag caa acg caa tac tac tat gta gat agg gaa aat aaa acg caa	1200
Ile Lys Gln Thr Gln Tyr Tyr Tyr Val Asp Arg Glu Asn Lys Thr Gln	
385 390 395 400	
aat atc ggt ggt tgt gtg gat tta caa ggc gct caa tac gcc atg caa	1248
Asn Ile Gly Gly Cys Val Asp Leu Gln Gly Ala Gln Tyr Ala Met Gln	
405 410 415	
ctt tac aaa gat gac agc aaa tgc gcc tta caa acc acg agc gat aaa	1296
Leu Tyr Lys Asp Asp Ser Lys Cys Ala Leu Gln Thr Thr Ser Asp Lys	
420 425 430	
ggt tat ggt atg ggg aaa acg caa acc ttt caa act gaa atc gtg ttt	1344
Gly Tyr Gly Met Gly Lys Thr Gln Thr Phe Gln Thr Glu Ile Val Phe	
435 440 445	
cgt ggg atg gac aat tta atc cat gtc gct gtg cct tgc agc gat tat	1392
Arg Gly Met Asp Asn Leu Ile His Val Ala Val Pro Cys Ser Asp Tyr	
450 455 460	
gca agg gtg caa gac agg att gtt agg tat gaa aaa aat gat aaa acc	1440
Ala Arg Val Gln Asp Arg Ile Val Arg Tyr Glu Lys Asn Asp Lys Thr	
465 470 475 480	
caa acc tta acg cct ata gtg gat cag tat tat aat gat cct aac aac	1488
Gln Thr Leu Thr Pro Ile Val Asp Gln Tyr Tyr Asn Asp Pro Asn Asn	

485								490				495					
cct	aac	aag	caa	gag	att	tta	aat	cgt	ggg	att	gcc	acc	caa	tta	agc	1536	
Pro	Asn	Lys	Gln	Glu	Ile	Leu	Asn	Arg	Gly	Ile	Ala	Thr	Gln	Leu	Ser		
			500					505					510				
tcg	caa	tat	caa	gaa	ttt	gca	tgc	ggg	caa	tgg	gaa	tac	aat	gac	gct	1584	
Ser	Gln	Tyr	Gln	Glu	Phe	Ala	Cys	Gly	Gln	Trp	Glu	Tyr	Asn	Asp	Ala		
		515					520					525					
aaa	tta	gaa	gcc	aaa	aga	cct	aca	atg	cta	aaa	agc	tat	aac	aag	ctt	1632	
Lys	Leu	Glu	Ala	Lys	Arg	Pro	Thr	Met	Leu	Lys	Ser	Tyr	Asn	Lys	Leu		
		530				535					540						
aat	gga	gaa	tgg	gta	gaa	ggt	acg	ccc	tgt	aat	ttt	gaa	gca	ggg	att	1680	
Asn	Gly	Glu	Trp	Val	Glu	Val	Thr	Pro	Cys	Asn	Phe	Glu	Ala	Gly	Ile		
545					550					555					560		
aaa	agc	ggg	gcg	ggt	ggt	agc	cct	tat	gtg	atg	ggc	gtg	cct	agt	tct	1728	
Lys	Ser	Gly	Ala	Val	Val	Ser	Pro	Tyr	Val	Met	Gly	Val	Pro	Ser	Ser		
				565					570					575			
aaa	gtc	tta	agc	gat	att	act	aca	agc	cat	tat	ttt	agg	ata	gaa	agg	1776	
Lys	Val	Leu	Ser	Asp	Ile	Thr	Thr	Ser	His	Tyr	Phe	Arg	Ile	Glu	Arg		
			580					585					590				
aaa	aat	tat	ggg	gag	aga	gaa	caa	tgc	caa	aaa	ctt	tat	gga	gtc	aat	1824	
Lys	Asn	Tyr	Gly	Glu	Arg	Glu	Gln	Cys	Gln	Lys	Leu	Tyr	Gly	Val	Asn		
		595					600					605					
cgt	tgc	caa	ccg	caa	tat	tcc	ata	ctg	atc	cta	gta	tca	ccg	att	gga	1872	
Arg	Cys	Gln	Pro	Gln	Tyr	Ser	Ile	Leu	Ile	Leu	Val	Ser	Pro	Ile	Gly		
	610					615					620						
gcg	cca	ctt	aca	aaa	cca	cta	cca	ccc	aaa	cca	ctc	aac	ctt	att	tac	1920	
Ala	Pro	Leu	Thr	Lys	Pro	Leu	Pro	Pro	Lys	Pro	Leu	Asn	Leu	Ile	Tyr		
	625				630				635						640		
gcc	cag	ccc	aag	ata	atg	aaa	aac	acc	cca	caa	cct	ata	atc	tta	tca	1968	
Ala	Gln	Pro	Lys	Ile	Met	Lys	Asn	Thr	Pro	Gln	Pro	Ile	Ile	Leu	Ser		
				645				650						655			
cca	ctc	aaa	cca	cca	tca	aca	gga	ctc	aaa	gcg	ttt	tga				2007	
Pro	Leu	Lys	Pro	Pro	Ser	Thr	Gly	Leu	Lys	Ala	Phe						
			660					665									

<210> 168  
 <211> 668  
 <212> PRT  
 <213> Helicobacter pylori

<400> 168

Met Lys Asn Gln His Lys Asn Pro Leu Thr Lys Ala Leu Met Lys Thr

1		5		10		15										
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			20					25					30			
Leu	Leu	Gly	Leu	Leu	Ser	Pro	Ala	Tyr	Ala	Leu	Ser	Ile	Ile	Thr	Thr	
		35					40					45				
Lys	Glu	Ile	Asp	Ala	Asn	Leu	Leu	Asn	Gly	Ala	Ile	Glu	Ser	Arg	Val	
	50					55					60					
Val	Leu	Gly	Lys	Arg	Val	Phe	Lys	Val	Glu	Ala	His	Gly	Phe	Tyr	Phe	
65					70					75					80	
Arg	Asn	Asn	Ala	Thr	Asn	Ser	Ile	Asp	Ile	Glu	Ile	Thr	Ser	Leu	Leu	
				85					90					95		
Arg	Asp	Asn	Gln	Ser	Phe	Pro	Leu	Thr	Ser	Ser	Ala	Lys	Thr	Ser	Leu	
			100					105					110			
Lys	Ile	Pro	Pro	Asn	Ala	Lys	Ile	Lys	Lys	Ser	Thr	Ile	Leu	Val	Leu	
		115					120					125				
Lys	Gly	Glu	Asn	Ala	Glu	Glu	Val	Ala	Lys	Ile	Leu	Gly	Val	Ser	Lys	
	130					135					140					
Glu	Glu	Tyr	Gln	Lys	Leu	Glu	Asn	Ile	Ala	Gln	Thr	Lys	Ala	Ala	Asn	
145					150					155					160	
Asp	Pro	Met	Tyr	Ala	Asn	Thr	Pro	Phe	Ser	Asn	Gly	Ser	Asp	Ser	Ser	
				165					170					175		
Phe	Tyr	Asp	Asn	Asn	Pro	Asn	Ser	Pro	Ser	Asn	Asn	Ala	Ile	Asn	Gly	
			180					185					190			
Lys	Asp	Gly	Ala	Asn	Gly	Ser	Asn	Gly	Tyr	Gly	Ala	Asn	Gly	Asn	Asp	
		195					200					205				
Gly	Val	Asn	Gly	Ile	Ser	Gly	Ser	Asn	Gly	Ala	Asn	Gly	Ser	His	Ser	
	210					215					220					

Asn Asn Asn Ala Ile Gly Ser Gly Ile Asp Thr Asp Gly Val Leu Gly  
 225 230 235 240

Val Asp Gly Val Asn Gly Ser Ser Ser Ser Ser Gly Gly Ser Val Gly  
 245 250 255

Gly Tyr Glu Asn Asn Phe Thr Asn His Gly Ser Thr Asn Asn Asn Thr  
 260 265 270

Gly Gly Tyr Asp Asn Phe Asn Asn Gly Ser Ser Ser Gly Gly Ser Leu  
 275 280 285

Gly Asn Gly Gly Leu Phe Pro Ile Pro Phe Gly Asn Gly Asp Thr Asn  
 290 295 300

Asn Ser Asn Asn Ser Thr Asn Thr Thr Ser Pro Thr Asn Gly Ser Ser  
 305 310 315 320

Ser Asn Asn Ala Thr Asn Pro Ser Ser Gln Glu Asn Asn Tyr Ser Ser  
 325 330 335

Gln Tyr Cys Lys Val Pro Glu Leu Ser Pro Asn Asn Thr Met Lys Leu  
 340 345 350

Asp Val Ile Ala Lys Asp Gly Ser Cys Ile Ser Met Asn Ala Leu Arg  
 355 360 365

Asp Asp Thr Lys Cys Ala Tyr Arg Tyr Asp Phe Glu Ala Gly Lys Ala  
 370 375 380

Ile Lys Gln Thr Gln Tyr Tyr Tyr Val Asp Arg Glu Asn Lys Thr Gln  
 385 390 395 400

Asn Ile Gly Gly Cys Val Asp Leu Gln Gly Ala Gln Tyr Ala Met Gln  
 405 410 415

Leu Tyr Lys Asp Asp Ser Lys Cys Ala Leu Gln Thr Thr Ser Asp Lys  
 420 425 430

Gly Tyr Gly Met Gly Lys Thr Gln Thr Phe Gln Thr Glu Ile Val Phe  
 435 440 445



Arg Gly Met Asp Asn Leu Ile His Val Ala Val Pro Cys Ser Asp Tyr  
 450 455 460

Ala Arg Val Gln Asp Arg Ile Val Arg Tyr Glu Lys Asn Asp Lys Thr  
 465 470 475 480

Gln Thr Leu Thr Pro Ile Val Asp Gln Tyr Tyr Asn Asp Pro Asn Asn  
 485 490 495

Pro Asn Lys Gln Glu Ile Leu Asn Arg Gly Ile Ala Thr Gln Leu Ser  
 500 505 510

Ser Gln Tyr Gln Glu Phe Ala Cys Gly Gln Trp Glu Tyr Asn Asp Ala  
 515 520 525

Lys Leu Glu Ala Lys Arg Pro Thr Met Leu Lys Ser Tyr Asn Lys Leu  
 530 535 540

Asn Gly Glu Trp Val Glu Val Thr Pro Cys Asn Phe Glu Ala Gly Ile  
 545 550 555 560

Lys Ser Gly Ala Val Val Ser Pro Tyr Val Met Gly Val Pro Ser Ser  
 565 570 575

Lys Val Leu Ser Asp Ile Thr Thr Ser His Tyr Phe Arg Ile Glu Arg  
 580 585 590

Lys Asn Tyr Gly Glu Arg Glu Gln Cys Gln Lys Leu Tyr Gly Val Asn  
 595 600 605

Arg Cys Gln Pro Gln Tyr Ser Ile Leu Ile Leu Val Ser Pro Ile Gly  
 610 615 620

Ala Pro Leu Thr Lys Pro Leu Pro Pro Lys Pro Leu Asn Leu Ile Tyr  
 625 630 635 640

Ala Gln Pro Lys Ile Met Lys Asn Thr Pro Gln Pro Ile Ile Leu Ser  
 645 650 655

Pro Leu Lys Pro Pro Ser Thr Gly Leu Lys Ala Phe  
 660 665

<210> 169  
 <211> 771  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(771)

<400> 169  
 atg ttg ggg agc gtc aaa aaa gcg gtt ttt agg gtt ttg tgt ttg ggg 48  
 Met Leu Gly Ser Val Lys Lys Ala Val Phe Arg Val Leu Cys Leu Gly  
 1 5 10 15  
 gcg ttg tgt tta tgc ggg ggg tta atg gca gag caa gat cct aaa gag 96  
 Ala Leu Cys Leu Cys Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu  
 20 25 30  
 ctt ata ttt tca ggt ata act att tac acg gat aaa aat ttc act aga 144  
 Leu Ile Phe Ser Gly Ile Thr Ile Tyr Thr Asp Lys Asn Phe Thr Arg  
 35 40 45  
 gct aag aaa tat ttt gaa aaa gct tgc aaa tca aac gat gct gat ggc 192  
 Ala Lys Lys Tyr Phe Glu Lys Ala Cys Lys Ser Asn Asp Ala Asp Gly  
 50 55 60  
 tgt gca atc tta aga gag gtt tat tct agt ggt aaa gcc ata gcg aga 240  
 Cys Ala Ile Leu Arg Glu Val Tyr Ser Ser Gly Lys Ala Ile Ala Arg  
 65 70 75 80  
 gaa aac gca aga gag agc att gaa aaa gct ctt gaa cac acc gct act 288  
 Glu Asn Ala Arg Glu Ser Ile Glu Lys Ala Leu Glu His Thr Ala Thr  
 85 90 95  
 gct aaa gtt tgt aaa tta aac gat gct gaa aaa tgc aag gac tta gca 336  
 Ala Lys Val Cys Lys Leu Asn Asp Ala Glu Lys Cys Lys Asp Leu Ala  
 100 105 110  
 gag ttt tat ttt aat gta aac gat ctt aaa aat gct tta gaa tat tac 384  
 Glu Phe Tyr Phe Asn Val Asn Asp Leu Lys Asn Ala Leu Glu Tyr Tyr  
 115 120 125  
 tct aaa tct tgt aag tta aat aat gtt gaa ggg tgt atg ctg tca gca 432  
 Ser Lys Ser Cys Lys Leu Asn Asn Val Glu Gly Cys Met Leu Ser Ala  
 130 135 140  
 act ttt tat aac gat atg ata aag ggt ttg aaa aaa gat aaa aaa gat 480  
 Thr Phe Tyr Asn Asp Met Ile Lys Gly Leu Lys Lys Asp Lys Lys Asp  
 145 150 155 160  
 cta gaa tat tat tct aaa gct tgc gag tta aat aac ggt gga ggg tgt 528  
 Leu Glu Tyr Tyr Ser Lys Ala Cys Glu Leu Asn Asn Gly Gly Gly Cys

165								170					175					
tct	aaa	tta	gga	ggg	gat	tat	ttt	ttt	ggt	gaa	ggc	gta	aca	aaa	gat	576		
Ser	Lys	Leu	Gly	Gly	Asp	Tyr	Phe	Phe	Gly	Glu	Gly	Val	Thr	Lys	Asp			
			180					185					190					
ttc	aaa	aaa	gct	ttt	gaa	tat	tct	gcc	aaa	gct	tgt	gag	ttg	aac	gat	624		
Phe	Lys	Lys	Ala	Phe	Glu	Tyr	Ser	Ala	Lys	Ala	Cys	Glu	Leu	Asn	Asp			
		195					200					205						
gct	aaa	ggg	tgt	tac	gct	cta	gca	gcg	ttt	tat	aat	gag	ggt	aaa	ggc	672		
Ala	Lys	Gly	Cys	Tyr	Ala	Leu	Ala	Ala	Phe	Tyr	Asn	Glu	Gly	Lys	Gly			
	210					215					220							
gtg	gca	aag	gat	gaa	aag	caa	acg	aca	gaa	aac	ctt	gaa	aag	agt	tgc	720		
Val	Ala	Lys	Asp	Glu	Lys	Gln	Thr	Thr	Glu	Asn	Leu	Glu	Lys	Ser	Cys			
225					230					235					240			
aag	cta	gga	tta	aaa	gaa	gca	tgc	gat	att	ctc	aaa	gaa	caa	aaa	caa	768		
Lys	Leu	Gly	Leu	Lys	Glu	Ala	Cys	Asp	Ile	Leu	Lys	Glu	Gln	Lys	Gln			
			245					250						255				
taa																771		

<210> 170  
 <211> 256  
 <212> PRT  
 <213> Helicobacter pylori

<400> 170

Met	Leu	Gly	Ser	Val	Lys	Lys	Ala	Val	Phe	Arg	Val	Leu	Cys	Leu	Gly
1				5					10					15	
Ala	Leu	Cys	Leu	Cys	Gly	Gly	Leu	Met	Ala	Glu	Gln	Asp	Pro	Lys	Glu
			20					25					30		
Leu	Ile	Phe	Ser	Gly	Ile	Thr	Ile	Tyr	Thr	Asp	Lys	Asn	Phe	Thr	Arg
		35					40					45			
Ala	Lys	Lys	Tyr	Phe	Glu	Lys	Ala	Cys	Lys	Ser	Asn	Asp	Ala	Asp	Gly
	50					55					60				
Cys	Ala	Ile	Leu	Arg	Glu	Val	Tyr	Ser	Ser	Gly	Lys	Ala	Ile	Ala	Arg
65					70					75					80
Glu	Asn	Ala	Arg	Glu	Ser	Ile	Glu	Lys	Ala	Leu	Glu	His	Thr	Ala	Thr
			85					90						95	

Ala Lys Val Cys Lys Leu Asn Asp Ala Glu Lys Cys Lys Asp Leu Ala  
100 105 110

Glu Phe Tyr Phe Asn Val Asn Asp Leu Lys Asn Ala Leu Glu Tyr Tyr  
115 120 125

Ser Lys Ser Cys Lys Leu Asn Asn Val Glu Gly Cys Met Leu Ser Ala  
130 135 140

Thr Phe Tyr Asn Asp Met Ile Lys Gly Leu Lys Lys Asp Lys Lys Asp  
145 150 155 160

Leu Glu Tyr Tyr Ser Lys Ala Cys Glu Leu Asn Asn Gly Gly Gly Cys  
165 170 175

Ser Lys Leu Gly Gly Asp Tyr Phe Phe Gly Glu Gly Val Thr Lys Asp  
180 185 190

Phe Lys Lys Ala Phe Glu Tyr Ser Ala Lys Ala Cys Glu Leu Asn Asp  
195 200 205

Ala Lys Gly Cys Tyr Ala Leu Ala Ala Phe Tyr Asn Glu Gly Lys Gly  
210 215 220

Val Ala Lys Asp Glu Lys Gln Thr Thr Glu Asn Leu Glu Lys Ser Cys  
225 230 235 240

Lys Leu Gly Leu Lys Glu Ala Cys Asp Ile Leu Lys Glu Gln Lys Gln  
245 250 255

<210> 171  
<211> 1641  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(1641)

<400> 171  
atg aat aaa aac aac aac acg aat ctt att tta gcg atc gct ctg tct  
Met Asn Lys Asn Asn Asn Thr Asn Leu Ile Leu Ala Ile Ala Leu Ser  
1 5 10 15

48

ttc ttg ttt atc gct ctt tat agc tat ttt ttc caa aaa cca aac aaa	96
Phe Leu Phe Ile Ala Leu Tyr Ser Tyr Phe Phe Gln Lys Pro Asn Lys	
20 25 30	
aca aca acc caa acc aca aag caa gaa aca gcc aac aac cac aca gca	144
Thr Thr Thr Gln Thr Thr Lys Gln Glu Thr Ala Asn Asn His Thr Ala	
35 40 45	
aca agt cct aac gcg ccc aac gcc caa aat ttt agc gtt act caa acc	192
Thr Ser Pro Asn Ala Pro Asn Ala Gln Asn Phe Ser Val Thr Gln Thr	
50 55 60	
atc ccc caa gag agt ttg tta agc acg att tct ttt gag cat gcc agg	240
Ile Pro Gln Glu Ser Leu Leu Ser Thr Ile Ser Phe Glu His Ala Arg	
65 70 75 80	
att gaa att gat tct tta ggg cgc atc aaa cag gtt tat ctc aag gat	288
Ile Glu Ile Asp Ser Leu Gly Arg Ile Lys Gln Val Tyr Leu Lys Asp	
85 90 95	
aaa aag tat cta acc cct aaa caa aag ggc ttt tta gag cat gtg agc	336
Lys Lys Tyr Leu Thr Pro Lys Gln Lys Gly Phe Leu Glu His Val Ser	
100 105 110	
cat ctt ttt aac ccc aaa gct aac ccg caa ccc ccc cta aaa gag ctc	384
His Leu Phe Asn Pro Lys Ala Asn Pro Gln Pro Pro Leu Lys Glu Leu	
115 120 125	
ccc ctt tta gcg gcc gat aaa ctc aag cct tta gaa gtg cgt ttt tta	432
Pro Leu Leu Ala Ala Asp Lys Leu Lys Pro Leu Glu Val Arg Phe Leu	
130 135 140	
gac ccc acg ctc aat aac aaa gcg ttc aac acc cct tat agt gct tca	480
Asp Pro Thr Leu Asn Asn Lys Ala Phe Asn Thr Pro Tyr Ser Ala Ser	
145 150 155 160	
aaa acc act ctt ggg cct aat gaa cag ctt gtt tta acc caa gat tta	528
Lys Thr Thr Leu Gly Pro Asn Glu Gln Leu Val Leu Thr Gln Asp Leu	
165 170 175	
ggc gct ctt acc atc att aaa acc ctg act ttt tat gat gat ttg cat	576
Gly Ala Leu Thr Ile Ile Lys Thr Leu Thr Phe Tyr Asp Asp Leu His	
180 185 190	
tat gat tta aaa atc gcc ttc aaa tcg cct aac aat att atc cct agc	624
Tyr Asp Leu Lys Ile Ala Phe Lys Ser Pro Asn Asn Ile Ile Pro Ser	
195 200 205	
tat gtg atc act aat ggt tac aga ccg gtg gct gat ttg gac agc tac	672
Tyr Val Ile Thr Asn Gly Tyr Arg Pro Val Ala Asp Leu Asp Ser Tyr	
210 215 220	
acc ttt tcg ggc gtg ctt tta gaa aac aac gac aaa aaa att gaa aaa	720
Thr Phe Ser Gly Val Leu Leu Glu Asn Asn Asp Lys Lys Ile Glu Lys	

225		230		235		240	
att gaa gat aaa gac gct aaa gaa atc aaa cgc ttt tct aac acc ctc							768
Ile Glu Asp Lys	Asp	Ala Lys Glu	Ile Lys	Arg Phe Ser	Asn Thr Leu		
	245		250		255		
ttt tta tcc agc gtg gat agg tat ttc acc act ttg ctt ttc act aaa							816
Phe Leu Ser Ser	Val Asp Arg	Tyr Phe Thr	Thr Leu Leu	Phe Thr Lys			
	260		265		270		
gat tct caa ggt ttt gaa gcc tta att gat tca gaa atc ggc act aaa							864
Asp Ser Gln Gly	Phe Glu Ala	Leu Ile Asp	Ser Glu Ile	Gly Thr Lys			
	275		280		285		
aaa ccc tta ggg ttc att tcc ctt aaa aat gaa gcg aat ttg cat ggt							912
Lys Pro Leu Gly	Phe Ile Ser	Leu Lys Asn	Glu Ala Asn	Leu His Gly			
	290		295		300		
tat att ggc cct aaa gat tac cgc tct ttg aaa gcg att tca ccc atg							960
Tyr Ile Gly Pro	Lys Asp Tyr	Arg Ser Leu	Lys Ala Ile	Ser Pro Met			
	310		315				
ctc act gat gtg ata gag tat ggt tta atc act ttc ttt gcg aaa ggc							1008
Leu Thr Asp Val	Ile Glu Tyr	Gly Leu Ile	Thr Phe Phe	Ala Lys Gly			
	325		330		335		
gtg ttt gtt tta ctg gat tat ttg tat caa ttc gtg ggc aat tgg ggt							1056
Val Phe Val Leu	Leu Asp Tyr	Leu Tyr Gln	Phe Val Gly	Asn Trp Gly			
	340		345		350		
tgg gct atc att ttt tta acg att atc gtg cgc cta atc ctt tac ccc							1104
Trp Ala Ile Ile	Phe Leu Thr	Ile Ile Val	Arg Leu Ile	Leu Tyr Pro			
	355		360		365		
tta agc tat aaa ggc atg gtg agc atg caa aag ctc aaa gaa tta gcc							1152
Leu Ser Tyr Lys	Gly Met Val	Ser Met Gln	Lys Leu Lys	Glu Leu Ala			
	370		375		380		
ccc aaa atg aaa gaa ctc caa gaa aaa tac aag ggc gaa ccc caa aag							1200
Pro Lys Met Lys	Glu Leu Gln	Glu Lys Tyr	Lys Gly Glu	Pro Gln Lys			
	385		390		395		400
ttg caa gcc cac atg atg cag ctt tac aaa aaa cat ggg gcc aac ccg							1248
Leu Gln Ala His	Met Met Gln	Leu Tyr Lys	Lys His Gly	Ala Asn Pro			
	405		410		415		
cta ggg ggt tgt ctg ccc tta atc tta caa atc ccg gtg ttt ttt gcg							1296
Leu Gly Gly Cys	Leu Pro Leu	Ile Leu Gln	Ile Pro Val	Phe Phe Ala			
	420		425		430		
att tat aga gtg ctt tat aac gct gtg gaa ttg aaa agc tca gag tgg							1344
Ile Tyr Arg Val	Leu Tyr Asn	Ala Val Glu	Leu Lys Ser	Ser Ser Glu	Trp		
	435		440		445		
atc tta tgg att cat gat tta tcc atc atg gat ccg tat ttt att tta							1392

Ile	Leu	Trp	Ile	His	Asp	Leu	Ser	Ile	Met	Asp	Pro	Tyr	Phe	Ile	Leu		
450						455					460						
ccg	ctt	ctt	atg	gga	gcg	tct	atg	tat	tgg	cac	caa	agc	gtt	acg	cca		1440
Pro	Leu	Leu	Met	Gly	Ala	Ser	Met	Tyr	Trp	His	Gln	Ser	Val	Thr	Pro		
465					470					475					480		
aac	acc	atg	acc	gat	ccc	atg	caa	gcg	aag	att	ttt	aaa	ctc	tta	ccc		1488
Asn	Thr	Met	Thr	Asp	Pro	Met	Gln	Ala	Lys	Ile	Phe	Lys	Leu	Leu	Pro		
				485					490					495			
cta	tta	ttt	aca	atc	ttt	tta	atc	act	ttc	cct	gca	ggg	tta	gtc	ttg		1536
Leu	Leu	Phe		Thr	Ile	Phe	Leu	Ile	Thr	Phe	Pro	Ala	Gly	Leu	Val	Leu	
			500					505					510				
tat	tgg	acc	aca	aac	aac	atc	ctt	tcg	gtg	ttg	caa	caa	ctc	att	att		1584
Tyr	Trp	Thr	Thr	Asn	Asn	Ile	Leu	Ser	Val	Leu	Gln	Gln	Leu	Ile	Ile		
		515				520						525					
aat	aaa	gtt	tta	gag	aat	aaa	aaa	cga	gcg	cac	cgc	gaa	aac	aaa	aag		1632
Asn	Lys	Val	Leu	Glu	Asn	Lys	Lys	Arg	Ala	His	Arg	Glu	Asn	Lys	Lys		
	530					535					540						
gaa	cat	tga															1641
Glu	His																
545																	

<210> 172  
 <211> 546  
 <212> PRT  
 <213> Helicobacter pylori

<400> 172

Met	Asn	Lys	Asn	Asn	Asn	Thr	Asn	Leu	Ile	Leu	Ala	Ile	Ala	Leu	Ser		
1				5					10					15			
Phe	Leu	Phe	Ile	Ala	Leu	Tyr	Ser	Tyr	Phe	Phe	Gln	Lys	Pro	Asn	Lys		
			20					25					30				
Thr	Thr	Thr	Gln	Thr	Thr	Lys	Gln	Glu	Thr	Ala	Asn	Asn	His	Thr	Ala		
		35					40					45					
Thr	Ser	Pro	Asn	Ala	Pro	Asn	Ala	Gln	Asn	Phe	Ser	Val	Thr	Gln	Thr		
	50					55					60						
Ile	Pro	Gln	Glu	Ser	Leu	Leu	Ser	Thr	Ile	Ser	Phe	Glu	His	Ala	Arg		
65					70					75					80		

Ile	Glu	Ile	Asp	Ser	Leu	Gly	Arg	Ile	Lys	Gln	Val	Tyr	Leu	Lys	Asp	85	90	95
Lys	Lys	Tyr	Leu	Thr	Pro	Lys	Gln	Lys	Gly	Phe	Leu	Glu	His	Val	Ser	100	105	110
His	Leu	Phe	Asn	Pro	Lys	Ala	Asn	Pro	Gln	Pro	Pro	Leu	Lys	Glu	Leu	115	120	125
Pro	Leu	Leu	Ala	Ala	Asp	Lys	Leu	Lys	Pro	Leu	Glu	Val	Arg	Phe	Leu	130	135	140
Asp	Pro	Thr	Leu	Asn	Asn	Lys	Ala	Phe	Asn	Thr	Pro	Tyr	Ser	Ala	Ser	145	150	155
Lys	Thr	Thr	Leu	Gly	Pro	Asn	Glu	Gln	Leu	Val	Leu	Thr	Gln	Asp	Leu	165	170	175
Gly	Ala	Leu	Thr	Ile	Ile	Lys	Thr	Leu	Thr	Phe	Tyr	Asp	Asp	Leu	His	180	185	190
Tyr	Asp	Leu	Lys	Ile	Ala	Phe	Lys	Ser	Pro	Asn	Asn	Ile	Ile	Pro	Ser	195	200	205
Tyr	Val	Ile	Thr	Asn	Gly	Tyr	Arg	Pro	Val	Ala	Asp	Leu	Asp	Ser	Tyr	210	215	220
Thr	Phe	Ser	Gly	Val	Leu	Leu	Glu	Asn	Asn	Asp	Lys	Lys	Ile	Glu	Lys	225	230	235
Ile	Glu	Asp	Lys	Asp	Ala	Lys	Glu	Ile	Lys	Arg	Phe	Ser	Asn	Thr	Leu	245	250	255
Phe	Leu	Ser	Ser	Val	Asp	Arg	Tyr	Phe	Thr	Thr	Leu	Leu	Phe	Thr	Lys	260	265	270
Asp	Ser	Gln	Gly	Phe	Glu	Ala	Leu	Ile	Asp	Ser	Glu	Ile	Gly	Thr	Lys	275	280	285
Lys	Pro	Leu	Gly	Phe	Ile	Ser	Leu	Lys	Asn	Glu	Ala	Asn	Leu	His	Gly	290	295	300



Tyr Ile Gly Pro Lys Asp Tyr Arg Ser Leu Lys Ala Ile Ser Pro Met  
 305 310 315 320

Leu Thr Asp Val Ile Glu Tyr Gly Leu Ile Thr Phe Phe Ala Lys Gly  
 325 330 335

Val Phe Val Leu Leu Asp Tyr Leu Tyr Gln Phe Val Gly Asn Trp Gly  
 340 345 350

Trp Ala Ile Ile Phe Leu Thr Ile Ile Val Arg Leu Ile Leu Tyr Pro  
 355 360 365

Leu Ser Tyr Lys Gly Met Val Ser Met Gln Lys Leu Lys Glu Leu Ala  
 370 375 380

Pro Lys Met Lys Glu Leu Gln Glu Lys Tyr Lys Gly Glu Pro Gln Lys  
 385 390 395 400

Leu Gln Ala His Met Met Gln Leu Tyr Lys Lys His Gly Ala Asn Pro  
 405 410 415

Leu Gly Gly Cys Leu Pro Leu Ile Leu Gln Ile Pro Val Phe Phe Ala  
 420 425 430

Ile Tyr Arg Val Leu Tyr Asn Ala Val Glu Leu Lys Ser Ser Glu Trp  
 435 440 445

Ile Leu Trp Ile His Asp Leu Ser Ile Met Asp Pro Tyr Phe Ile Leu  
 450 455 460

Pro Leu Leu Met Gly Ala Ser Met Tyr Trp His Gln Ser Val Thr Pro  
 465 470 475 480

Asn Thr Met Thr Asp Pro Met Gln Ala Lys Ile Phe Lys Leu Leu Pro  
 485 490 495

Leu Leu Phe Thr Ile Phe Leu Ile Thr Phe Pro Ala Gly Leu Val Leu  
 500 505 510

Tyr Trp Thr Thr Asn Asn Ile Leu Ser Val Leu Gln Gln Leu Ile Ile  
 515 520 525

Asn Lys Val Leu Glu Asn Lys Lys Arg Ala His Arg Glu Asn Lys Lys  
 530 535 540

Glu His  
 545

<210> 173  
 <211> 783  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(783)

<400> 173  
 gtg agg caa gaa aag tat ttt ttg act tct tct tta tcg ctt tta tcg 48  
 Val Arg Gln Glu Lys Tyr Phe Leu Thr Ser Ser Leu Ser Leu Ser  
 1 5 10 15  
 ttt tta tta tgt cct gta gaa gct ttt gat tat cgg ttt agt ggt cgt 96  
 Phe Leu Leu Cys Pro Val Glu Ala Phe Asp Tyr Arg Phe Ser Gly Arg  
 20 25 30  
 gtg gag aac ttt tct aag att ggt ttt aac aat tct caa atc aat act 144  
 Val Glu Asn Phe Ser Lys Ile Gly Phe Asn Asn Ser Gln Ile Asn Thr  
 35 40 45  
 aaa aaa ggg att tat cct act gaa agt ttt ata gat att gta act tta 192  
 Lys Lys Gly Ile Tyr Pro Thr Glu Ser Phe Ile Asp Ile Val Thr Leu  
 50 55 60  
 gca caa gtc aaa gtc aat tta ctc cct aaa ggc acc gaa aac cat agg 240  
 Ala Gln Val Lys Val Asn Leu Leu Pro Lys Gly Thr Glu Asn His Arg  
 65 70 75 80  
 ctc tct gtt tct ttg ggt ggg gcg att gca gcc att cct tac gat aag 288  
 Leu Ser Val Ser Leu Gly Gly Ala Ile Ala Ala Ile Pro Tyr Asp Lys  
 85 90 95  
 act aaa tat tat att aac cag gct aac ggg aag gtt ttt ggc tca att 336  
 Thr Lys Tyr Tyr Ile Asn Gln Ala Asn Gly Lys Val Phe Gly Ser Ile  
 100 105 110  
 gtg gag aat ttc att ggg ggc tat cat gga tac ttt ttt aac aag tat 384  
 Val Glu Asn Phe Ile Gly Gly Tyr His Gly Tyr Phe Phe Asn Lys Tyr  
 115 120 125  
 ctt ggc cct gct tat gcg ggg act tct caa tca gcg agc tat cat gca 432  
 Leu Gly Pro Ala Tyr Ala Gly Thr Ser Gln Ser Ala Ser Tyr His Ala

130	135	140	
agg cct tat gtg gtg gat acc gct ttt tta cga tac gat tac aaa gat			480
Arg Pro Tyr Val Val Asp Thr Ala Phe Leu Arg Tyr Asp Tyr Lys Asp			
145	150	155	160
ggt ttt ggg ttt aaa gcg ggg cgc tat gaa gcg aat att gat ttc atg			528
Val Phe Gly Phe Lys Ala Gly Arg Tyr Glu Ala Asn Ile Asp Phe Met			
	165	170	175
agc gga tcg aat caa ggg tgg gaa gtg tat tat cag ccc tat aag act			576
Ser Gly Ser Asn Gln Gly Trp Glu Val Tyr Tyr Gln Pro Tyr Lys Thr			
	180	185	190
gag acg caa agg tta agg ttt tgg tgg tgg agt tct ttt ggg aga ggt			624
Glu Thr Gln Arg Leu Arg Phe Trp Trp Trp Ser Ser Phe Gly Arg Gly			
	195	200	205
tta gcg ttt aac tct tgg att tat gag ttt ttc gcg acc gtg cct tat			672
Leu Ala Phe Asn Ser Trp Ile Tyr Glu Phe Phe Ala Thr Val Pro Tyr			
	210	215	220
ttg aaa aag gga ggc aat cct gat aac agc aac gat ttc atc aat tat			720
Leu Lys Lys Gly Gly Asn Pro Asp Asn Ser Asn Asp Phe Ile Asn Tyr			
	225	230	235
ggc tgg cat ggg atc acc aca acc tat tct tat aaa ggt tta gac gct			768
Gly Trp His Gly Ile Thr Thr Thr Tyr Ser Tyr Lys Gly Leu Asp Ala			
	245	250	255
caa ttt ttt tat att			783
Gln Phe Phe Tyr Ile			
	260		

<210> 174

<211> 261

<212> PRT

<213> Helicobacter pylori

<400> 174

Val Arg Gln Glu Lys Tyr Phe Leu Thr Ser Ser Leu Ser Leu Leu Ser
1 5 10 15

Phe Leu Leu Cys Pro Val Glu Ala Phe Asp Tyr Arg Phe Ser Gly Arg
20 25 30

Val Glu Asn Phe Ser Lys Ile Gly Phe Asn Asn Ser Gln Ile Asn Thr
35 40 45

Lys Lys Gly Ile Tyr Pro Thr Glu Ser Phe Ile Asp Ile Val Thr Leu
---

50		55		60
Ala Gln Val Lys Val Asn Leu Leu Pro Lys Gly Thr Glu Asn His Arg				
65		70		75 80
Leu Ser Val Ser Leu Gly Gly Ala Ile Ala Ala Ile Pro Tyr Asp Lys				
	85		90	95
Thr Lys Tyr Tyr Ile Asn Gln Ala Asn Gly Lys Val Phe Gly Ser Ile				
	100		105	110
Val Glu Asn Phe Ile Gly Gly Tyr His Gly Tyr Phe Phe Asn Lys Tyr				
	115		120	125
Leu Gly Pro Ala Tyr Ala Gly Thr Ser Gln Ser Ala Ser Tyr His Ala				
	130		135	140
Arg Pro Tyr Val Val Asp Thr Ala Phe Leu Arg Tyr Asp Tyr Lys Asp				
145		150		155 160
Val Phe Gly Phe Lys Ala Gly Arg Tyr Glu Ala Asn Ile Asp Phe Met				
	165		170	175
Ser Gly Ser Asn Gln Gly Trp Glu Val Tyr Tyr Gln Pro Tyr Lys Thr				
	180		185	190
Glu Thr Gln Arg Leu Arg Phe Trp Trp Trp Ser Ser Phe Gly Arg Gly				
	195		200	205
Leu Ala Phe Asn Ser Trp Ile Tyr Glu Phe Phe Ala Thr Val Pro Tyr				
	210		215	220
Leu Lys Lys Gly Gly Asn Pro Asp Asn Ser Asn Asp Phe Ile Asn Tyr				
225		230		235 240
Gly Trp His Gly Ile Thr Thr Thr Tyr Ser Tyr Lys Gly Leu Asp Ala				
	245		250	255
Gln Phe Phe Tyr Ile				
	260			

<210> 175  
 <211> 1131  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1131)

<400> 175  
 atg aat ttt ttt aaa atc ctt tta atg gaa tta agg gct att gtt tct 48  
 Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val Ser  
 1 5 10 15  
 cat aaa ggc gtt tta tta atc ctt ata ggc gct cct tta atc tat ggc 96  
 His Lys Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr Gly  
 20 25 30  
 ttg tta tac cct ttg cct tat tta aaa gac atc gta acg cag caa aaa 144  
 Leu Leu Tyr Pro Leu Pro Tyr Leu Lys Asp Ile Val Thr Gln Gln Lys  
 35 40 45  
 atc gcc ctt gta gat gaa gac aat tcc ttc ctt tct agg caa tta gcc 192  
 Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu Ala  
 50 55 60  
 ttc atg gcg caa agc tcc aac gag tta gaa atc gct ttt ttt agc ccc 240  
 Phe Met Ala Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser Pro  
 65 70 75 80  
 tct atg ctg gaa gcc aaa aag ctt tta aaa gaa gaa aaa att tat ggg 288  
 Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr Gly  
 85 90 95  
 atc ttg cat atc cct tcg tat ttt gaa gcc aat atc cat aag cag gtg 336  
 Ile Leu His Ile Pro Ser Tyr Phe Glu Ala Asn Ile His Lys Gln Val  
 100 105 110  
 cct gta acg ata gat ttt tat gcg aat tcc aat tac ttt ttg att tat 384  
 Pro Val Thr Ile Asp Phe Tyr Ala Asn Ser Asn Tyr Phe Leu Ile Tyr  
 115 120 125  
 ggc acc tta gcg aat gcg gtg gtg gag agc atc aac gct tta aat gat 432  
 Gly Thr Leu Ala Asn Ala Val Val Glu Ser Ile Asn Ala Leu Asn Asp  
 130 135 140  
 gag ata aga ttc aaa cgc aac gcc caa ata gaa gaa gct gaa tta ggg 480  
 Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu Leu Gly  
 145 150 155 160  
 aca gac ggg att aaa atc agg cct atc gct ttg tat aac cct agt gag 528  
 Thr Asp Gly Ile Lys Ile Arg Pro Ile Ala Leu Tyr Asn Pro Ser Glu  
 165 170 175

ggg tat ttg aat tac gcg ctc tct agc gtg ttt att ttc ayy tta cac	576
Gly Tyr Leu Asn Tyr Ala Leu Ser Ser Val Phe Ile Phe Xaa Leu His	
180 185 190	
cag gtg atg ctc att gca agc agc atg ttt act agc tct agg cgt ttg	624
Gln Val Met Leu Ile Ala Ser Ser Met Phe Thr Ser Ser Arg Arg Leu	
195 200 205	
gaa tta gcc ctt tta gat aaa aag caa atc gct tta agg ctg tgc gca	672
Glu Leu Ala Leu Leu Asp Lys Lys Gln Ile Ala Leu Arg Leu Cys Ala	
210 215 220	
aga ctc ttg gtg ttt atg gca gcg ttt agc gkt ttt gtt ttg ttg tat	720
Arg Leu Leu Val Phe Met Ala Ala Phe Ser Xaa Phe Val Leu Leu Tyr	
225 230 235 240	
ttt ggg gcg ctg ttt tct ttt tat ggg atc gaa cgg cat gcg agt gct	768
Phe Gly Ala Leu Phe Ser Phe Tyr Gly Ile Glu Arg His Ala Ser Ala	
245 250 255	
tta atg gtg ttt ttg aat agc tcc ata ttc atg ctt gca acc ttg agt	816
Leu Met Val Phe Leu Asn Ser Ser Ile Phe Met Leu Ala Thr Leu Ser	
260 265 270	
ttg ggg tgc ttt tta ggc gca tgg atc aaa aat gaa gcc cac acc act	864
Leu Gly Ser Phe Leu Gly Ala Trp Ile Lys Asn Glu Ala His Thr Thr	
275 280 285	
caa atc gtt ttg att tct tct ttg ccc ttg att ttt atg atg ggt ttt	912
Gln Ile Val Leu Ile Ser Ser Leu Pro Leu Ile Phe Met Met Gly Phe	
290 295 300	
gtg tgg cct ttt gaa tcc ttg ccc tct tat ttg cag gtt ttc gtt caa	960
Val Trp Pro Phe Glu Ser Leu Pro Ser Tyr Leu Gln Val Phe Val Gln	
305 310 315 320	
ata gtg cct gct tat cat ggg atc agt ttg tta ggg cga ttg aat caa	1008
Ile Val Pro Ala Tyr His Gly Ile Ser Leu Leu Gly Arg Leu Asn Gln	
325 330 335	
atg cat gcg gaa ttt ata gat gtt tct gtc cat ttt tat gcg ctt att	1056
Met His Ala Glu Phe Ile Asp Val Ser Val His Phe Tyr Ala Leu Ile	
340 345 350	
gcg att ttt att gcg agt ttt ata ggg agt gtc ttt aaa ctc agc tct	1104
Ala Ile Phe Ile Ala Ser Phe Ile Gly Ser Val Phe Lys Leu Ser Ser	
355 360 365	
tta aag aaa gct tgt gaa aac gct taa	1131
Leu Lys Lys Ala Cys Glu Asn Ala	
370 375	

<210> 176

<211> 376

<212> PRT  
<213> Helicobacter pylori

<220>  
<221> misc\_feature  
<222> (190)..(190)  
<223> The 'Xaa' at location 190 stands for Thr, or Ile.

<220>  
<221> misc\_feature  
<222> (235)..(235)  
<223> The 'Xaa' at location 235 stands for Gly, or Val.

<400> 176

Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val Ser  
1 5 10 15

His Lys Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr Gly  
20 25 30

Leu Leu Tyr Pro Leu Pro Tyr Leu Lys Asp Ile Val Thr Gln Gln Lys  
35 40 45

Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu Ala  
50 55 60

Phe Met Ala Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser Pro  
65 70 75 80

Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr Gly  
85 90 95

Ile Leu His Ile Pro Ser Tyr Phe Glu Ala Asn Ile His Lys Gln Val  
100 105 110

Pro Val Thr Ile Asp Phe Tyr Ala Asn Ser Asn Tyr Phe Leu Ile Tyr  
115 120 125

Gly Thr Leu Ala Asn Ala Val Val Glu Ser Ile Asn Ala Leu Asn Asp  
130 135 140

Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu Leu Gly  
145 150 155 160

Thr Asp Gly Ile Lys Ile Arg Pro Ile Ala Leu Tyr Asn Pro Ser Glu  
165 170 175

Gly Tyr Leu Asn Tyr Ala Leu Ser Ser Val Phe Ile Phe Xaa Leu His  
180 185 190

Gln Val Met Leu Ile Ala Ser Ser Met Phe Thr Ser Ser Arg Arg Leu  
195 200 205

Glu Leu Ala Leu Leu Asp Lys Lys Gln Ile Ala Leu Arg Leu Cys Ala  
210 215 220

Arg Leu Leu Val Phe Met Ala Ala Phe Ser Xaa Phe Val Leu Leu Tyr  
225 230 235 240

Phe Gly Ala Leu Phe Ser Phe Tyr Gly Ile Glu Arg His Ala Ser Ala  
245 250 255

Leu Met Val Phe Leu Asn Ser Ser Ile Phe Met Leu Ala Thr Leu Ser  
260 265 270

Leu Gly Ser Phe Leu Gly Ala Trp Ile Lys Asn Glu Ala His Thr Thr  
275 280 285

Gln Ile Val Leu Ile Ser Ser Leu Pro Leu Ile Phe Met Met Gly Phe  
290 295 300

Val Trp Pro Phe Glu Ser Leu Pro Ser Tyr Leu Gln Val Phe Val Gln  
305 310 315 320

Ile Val Pro Ala Tyr His Gly Ile Ser Leu Leu Gly Arg Leu Asn Gln  
325 330 335

Met His Ala Glu Phe Ile Asp Val Ser Val His Phe Tyr Ala Leu Ile  
340 345 350

Ala Ile Phe Ile Ala Ser Phe Ile Gly Ser Val Phe Lys Leu Ser Ser  
355 360 365

Leu Lys Lys Ala Cys Glu Asn Ala  
370 375



<210> 177  
 <211> 675  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(675)

<400> 177  
 atg aaa gcg tta aag att ttt tta aaa aaa tcc ctt att ctg ttg ttg 48  
 Met Lys Ala Leu Lys Ile Phe Leu Lys Lys Ser Leu Ile Leu Leu Leu  
 1 5 10 15  
 gcg att gct tta agc cac ctg aac gct gtg gct atg att gtg gat aat 96  
 Ala Ile Ala Leu Ser His Leu Asn Ala Val Ala Met Ile Val Asp Asn  
 20 25 30  
 cct acg cag aat atc tgg caa caa gca aaa gac gct ata gac aag tct 144  
 Pro Thr Gln Asn Ile Trp Gln Gln Ala Lys Asp Ala Ile Asp Lys Ser  
 35 40 45  
 cgc ttt gtt caa cag gtc aat cat tgg gct gac caa atc aaa aaa tac 192  
 Arg Phe Val Gln Gln Val Asn His Trp Ala Asp Gln Ile Lys Lys Tyr  
 50 55 60  
 caa gat atg ata gaa aaa gct caa tca acc att aac caa cta aat aaa 240  
 Gln Asp Met Ile Glu Lys Ala Gln Ser Thr Ile Asn Gln Leu Asn Lys  
 65 70 75 80  
 gtg aat gat att tta ctg aaa acc aat cag ttt atg aat ggt tct att 288  
 Val Asn Asp Ile Leu Leu Lys Thr Asn Gln Phe Met Asn Gly Ser Ile  
 85 90 95  
 tta aat atc cct aac cct atg ggt tta gta gaa aat gca act caa att 336  
 Leu Asn Ile Pro Asn Pro Met Gly Leu Val Glu Asn Ala Thr Gln Ile  
 100 105 110  
 gcc aag aat gta aag tca aac gct ctc gcc cta caa gaa agc gct aaa 384  
 Ala Lys Asn Val Lys Ser Asn Ala Leu Ala Leu Gln Glu Ser Ala Lys  
 115 120 125  
 aac tac aat cta gcc gaa aaa ttt tta tta cga aat att gct agc aaa 432  
 Asn Tyr Asn Leu Ala Glu Lys Phe Leu Leu Arg Asn Ile Ala Ser Lys  
 130 135 140  
 tgc cct gaa tta gat atg aat aaa att aac cca aaa aca aaa gag att 480  
 Cys Pro Glu Leu Asp Met Asn Lys Ile Asn Pro Lys Thr Lys Glu Ile  
 145 150 155 160  
 ttt ttc tcc gat aag gga aaa gaa aag agt gcc gct aga caa gct tta 528  
 Phe Phe Ser Asp Lys Gly Lys Glu Lys Ser Ala Ala Arg Gln Ala Leu  
 165 170 175

gaa aat tta gct aat gca ctt gga aat aca caa att aca acc act caa	576
Glu Asn Leu Ala Asn Ala Leu Gly Asn Thr Gln Ile Thr Thr Thr Gln	
180 185 190	

cat ata aca aca agt tta agt ggt agg gct tty agc aga ctt yat ttg	624
His Ile Thr Thr Ser Leu Ser Gly Arg Ala Phe Ser Arg Leu Xaa Leu	
195 200 205	

caa aac aaa aga gca aga act ttt agc aga yaa aaa agc aac aat acc	672
Gln Asn Lys Arg Ala Arg Thr Phe Ser Arg Xaa Lys Ser Asn Asn Thr	
210 215 220	

tag	675
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<210> 178  
 <211> 224  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <221> misc\_feature  
 <222> (207)..(207)  
 <223> The 'Xaa' at location 207 stands for His, or Tyr.

<220>  
 <221> misc\_feature  
 <222> (219)..(219)  
 <223> The 'Xaa' at location 219 stands for Gln.

<400> 178

Met Lys Ala Leu Lys Ile Phe Leu Lys Lys Ser Leu Ile Leu Leu Leu
1 5 10 15

Ala Ile Ala Leu Ser His Leu Asn Ala Val Ala Met Ile Val Asp Asn
20 25 30

Pro Thr Gln Asn Ile Trp Gln Gln Ala Lys Asp Ala Ile Asp Lys Ser
35 40 45

Arg Phe Val Gln Gln Val Asn His Trp Ala Asp Gln Ile Lys Lys Tyr
50 55 60

Gln Asp Met Ile Glu Lys Ala Gln Ser Thr Ile Asn Gln Leu Asn Lys
65 70 75 80

Val Asn Asp Ile Leu Leu Lys Thr Asn Gln Phe Met Asn Gly Ser Ile
85 90 95

Leu Asn Ile Pro Asn Pro Met Gly Leu Val Glu Asn Ala Thr Gln Ile  
100 105 110

Ala Lys Asn Val Lys Ser Asn Ala Leu Ala Leu Gln Glu Ser Ala Lys  
115 120 125

Asn Tyr Asn Leu Ala Glu Lys Phe Leu Leu Arg Asn Ile Ala Ser Lys  
130 135 140

Cys Pro Glu Leu Asp Met Asn Lys Ile Asn Pro Lys Thr Lys Glu Ile  
145 150 155 160

Phe Phe Ser Asp Lys Gly Lys Glu Lys Ser Ala Ala Arg Gln Ala Leu  
165 170 175

Glu Asn Leu Ala Asn Ala Leu Gly Asn Thr Gln Ile Thr Thr Thr Gln  
180 185 190

His Ile Thr Thr Ser Leu Ser Gly Arg Ala Phe Ser Arg Leu Xaa Leu  
195 200 205

Gln Asn Lys Arg Ala Arg Thr Phe Ser Arg Xaa Lys Ser Asn Asn Thr  
210 215 220

<210> 179  
<211> 348  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(348)

<400>	179	
atg atg ttt tct tca atg ttt gct tcg tta ggg act cgt atc atg ctg		48
Met Met Phe Ser Ser Met Phe Ala Ser Leu Gly Thr Arg Ile Met Leu		
1 5 10 15		
gtc gtg tta gcc gct ctt ttg ggt tta ggg ggg ctt ttt att ggt ttt		96
Val Val Leu Ala Ala Leu Leu Gly Leu Gly Gly Leu Phe Ile Gly Phe		
20 25 30		
gta aag gtt atg caa aaa gat gtg cta gcg caa ctc atg gag cat tta		144
Val Lys Val Met Gln Lys Asp Val Leu Ala Gln Leu Met Glu His Leu		

35					40					45							
gaa	acc	ggg	caa	tac	aaa	aag	cgt	gaa	aaa	acg	ctc	gct	tac	atg	aca	192	
Glu	Thr	Gly	Gln	Tyr	Lys	Lys	Arg	Glu	Lys	Thr	Leu	Ala	Tyr	Met	Thr		
50					55					60							
aaa	ctt	ctt	gaa	cag	ggc	att	cat	gaa	tat	tac	aaa	agt	ttt	gac	aat	240	
Lys	Leu	Leu	Glu	Gln	Gly	Ile	His	Glu	Tyr	Tyr	Lys	Ser	Phe	Asp	Asn		
65					70					75					80		
gct	act	gca	aga	aaa	atg	gcg	ttg	gat	tat	ttt	aaa	cgc	atc	aac	gac	288	
Ala	Thr	Ala	Arg	Lys	Met	Ala	Leu	Asp	Tyr	Phe	Lys	Arg	Ile	Asn	Asp		
85					90					95							
gat	aaa	ggc	atg	att	tat	atg	gtg	gtg	gtg	gat	aaa	aac	ggg	gtg	gtg	336	
Asp	Lys	Gly	Met	Ile	Tyr	Met	Val	Val	Val	Asp	Lys	Asn	Gly	Val	Val		
100					105					110							
ctg	ttt	gat	ccg													348	
Leu	Phe	Asp	Pro														
115																	

<210> 180  
 <211> 116  
 <212> PRT  
 <213> Helicobacter pylori

<400> 180

Met	Met	Phe	Ser	Ser	Met	Phe	Ala	Ser	Leu	Gly	Thr	Arg	Ile	Met	Leu
1				5					10					15	

Val	Val	Leu	Ala	Ala	Leu	Leu	Gly	Leu	Gly	Gly	Leu	Phe	Ile	Gly	Phe
			20					25					30		

Val	Lys	Val	Met	Gln	Lys	Asp	Val	Leu	Ala	Gln	Leu	Met	Glu	His	Leu
	35						40					45			

Glu	Thr	Gly	Gln	Tyr	Lys	Lys	Arg	Glu	Lys	Thr	Leu	Ala	Tyr	Met	Thr
50					55					60					

Lys	Leu	Leu	Glu	Gln	Gly	Ile	His	Glu	Tyr	Tyr	Lys	Ser	Phe	Asp	Asn	
65					70					75					80	

Ala	Thr	Ala	Arg	Lys	Met	Ala	Leu	Asp	Tyr	Phe	Lys	Arg	Ile	Asn	Asp
85					90					95					

Asp	Lys	Gly	Met	Ile	Tyr	Met	Val	Val	Val	Asp	Lys	Asn	Gly	Val	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100

105

110

Leu Phe Asp Pro  
115

&lt;210&gt; 181

&lt;211&gt; 1359

&lt;212&gt; DNA

&lt;213&gt; Helicobacter pylori

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1359)

&lt;400&gt; 181

atg	aaa	aaa	ttg	gtt	tta	atc	atc	ttt	tta	acg	cta	aca	ctt	tca	ata	48
Met	Lys	Lys	Leu	Val	Leu	Ile	Ile	Phe	Leu	Thr	Leu	Thr	Leu	Ser	Ile	
1				5					10					15		

tct	gca	aaa	gaa	gtg	aaa	ata	gtg	ttt	tta	gaa	act	tca	gac	att	cat	96
Ser	Ala	Lys	Glu	Val	Lys	Ile	Val	Phe	Leu	Glu	Thr	Ser	Asp	Ile	His	
			20					25					30			

ggg	cgg	ctt	ttt	tcg	tat	gat	tat	gcg	act	ggc	gag	caa	aaa	ccc	gat	144
Gly	Arg	Leu	Phe	Ser	Tyr	Asp	Tyr	Ala	Thr	Gly	Glu	Gln	Lys	Pro	Asp	
		35					40					45				

aac	ggc	ttg	aca	agg	att	gcg	act	tta	atc	aaa	aag	caa	agg	gct	gaa	192
Asn	Gly	Leu	Thr	Arg	Ile	Ala	Thr	Leu	Ile	Lys	Lys	Gln	Arg	Ala	Glu	
	50					55					60					

aat	aaa	aat	gtg	gtt	ttg	att	gac	agc	ggg	gat	ttg	ttg	cag	ggc	aat	240
Asn	Lys	Asn	Val	Val	Leu	Ile	Asp	Ser	Gly	Asp	Leu	Leu	Gln	Gly	Asn	
65					70				75						80	

agc	gcg	gag	ttg	ttt	aac	gat	gag	ccc	att	cac	ccg	ctc	gtt	tta	gcc	288
Ser	Ala	Glu	Leu	Phe	Asn	Asp	Glu	Pro	Ile	His	Pro	Leu	Val	Leu	Ala	
				85					90					95		

gaa	aac	gat	ttg	aaa	ttt	gat	att	cgt	gtg	ctt	ggg	aat	cac	gag	ttt	336
Glu	Asn	Asp	Leu	Lys	Phe	Asp	Ile	Arg	Val	Leu	Gly	Asn	His	Glu	Phe	
			100					105					110			

aat	ttc	agt	aag	gat	ttt	tta	gag	aaa	aac	att	aag	ggg	ttt	aat	ggt	384
Asn	Phe	Ser	Lys	Asp	Phe	Leu	Glu	Lys	Asn	Ile	Lys	Gly	Phe	Asn	Gly	
		115					120					125				

gat	gtc	gtg	aat	gcg	aat	atc	atc	aag	act	ata	gac	aat	aag	ccg	ttt	432
Asp	Val	Val	Asn	Ala	Asn	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Lys	Pro	Phe	
	130					135					140					

gta	aag	cct	tat	gca	att	aaa	aca	att	gat	ggc	gtg	agg	gtg	gcg	gtt	480
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Val 145	Lys	Pro	Tyr	Ala	Ile 150	Lys	Thr	Ile	Asp	Gly 155	Val	Arg	Val	Ala	Val 160	
gtg	ggg	tat	gtg	gtg	gcg	cac	atc	ccc	act	tgg	gag	gcc	gct	acg	cct	528
Val	Gly	Tyr	Val	Val	Ala	His	Ile	Pro	Thr	Trp	Glu	Ala	Ala	Thr	Pro	
				165					170					175		
gaa	cat	ttt	gca	ggg	tta	aag	ttt	ttg	gac	gcc	aaa	gaa	gcg	tta	aaa	576
Glu	His	Phe	Ala	Gly	Leu	Lys	Phe	Leu	Asp	Ala	Lys	Glu	Ala	Leu	Lys	
			180					185					190			
aag	act	ttg	aaa	gag	cta	aaa	ggg	aag	tat	gat	att	ttg	att	ggg	gct	624
Lys	Thr	Leu	Lys	Glu	Leu	Lys	Gly	Lys	Tyr	Asp	Ile	Leu	Ile	Gly	Ala	
		195					200					205				
ttt	cat	ttg	ggg	cga	gaa	gat	gag	aaa	ggg	ggc	gac	gga	ata	cct	gat	672
Phe	His	Leu	Gly	Arg	Glu	Asp	Glu	Lys	Gly	Gly	Asp	Gly	Ile	Pro	Asp	
	210					215					220					
ctg	gcg	aaa	aaa	ttc	ccg	caa	ttt	gac	atc	att	ttt	gca	ggg	cat	gag	720
Leu	Ala	Lys	Lys	Phe	Pro	Gln	Phe	Asp	Ile	Ile	Phe	Ala	Gly	His	Glu	
225					230					235					240	
cat	gcg	gtt	tat	aac	acc	aaa	ata	gga	aag	gtg	cat	acc	att	gag	cct	768
His	Ala	Val	Tyr	Asn	Thr	Lys	Ile	Gly	Lys	Val	His	Thr	Ile	Glu	Pro	
				245					250					255		
gga	gcg	tat	ggg	gct	tat	ctg	gca	aaa	ggc	gtg	gta	gta	ttt	gac	acc	816
Gly	Ala	Tyr	Gly	Ala	Tyr	Leu	Ala	Lys	Gly	Val	Val	Val	Phe	Asp	Thr	
			260					265					270			
aaa	acg	aag	aaa	aaa	atc	gta	acg	act	gaa	aat	tta	ccc	aca	aaa	ggc	864
Lys	Thr	Lys	Lys	Lys	Ile	Val	Thr	Thr	Glu	Asn	Leu	Pro	Thr	Lys	Gly	
		275					280					285				
gtg	cca	gaa	gat	gaa	gaa	tta	gcg	aaa	aaa	tat	gaa	tat	gtg	gat	aaa	912
Val	Pro	Glu	Asp	Glu	Glu	Leu	Ala	Lys	Lys	Tyr	Glu	Tyr	Val	Asp	Lys	
	290					295					300					
aaa	tca	aaa	gaa	tac	gct	aat	gaa	gtg	gtt	ggc	gaa	gtt	aca	aaa	acc	960
Lys	Ser	Lys	Glu	Tyr	Ala	Asn	Glu	Val	Val	Gly	Glu	Val	Thr	Lys	Thr	
305					310					315					320	
ttt	att	gac	agg	cct	gat	ttc	atc	aca	gga	gga	gaa	aaa	atc	act	acg	1008
Phe	Ile	Asp	Arg	Pro	Asp	Phe	Ile	Thr	Gly	Gly	Glu	Lys	Ile	Thr	Thr	
				325					330					335		
atg	ccc	acc	gcc	gcc	ttg	caa	gaa	aca	ccg	gtg	ata	gaa	ttg	atc	aat	1056
Met	Pro	Thr	Ala	Ala	Leu	Gln	Glu	Thr	Pro	Val	Ile	Glu	Leu	Ile	Asn	
			340					345					350			
aaa	gtg	caa	aaa	tat	tac	gca	aaa	gcc	gat	gtt	tca	gcg	gcc	gcc	tta	1104
Lys	Val	Gln	Lys	Tyr	Tyr	Ala	Lys	Ala	Asp	Val	Ser	Ala	Ala	Ala	Leu	
		355					360					365				

ttc aat ttt ggg gcc aat ttg aaa aaa ggg cct ttc aaa aga aaa gat	1152
Phe Asn Phe Gly Ala Asn Leu Lys Lys Gly Pro Phe Lys Arg Lys Asp	
370 375 380	
gtc gcc tac att tac aag ttc gct aac acg ctc att gga gtg gag ata	1200
Val Ala Tyr Ile Tyr Lys Phe Ala Asn Thr Leu Ile Gly Val Glu Ile	
385 390 395 400	
acg ggt gaa aat ctg ttg aaa tac atg gaa tgg tcg tat caa ttt tac	1248
Thr Gly Glu Asn Leu Leu Lys Tyr Met Glu Trp Ser Tyr Gln Phe Tyr	
405 410 415	
aat cag ttg caa cca ggc gat tta acg atc agt ttt aat gaa aat att	1296
Asn Gln Leu Gln Pro Gly Asp Leu Thr Ile Ser Phe Asn Glu Asn Ile	
420 425 430	
cgt ggt tat aac ttt gat atg ttt tct ggc gtg aaa tac cag gtt gat	1344
Arg Gly Tyr Asn Phe Asp Met Phe Ser Gly Val Lys Tyr Gln Val Asp	
435 440 445	
gtt aca aaa ccc gcc	1359
Val Thr Lys Pro Ala	
450	

<210> 182  
 <211> 453  
 <212> PRT  
 <213> Helicobacter pylori

<400> 182

Met Lys Lys Leu Val Leu Ile Ile Phe Leu Thr Leu Thr Leu Ser Ile	
1 5 10 15	
Ser Ala Lys Glu Val Lys Ile Val Phe Leu Glu Thr Ser Asp Ile His	
20 25 30	
Gly Arg Leu Phe Ser Tyr Asp Tyr Ala Thr Gly Glu Gln Lys Pro Asp	
35 40 45	
Asn Gly Leu Thr Arg Ile Ala Thr Leu Ile Lys Lys Gln Arg Ala Glu	
50 55 60	
Asn Lys Asn Val Val Leu Ile Asp Ser Gly Asp Leu Leu Gln Gly Asn	
65 70 75 80	
Ser Ala Glu Leu Phe Asn Asp Glu Pro Ile His Pro Leu Val Leu Ala	
85 90 95	

Glu	Asn	Asp	Leu	Lys	Phe	Asp	Ile	Arg	Val	Leu	Gly	Asn	His	Glu	Phe	100	105	110
Asn	Phe	Ser	Lys	Asp	Phe	Leu	Glu	Lys	Asn	Ile	Lys	Gly	Phe	Asn	Gly	115	120	125
Asp	Val	Val	Asn	Ala	Asn	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Lys	Pro	Phe	130	135	140
Val	Lys	Pro	Tyr	Ala	Ile	Lys	Thr	Ile	Asp	Gly	Val	Arg	Val	Ala	Val	145	150	155
Val	Gly	Tyr	Val	Val	Ala	His	Ile	Pro	Thr	Trp	Glu	Ala	Ala	Thr	Pro	165	170	175
Glu	His	Phe	Ala	Gly	Leu	Lys	Phe	Leu	Asp	Ala	Lys	Glu	Ala	Leu	Lys	180	185	190
Lys	Thr	Leu	Lys	Glu	Leu	Lys	Gly	Lys	Tyr	Asp	Ile	Leu	Ile	Gly	Ala	195	200	205
Phe	His	Leu	Gly	Arg	Glu	Asp	Glu	Lys	Gly	Gly	Asp	Gly	Ile	Pro	Asp	210	215	220
Leu	Ala	Lys	Lys	Phe	Pro	Gln	Phe	Asp	Ile	Ile	Phe	Ala	Gly	His	Glu	225	230	235
His	Ala	Val	Tyr	Asn	Thr	Lys	Ile	Gly	Lys	Val	His	Thr	Ile	Glu	Pro	245	250	255
Gly	Ala	Tyr	Gly	Ala	Tyr	Leu	Ala	Lys	Gly	Val	Val	Val	Phe	Asp	Thr	260	265	270
Lys	Thr	Lys	Lys	Lys	Ile	Val	Thr	Thr	Glu	Asn	Leu	Pro	Thr	Lys	Gly	275	280	285
Val	Pro	Glu	Asp	Glu	Glu	Leu	Ala	Lys	Lys	Tyr	Glu	Tyr	Val	Asp	Lys	290	295	300
Lys	Ser	Lys	Glu	Tyr	Ala	Asn	Glu	Val	Val	Gly	Glu	Val	Thr	Lys	Thr	305	310	315



Phe Ile Asp Arg Pro Asp Phe Ile Thr Gly Gly Glu Lys Ile Thr Thr  
325 330 335

Met Pro Thr Ala Ala Leu Gln Glu Thr Pro Val Ile Glu Leu Ile Asn  
340 345 350

Lys Val Gln Lys Tyr Tyr Ala Lys Ala Asp Val Ser Ala Ala Ala Leu  
355 360 365

Phe Asn Phe Gly Ala Asn Leu Lys Lys Gly Pro Phe Lys Arg Lys Asp  
370 375 380

Val Ala Tyr Ile Tyr Lys Phe Ala Asn Thr Leu Ile Gly Val Glu Ile  
385 390 395 400

Thr Gly Glu Asn Leu Leu Lys Tyr Met Glu Trp Ser Tyr Gln Phe Tyr  
405 410 415

Asn Gln Leu Gln Pro Gly Asp Leu Thr Ile Ser Phe Asn Glu Asn Ile  
420 425 430

Arg Gly Tyr Asn Phe Asp Met Phe Ser Gly Val Lys Tyr Gln Val Asp  
435 440 445

Val Thr Lys Pro Ala  
450

<210> 183  
<211> 858  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(858)

<220>  
<221> misc\_feature  
<222> (91)..(91)  
<223> n is a, c, g, or t

<400> 183  
ttg ggt atc aat atg tgt tct aaa aaa ata aga aat ttc att tta tgc

Leu 1	Gly	Ile	Asn	Met 5	Cys	Ser	Lys	Lys	Ile 10	Arg	Asn	Phe	Ile	Leu 15	Cys	
ttt Phe	ggt Gly	ttt Phe	att Ile 20	tta Leu	agc Ser	ttg Leu	cac His	gct Ala 25	gaa Glu	gag Glu	agt Ser	atg Met	act Thr 30	ntg Xaa	act Thr	96
gaa Glu	gaa Glu	aat Asn 35	acc Thr	cct Pro	aaa Lys	gac Asp	gct Ala 40	ccc Pro	att Ile	ctt Leu	ttg Leu	gaa Glu 45	gaa Glu	aaa Lys	cgc Arg	144
gcc Ala 50	caa Gln	acg Thr	cta Leu	gag Glu	ttt Phe	gaa Glu 55	gaa Glu	aac Asn	aag Lys	gaa Glu	gtt Val 60	aaa Lys	aag Lys	aat Asn	att Ile	192
gat Asp 65	gaa Glu	aaa Lys	agc Ser	ctg Leu 70	ctt Leu	gaa Glu	gaa Glu	atc Ile	cat His	aag Lys 75	aaa Lys	aaa Lys	cgc Arg	cag Gln	ctt Leu 80	240
tac Tyr	atg Met	ctc Leu	aaa Lys 85	ggg Gly	gaa Glu	ttg Leu	cat His	gaa Glu 90	aaa Lys	aat Asn	gaa Glu	tcc Ser	att Ile 95	tta Leu	ttc Phe	288
caa Gln	cga Arg	atg Met	gct Ala 100	aaa Lys	aac Asn	aag Lys	agc Ser	ggg Gly 105	ttt Phe	ttt Phe	ata Ile	ggc Gly	gta Val 110	att Ile	ctt Leu	336
ggc Gly	gat Asp	ata Ile 115	ggg Gly	att Ile	aac Asn	gct Ala	cat His 120	cct Pro	aac Asn	acc Thr	cga Arg	tct Ser	tat Tyr	gag Glu	agc Ser	384
ttt Phe 130	gaa Glu	cct Pro	tta Leu	agc Ser	aac Asn	att Ile 135	caa Gln	gat Asp	tct Ser	cct Pro	tta Leu 140	ttg Leu	tat Tyr	ggc Gly	tta Leu	432
agg Arg 145	agc Ser	ggg Gly	tat Tyr	caa Gln	aag Lys 150	tat Tyr	ttt Phe	gct Ala	aac Asn 155	ggg Gly	att Ile	agc Ser	gcc Ala	tta Leu	cgc Arg 160	480
ttt Phe	tat Tyr	ggg Gly	gag Glu	tat Tyr 165	tta Leu	ggg Gly	ggg Gly	gcg Ala	atg Met 170	aaa Lys	ggg Gly	ttt Phe	aaa Lys	agc Ser 175	gat Asp	528
tct Ser	tta Leu	gcc Ala	tct Ser 180	tat Tyr	caa Gln	acc Thr	gca Ala	agc Ser 185	ttg Leu	aac Asn	att Ile	gat Asp	ttg Leu 190	ttg Leu	atg Met	576
gat Asp	aag Lys	cct Pro 195	att Ile	gat Asp	aaa Lys	gaa Glu	aaa Lys 200	agg Arg	ttt Phe	gcg Ala	tta Leu	ggg Gly 205	ata Ile	ttt Phe	gga Gly	624
ggc Gly 210	gtt Val	gga Gly	gtg Val	ggg Gly	tgg Trp	aat Asn 215	ggg Gly	atg Met	tat Tyr	caa Gln	aat Asn 220	tta Leu	aaa Lys	gag Glu	att Ile	672

aaa ggg tat tca cag cct aac gct ttt gga tta gtg cta aat tta ggg	720
Lys Gly Tyr Ser Gln Pro Asn Ala Phe Gly Leu Val Leu Asn Leu Gly	
225 230 235 240	

gtg agc atg acg ctt aac ctc aaa cac cgc ttt gaa tta gcc tta aaa	768
Val Ser Met Thr Leu Asn Leu Lys His Arg Phe Glu Leu Ala Leu Lys	
245 250 255	

atg cct ccc tta aaa gaa act tcg caa act ttt tta tat tat ttt aaa	816
Met Pro Pro Leu Lys Glu Thr Ser Gln Thr Phe Leu Tyr Tyr Phe Lys	
260 265 270	

agc act aat att tat tat att agt tac aac tat tta ttg taa	858
Ser Thr Asn Ile Tyr Tyr Ile Ser Tyr Asn Tyr Leu Leu	
275 280 285	

<210> 184

<211> 285

<212> PRT

<213> Helicobacter pylori

<220>

<221> misc\_feature

<222> (31)..(31)

<223> The 'Xaa' at location 31 stands for Met, Val, or Leu.

<400> 184

Leu Gly Ile Asn Met Cys Ser Lys Lys Ile Arg Asn Phe Ile Leu Cys
1 5 10 15

Phe Gly Phe Ile Leu Ser Leu His Ala Glu Glu Ser Met Thr Xaa Thr
20 25 30

Glu Glu Asn Thr Pro Lys Asp Ala Pro Ile Leu Leu Glu Glu Lys Arg
35 40 45

Ala Gln Thr Leu Glu Phe Glu Glu Asn Lys Glu Val Lys Lys Asn Ile
50 55 60

Asp Glu Lys Ser Leu Leu Glu Glu Ile His Lys Lys Lys Arg Gln Leu
65 70 75 80

Tyr Met Leu Lys Gly Glu Leu His Glu Lys Asn Glu Ser Ile Leu Phe
85 90 95

Gln Arg Met Ala Lys Asn Lys Ser Gly Phe Phe Ile Gly Val Ile Leu
100 105 110

Gly Asp Ile Gly Ile Asn Ala His Pro Asn Thr Arg Ser Tyr Glu Ser  
115 120 125

Phe Glu Pro Leu Ser Asn Ile Gln Asp Ser Pro Leu Leu Tyr Gly Leu  
130 135 140

Arg Ser Gly Tyr Gln Lys Tyr Phe Ala Asn Gly Ile Ser Ala Leu Arg  
145 150 155 160

Phe Tyr Gly Glu Tyr Leu Gly Gly Ala Met Lys Gly Phe Lys Ser Asp  
165 170 175

Ser Leu Ala Ser Tyr Gln Thr Ala Ser Leu Asn Ile Asp Leu Leu Met  
180 185 190

Asp Lys Pro Ile Asp Lys Glu Lys Arg Phe Ala Leu Gly Ile Phe Gly  
195 200 205

Gly Val Gly Val Gly Trp Asn Gly Met Tyr Gln Asn Leu Lys Glu Ile  
210 215 220

Lys Gly Tyr Ser Gln Pro Asn Ala Phe Gly Leu Val Leu Asn Leu Gly  
225 230 235 240

Val Ser Met Thr Leu Asn Leu Lys His Arg Phe Glu Leu Ala Leu Lys  
245 250 255

Met Pro Pro Leu Lys Glu Thr Ser Gln Thr Phe Leu Tyr Tyr Phe Lys  
260 265 270

Ser Thr Asn Ile Tyr Tyr Ile Ser Tyr Asn Tyr Leu Leu  
275 280 285

<210> 185  
<211> 804  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS

<222> (1)..(804)

<400> 185

atg tca gaa aaa gaa aga ctg aat gaa gtg atc tta gaa gaa gaa aat	48
Met Ser Glu Lys Glu Arg Leu Asn Glu Val Ile Leu Glu Glu Glu Asn	
1 5 10 15	
aat ggg ggc ggc act aaa aag gtg ttt ttg atc gtg gct ata gcc att	96
Asn Gly Gly Gly Thr Lys Lys Val Phe Leu Ile Val Ala Ile Ala Ile	
20 25 30	
atc att tta gcg gtg ctt tta atg gtg ttt tgg aaa agc acg aga gtc	144
Ile Ile Leu Ala Val Leu Leu Met Val Phe Trp Lys Ser Thr Arg Val	
35 40 45	
gct cct aaa gag act ttt tta caa acc gat agc ggg atg caa aaa ata	192
Ala Pro Lys Glu Thr Phe Leu Gln Thr Asp Ser Gly Met Gln Lys Ile	
50 55 60	
ggc aac act aaa gac gag aaa aaa gac gat gag ttt gaa agc ttg aat	240
Gly Asn Thr Lys Asp Glu Lys Lys Asp Asp Glu Phe Glu Ser Leu Asn	
65 70 75 80	
ttg gat cct tcc aag caa gaa gac aag cta gac aaa gta gcg gat aat	288
Leu Asp Pro Ser Lys Gln Glu Asp Lys Leu Asp Lys Val Ala Asp Asn	
85 90 95	
gtt aaa aaa caa gaa aat gat gcg ttt aac atg ccc act caa acc aat	336
Val Lys Lys Gln Glu Asn Asp Ala Phe Asn Met Pro Thr Gln Thr Asn	
100 105 110	
caa act caa acg gag atg aaa aca gca gaa gaa acg caa gaa gct caa	384
Gln Thr Gln Thr Glu Met Lys Thr Ala Glu Glu Thr Gln Glu Ala Gln	
115 120 125	
aaa gaa tta aaa gct gtt gag cac act agc gct caa aaa gaa tct caa	432
Lys Glu Leu Lys Ala Val Glu His Thr Ser Ala Gln Lys Glu Ser Gln	
130 135 140	
gct gtg gct aaa aaa gaa acc ccc cat aaa aag ccc aaa gca acc cct	480
Ala Val Ala Lys Lys Glu Thr Pro His Lys Lys Pro Lys Ala Thr Pro	
145 150 155 160	
aaa gat aag gaa gct cat aaa gat aaa gat aag cat gcg gtt aaa gag	528
Lys Asp Lys Glu Ala His Lys Asp Lys Asp Lys His Ala Val Lys Glu	
165 170 175	
cta aaa gtc aaa aaa gaa gct cat aaa gaa gtt cct aaa aaa gcc aat	576
Leu Lys Val Lys Lys Glu Ala His Lys Glu Val Pro Lys Lys Ala Asn	
180 185 190	
tct aaa acc act ctt act aaa ggg cat tat ttg caa gtg ggg gtt ttt	624
Ser Lys Thr Thr Leu Thr Lys Gly His Tyr Leu Gln Val Gly Val Phe	
195 200 205	

gcg	cac	acg	ccc	aat	aaa	gcc	ttt	ttg	caa	gcg	ttt	aac	caa	ttc	ccc	672
Ala	His	Thr	Pro	Asn	Lys	Ala	Phe	Leu	Gln	Ala	Phe	Asn	Gln	Phe	Pro	
210						215					220					

cat	aag	att	gaa	gat	agg	gga	gca	acg	aag	cgc	tat	ctc	ata	ggc	cct	720
His	Lys	Ile	Glu	Asp	Arg	Gly	Ala	Thr	Lys	Arg	Tyr	Leu	Ile	Gly	Pro	
225					230					235					240	

tat	aag	agc	aag	caa	gaa	gcc	tta	atg	cat	gct	gat	gaa	gtc	agc	aaa	768
Tyr	Lys	Ser	Lys	Gln	Glu	Ala	Leu	Met	His	Ala	Asp	Glu	Val	Ser	Lys	
				245					250					255		

aag	atg	act	aaa	ccg	gtt	gtc	ata	gaa	gcg	cat	tag					804
Lys	Met	Thr	Lys	Pro	Val	Val	Ile	Glu	Ala	His						
				260					265							

<210> 186

<211> 267

<212> PRT

<213> Helicobacter pylori

<400> 186

Met	Ser	Glu	Lys	Glu	Arg	Leu	Asn	Glu	Val	Ile	Leu	Glu	Glu	Glu	Asn
1				5					10					15	

Asn	Gly	Gly	Gly	Thr	Lys	Lys	Val	Phe	Leu	Ile	Val	Ala	Ile	Ala	Ile
			20					25					30		

Ile	Ile	Leu	Ala	Val	Leu	Leu	Met	Val	Phe	Trp	Lys	Ser	Thr	Arg	Val
		35					40					45			

Ala	Pro	Lys	Glu	Thr	Phe	Leu	Gln	Thr	Asp	Ser	Gly	Met	Gln	Lys	Ile
	50					55					60				

Gly	Asn	Thr	Lys	Asp	Glu	Lys	Lys	Asp	Asp	Glu	Phe	Glu	Ser	Leu	Asn
65					70					75					80

Leu	Asp	Pro	Ser	Lys	Gln	Glu	Asp	Lys	Leu	Asp	Lys	Val	Ala	Asp	Asn
				85					90					95	

Val	Lys	Lys	Gln	Glu	Asn	Asp	Ala	Phe	Asn	Met	Pro	Thr	Gln	Thr	Asn
			100					105					110		

Gln	Thr	Gln	Thr	Glu	Met	Lys	Thr	Ala	Glu	Glu	Thr	Gln	Glu	Ala	Gln
		115					120					125			

Lys Glu Leu Lys Ala Val Glu His Thr Ser Ala Gln Lys Glu Ser Gln  
 130 135 140

Ala Val Ala Lys Lys Glu Thr Pro His Lys Lys Pro Lys Ala Thr Pro  
 145 150 155 160

Lys Asp Lys Glu Ala His Lys Asp Lys Asp Lys His Ala Val Lys Glu  
 165 170 175

Leu Lys Val Lys Lys Glu Ala His Lys Glu Val Pro Lys Lys Ala Asn  
 180 185 190

Ser Lys Thr Thr Leu Thr Lys Gly His Tyr Leu Gln Val Gly Val Phe  
 195 200 205

Ala His Thr Pro Asn Lys Ala Phe Leu Gln Ala Phe Asn Gln Phe Pro  
 210 215 220

His Lys Ile Glu Asp Arg Gly Ala Thr Lys Arg Tyr Leu Ile Gly Pro  
 225 230 235 240

Tyr Lys Ser Lys Gln Glu Ala Leu Met His Ala Asp Glu Val Ser Lys  
 245 250 255

Lys Met Thr Lys Pro Val Val Ile Glu Ala His  
 260 265

<210> 187  
 <211> 1657  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1656)

<400> 187  
 atg aaa tct aaa aaa ctt tat ttg gct tta atc ata ggg gtt tta tta  
 Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile Ile Gly Val Leu Leu  
 1 5 10 15

48

gcg ttt tta acc cta tct tca tgg ctg ggt aat agc ggt tta gtg ggg  
 Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn Ser Gly Leu Val Gly

96

20					25					30						
cgt	ttt	ggg	gtg	tgg	ttt	gcc	gca	ctc	aat	aaa	aaa	tat	ttt	ggg	tat	144
Arg	Phe	Gly	Val	Trp	Phe	Ala	Ala	Leu	Asn	Lys	Lys	Tyr	Phe	Gly	Tyr	
		35					40					45				
ctt	tca	ttc	att	aat	ctg	ccc	tat	tta	gcg	tgg	gtt	tta	ttc	ctt	tta	192
Leu	Ser	Phe	Ile	Asn	Leu	Pro	Tyr	Leu	Ala	Trp	Val	Leu	Phe	Leu	Leu	
	50					55					60					
tac	aag	act	ada	aac	cct	ttt	aca	gaa	atc	gtt	tta	gaa	aaa	act	tta	240
Tyr	Lys	Thr	Xaa	Asn	Pro	Phe	Thr	Glu	Ile	Val	Leu	Glu	Lys	Thr	Leu	
65					70					75					80	
ggg	cat	cta	tta	ggc	att	tta	tct	ttg	ctc	ttt	tta	caa	tct	agc	cta	288
Gly	His	Leu	Leu	Gly	Ile	Leu	Ser	Leu	Leu	Phe	Leu	Gln	Ser	Ser	Leu	
				85					90					95		
ttg	aat	caa	ggg	gaa	atc	ggc	aac	agc	gtg	cgt	ttg	ttt	tta	cgc	cct	336
Leu	Asn	Gln	Gly	Glu	Ile	Gly	Asn	Ser	Val	Arg	Leu	Phe	Leu	Arg	Pro	
			100					105					110			
ttt	ata	ggg	gat	ttt	ggg	ctt	tat	gcg	ctg	ata	acg	ctt	atg	gta	gtt	384
Phe	Ile	Gly	Asp	Phe	Gly	Leu	Tyr	Ala	Leu	Ile	Thr	Leu	Met	Val	Val	
		115					120					125				
att	tct	tat	ttg	att	tta	ttc	aaa	cta	ccc	cct	aaa	agc	gtt	ttt	tat	432
Ile	Ser	Tyr	Leu	Ile	Leu	Phe	Lys	Leu	Pro	Pro	Lys	Ser	Val	Phe	Tyr	
	130					135					140					
cct	tat	atg	aac	aaa	aca	caa	aac	ctt	tta	aaa	gag	att	tac	aaa	caa	480
Pro	Tyr	Met	Asn	Lys	Thr	Gln	Asn	Leu	Leu	Lys	Glu	Ile	Tyr	Lys	Gln	
145					150					155					160	
tgc	cta	caa	gcc	ttt	agc	cct	aat	ttt	agc	cca	aaa	aaa	gag	gat	ttt	528
Cys	Leu	Gln	Ala	Phe	Ser	Pro	Asn	Phe	Ser	Pro	Lys	Lys	Glu	Asp	Phe	
			165					170						175		
gaa	aac	acc	tta	tca	gat	ctt	caa	aaa	aaa	gaa	acc	aac	aac	gac	aaa	576
Glu	Asn	Thr	Leu	Ser	Asp	Leu	Gln	Lys	Lys	Glu	Thr	Asn	Asn	Asp	Lys	
			180					185					190			
gaa	aaa	gaa	aat	ctc	aaa	gaa	aac	cct	att	gat	gaa	aac	cac	aaa	acc	624
Glu	Lys	Glu	Asn	Leu	Lys	Glu	Asn	Pro	Ile	Asp	Glu	Asn	His	Lys	Thr	
		195					200					205				
cct	aac	gaa	gaa	tcg	ttt	cta	gcg	atc	cct	acc	ccc	tat	aac	acg	act	672
Pro	Asn	Glu	Glu	Ser	Phe	Leu	Ala	Ile	Pro	Thr	Pro	Tyr	Asn	Thr	Thr	
	210					215					220					
tta	aac	gat	tca	gag	ccg	caa	gaa	ggc	ttg	gtt	caa	att	tcc	cct	cac	720
Leu	Asn	Asp	Ser	Glu	Pro	Gln	Glu	Gly	Leu	Val	Gln	Ile	Ser	Pro	His	
225					230					235					240	
ccc	cct	acc	cat	tac	acc	att	tac	cct	aaa	aga	aac	cga	ttt	gat	gat	768



Pro	Pro	Thr	His	Tyr	Thr	Ile	Tyr	Pro	Lys	Arg	Asn	Arg	Phe	Asp	Asp	
				245					250					255		
ttg	act	aac	ccc	act	aac	ccc	cct	tta	aaa	gaa	cct	aag	caa	gaa	acc	816
Leu	Thr	Asn	Pro	Thr	Asn	Pro	Pro	Leu	Lys	Glu	Pro	Lys	Gln	Glu	Thr	
			260					265					270			
aaa	gaa	aga	gaa	ccc	atg	ccc	aca	aaa	gaa	act	ctt	acg	ccc	gcc	aca	864
Lys	Glu	Arg	Glu	Pro	Met	Pro	Thr	Lys	Glu	Thr	Leu	Thr	Pro	Ala	Thr	
		275					280					285				
ctc	aaa	cct	atc	ata	tca	gca	ccc	gtc	atg	ccc	gca	tct	gca	ccc	aac	912
Leu	Lys	Pro	Ile	Ile	Ser	Ala	Pro	Val	Met	Pro	Ala	Ser	Ala	Pro	Asn	
	290					295					300					
cta	gaa	aat	gac	aac	aaa	aca	gaa	aac	caa	aaa	acc	ccc	aac	cac	ccc	960
Leu	Glu	Asn	Asp	Asn	Lys	Thr	Glu	Asn	Gln	Lys	Thr	Pro	Asn	His	Pro	
305					310				315						320	
ata	aaa	gaa	gat	gat	tta	caa	gaa	agc	cca	cag	gaa	aac	cca	caa	aaa	1008
Ile	Lys	Glu	Asp	Asp	Leu	Gln	Glu	Ser	Pro	Gln	Glu	Asn	Pro	Gln	Lys	
				325					330					335		
gaa	aat	caa	aaa	gaa	aat	ata	gaa	gaa	aaa	gaa	aat	ctc	aaa	gaa	gaa	1056
Glu	Asn	Gln	Lys	Glu	Asn	Ile	Glu	Glu	Lys	Glu	Asn	Leu	Lys	Glu	Glu	
			340					345					350			
gaa	aaa	gaa	acg	caa	aac	gct	cca	aac	ttt	agc	cca	cta	acc	ccc	aca	1104
Glu	Lys	Glu	Thr	Gln	Asn	Ala	Pro	Asn	Phe	Ser	Pro	Leu	Thr	Pro	Thr	
		355					360					365				
aac	gct	aaa	aaa	ccc	gtt	atg	gtt	aaa	gaa	ttg	agc	gaa	aat	aaa	gag	1152
Asn	Ala	Lys	Lys	Pro	Val	Met	Val	Lys	Glu	Leu	Ser	Glu	Asn	Lys	Glu	
	370					375					380					
ata	tta	gac	gga	ttg	gat	tat	ggc	gaa	gtg	caa	aaa	mcc	caa	gat	tat	1200
Ile	Leu	Asp	Gly	Leu	Asp	Tyr	Gly	Glu	Val	Gln	Lys	Xaa	Gln	Asp	Tyr	
385					390					395					400	
gag	ctt	ccc	acc	acg	caa	tta	ttg	aat	gcg	gtt	tgt	ttg	aaa	gaa	act	1248
Glu	Leu	Pro	Thr	Thr	Gln	Leu	Leu	Asn	Ala	Val	Cys	Leu	Lys	Glu	Thr	
				405					410					415		
tct	tta	gac	gaa	aac	gag	att	gac	caa	aaa	att	cag	gat	cta	ttg	agc	1296
Ser	Leu	Asp	Glu	Asn	Glu	Ile	Asp	Gln	Lys	Ile	Gln	Asp	Leu	Leu	Ser	
			420					425					430			
aaa	ctg	cgc	acc	ttt	aaa	att	gat	ggc	gat	att	atc	cgc	act	tat	tca	1344
Lys	Leu	Arg	Thr	Phe	Lys	Ile	Asp	Gly	Asp	Ile	Ile	Arg	Thr	Tyr	Ser	
		435					440					445				
ggc	cct	att	gta	acc	act	ttt	gaa	ttc	cgc	cca	gct	cct	agc	gtt	aag	1392
Gly	Pro	Ile	Val	Thr	Thr	Phe	Glu	Phe	Arg	Pro	Ala	Pro	Ser	Val	Lys	
	450					455					460					

gtg agt cgt att tta gga ttg agc gat gat tta gcg atg act tta tgt	1440
Val Ser Arg Ile Leu Gly Leu Ser Asp Asp Leu Ala Met Thr Leu Cys	
465 470 475 480	
gct gaa tcc att cgc att caa gcc cct att aaa ggt aaa gat gtc gtt	1488
Ala Glu Ser Ile Arg Ile Gln Ala Pro Ile Lys Gly Lys Asp Val Val	
485 490 495	
ggc att gaa atc cct aac agc caa agc caa att att tac ttg aga gaa	1536
Gly Ile Glu Ile Pro Asn Ser Gln Ser Gln Ile Ile Tyr Leu Arg Glu	
500 505 510	
att tta gaa agc gaa ttg ttt caa aaa tcc agc tcg ccc tta act cta	1584
Ile Leu Glu Ser Glu Leu Phe Gln Lys Ser Ser Ser Pro Leu Thr Leu	
515 520 525	
gct tta ggc aaa gac att gtg ggt aac cct ttc atc acg gat tta aaa	1632
Ala Leu Gly Lys Asp Ile Val Gly Asn Pro Phe Ile Thr Asp Leu Lys	
530 535 540	
aag ctc ccc cat ttg ctc atc gcc g	1657
Lys Leu Pro His Leu Leu Ile Ala	
545 550	

<210> 188  
 <211> 552  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <221> misc\_feature  
 <222> (68)..(68)  
 <223> The 'Xaa' at location 68 stands for Lys, Arg, or Ile.

<220>  
 <221> misc\_feature  
 <222> (397)..(397)  
 <223> The 'Xaa' at location 397 stands for Thr, or Pro.

<400> 188

Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile Ile Gly Val Leu Leu	
1 5 10 15	
Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn Ser Gly Leu Val Gly	
20 25 30	
Arg Phe Gly Val Trp Phe Ala Ala Leu Asn Lys Lys Tyr Phe Gly Tyr	
35 40 45	
Leu Ser Phe Ile Asn Leu Pro Tyr Leu Ala Trp Val Leu Phe Leu Leu	

50		55		60												
Tyr	Lys	Thr	Xaa	Asn	Pro	Phe	Thr	Glu	Ile	Val	Leu	Glu	Lys	Thr	Leu	
65					70					75					80	
Gly	His	Leu	Leu	Gly	Ile	Leu	Ser	Leu	Leu	Phe	Leu	Gln	Ser	Ser	Leu	
				85					90					95		
Leu	Asn	Gln	Gly	Glu	Ile	Gly	Asn	Ser	Val	Arg	Leu	Phe	Leu	Arg	Pro	
			100					105					110			
Phe	Ile	Gly	Asp	Phe	Gly	Leu	Tyr	Ala	Leu	Ile	Thr	Leu	Met	Val	Val	
		115					120					125				
Ile	Ser	Tyr	Leu	Ile	Leu	Phe	Lys	Leu	Pro	Pro	Lys	Ser	Val	Phe	Tyr	
	130					135					140					
Pro	Tyr	Met	Asn	Lys	Thr	Gln	Asn	Leu	Leu	Lys	Glu	Ile	Tyr	Lys	Gln	
145					150					155					160	
Cys	Leu	Gln	Ala	Phe	Ser	Pro	Asn	Phe	Ser	Pro	Lys	Lys	Glu	Asp	Phe	
				165					170					175		
Glu	Asn	Thr	Leu	Ser	Asp	Leu	Gln	Lys	Lys	Glu	Thr	Asn	Asn	Asp	Lys	
			180					185					190			
Glu	Lys	Glu	Asn	Leu	Lys	Glu	Asn	Pro	Ile	Asp	Glu	Asn	His	Lys	Thr	
		195					200					205				
Pro	Asn	Glu	Glu	Ser	Phe	Leu	Ala	Ile	Pro	Thr	Pro	Tyr	Asn	Thr	Thr	
	210					215					220					
Leu	Asn	Asp	Ser	Glu	Pro	Gln	Glu	Gly	Leu	Val	Gln	Ile	Ser	Pro	His	
225					230					235					240	
Pro	Pro	Thr	His	Tyr	Thr	Ile	Tyr	Pro	Lys	Arg	Asn	Arg	Phe	Asp	Asp	
				245					250					255		
Leu	Thr	Asn	Pro	Thr	Asn	Pro	Pro	Leu	Lys	Glu	Pro	Lys	Gln	Glu	Thr	
			260					265					270			

Lys Glu Arg Glu Pro Met Pro Thr Lys Glu Thr Leu Thr Pro Ala Thr  
275 280 285

Leu Lys Pro Ile Ile Ser Ala Pro Val Met Pro Ala Ser Ala Pro Asn  
290 295 300

Leu Glu Asn Asp Asn Lys Thr Glu Asn Gln Lys Thr Pro Asn His Pro  
305 310 315 320

Ile Lys Glu Asp Asp Leu Gln Glu Ser Pro Gln Glu Asn Pro Gln Lys  
325 330 335

Glu Asn Gln Lys Glu Asn Ile Glu Glu Lys Glu Asn Leu Lys Glu Glu  
340 345 350

Glu Lys Glu Thr Gln Asn Ala Pro Asn Phe Ser Pro Leu Thr Pro Thr  
355 360 365

Asn Ala Lys Lys Pro Val Met Val Lys Glu Leu Ser Glu Asn Lys Glu  
370 375 380

Ile Leu Asp Gly Leu Asp Tyr Gly Glu Val Gln Lys Xaa Gln Asp Tyr  
385 390 395 400

Glu Leu Pro Thr Thr Gln Leu Leu Asn Ala Val Cys Leu Lys Glu Thr  
405 410 415

Ser Leu Asp Glu Asn Glu Ile Asp Gln Lys Ile Gln Asp Leu Leu Ser  
420 425 430

Lys Leu Arg Thr Phe Lys Ile Asp Gly Asp Ile Ile Arg Thr Tyr Ser  
435 440 445

Gly Pro Ile Val Thr Thr Phe Glu Phe Arg Pro Ala Pro Ser Val Lys  
450 455 460

Val Ser Arg Ile Leu Gly Leu Ser Asp Asp Leu Ala Met Thr Leu Cys  
465 470 475 480

Ala Glu Ser Ile Arg Ile Gln Ala Pro Ile Lys Gly Lys Asp Val Val  
485 490 495

Gly Ile Glu Ile Pro Asn Ser Gln Ser Gln Ile Ile Tyr Leu Arg Glu  
500 505 510

Ile Leu Glu Ser Glu Leu Phe Gln Lys Ser Ser Ser Pro Leu Thr Leu  
515 520 525

Ala Leu Gly Lys Asp Ile Val Gly Asn Pro Phe Ile Thr Asp Leu Lys  
530 535 540

Lys Leu Pro His Leu Leu Ile Ala  
545 550

<210> 189

<211> 648

<212> DNA

<213> *Helicobacter pylori*

<220>

<221> CDS

<222> (1)..(648)

<400> 189

atg	aaa	aaa	ccc	tac	aga	aag	att	tct	gat	tat	gcg	atc	gtg	ggg	ggg	48
Met	Lys	Lys	Pro	Tyr	Arg	Lys	Ile	Ser	Asp	Tyr	Ala	Ile	Val	Gly	Gly	
1				5				10					15			

ttg	agt	gcg	tta	gtg	atg	gtg	agc	att	gtg	ggg	tgt	aag	agc	aat	gcc	96
Leu	Ser	Ala	Leu	Val	Met	Val	Ser	Ile	Val	Gly	Cys	Lys	Ser	Asn	Ala	
			20					25					30			

gat	gac	aaa	ccc	aaa	gag	caa	agc	tct	tta	agt	caa	agc	gtt	caa	aaa	144
Asp	Asp	Lys	Pro	Lys	Glu	Gln	Ser	Ser	Leu	Ser	Gln	Ser	Val	Gln	Lys	
		35					40					45				

ggg	gag	ttt	gtg	att	tta	gaa	gag	caa	aag	gat	aaa	tct	tac	aag	gtt	192
Gly	Ala	Phe	Val	Ile	Leu	Glu	Glu	Gln	Lys	Asp	Lys	Ser	Tyr	Lys	Val	
	50					55					60					

gtt	gaa	gaa	tac	ccc	agc	tca	aga	acc	cac	atc	ata	gtg	cgc	gat	ttg	240
Val	Glu	Glu	Tyr	Pro	Ser	Ser	Arg	Thr	His	Ile	Ile	Val	Arg	Asp	Leu	
65					70				75						80	

caa	ggc	aat	gaa	cgc	gtg	ttg	agc	aat	gaa	gag	att	caa	aag	ctc	att	288
Gln	Gly	Asn	Glu	Arg	Val	Leu	Ser	Asn	Glu	Glu	Ile	Gln	Lys	Leu	Ile	
				85					90					95		

aaa	gaa	gaa	gag	gcc	aaa	att	gat	aac	ggc	acg	agc	aag	ctt	gtt	caa	336
Lys	Glu	Glu	Glu	Ala	Lys	Ile	Asp	Asn	Gly	Thr	Ser	Lys	Leu	Val	Gln	

100							105					110					
cct	aat	aat	gga	ggg	agt	aat	gaa	agc	tca	ggc	ttt	ggc	ttg	ggg	agt	384	
Pro	Asn	Asn	Gly	Gly	Ser	Asn	Glu	Ser	Ser	Gly	Phe	Gly	Leu	Gly	Ser		
		115					120					125					
gcg	att	tta	ggg	agc	gcg	gcg	ggg	gcg	att	tta	ggg	agt	tat	att	ggc	432	
Ala	Ile	Leu	Gly	Ser	Ala	Ala	Gly	Ala	Ile	Leu	Gly	Ser	Tyr	Ile	Gly		
	130					135					140						
aat	aag	ctt	ttc	aat	aac	cct	aat	tat	cag	caa	aac	gcc	caa	cgg	acc	480	
Asn	Lys	Leu	Phe	Asn	Asn	Pro	Asn	Tyr	Gln	Gln	Asn	Ala	Gln	Arg	Thr		
145					150					155					160		
tac	aaa	tcc	cca	caa	gct	tac	caa	cgc	tct	caa	aat	tcc	ttt	tct	aaa	528	
Tyr	Lys	Ser	Pro	Gln	Ala	Tyr	Gln	Arg	Ser	Gln	Asn	Ser	Phe	Ser	Lys		
				165					170					175			
agc	gca	ccc	agc	gct	tca	agc	atg	gga	gga	gcg	agt	aag	gga	cag	agc	576	
Ser	Ala	Pro	Ser	Ala	Ser	Ser	Met	Gly	Gly	Ala	Ser	Lys	Gly	Gln	Ser		
			180					185					190				
ggg	ttt	ttt	ggc	tct	agt	aga	cct	act	agt	tcg	cct	gcg	gta	agc	tct	624	
Gly	Phe	Phe	Gly	Ser	Ser	Arg	Pro	Thr	Ser	Ser	Pro	Ala	Val	Ser	Ser		
		195					200					205					
ggg	aca	agg	ggc	ttt	aac	tca	taa									648	
Gly	Thr	Arg	Gly	Phe	Asn	Ser											
	210					215											

<210> 190  
 <211> 215  
 <212> PRT  
 <213> Helicobacter pylori

<400> 190

Met	Lys	Lys	Pro	Tyr	Arg	Lys	Ile	Ser	Asp	Tyr	Ala	Ile	Val	Gly	Gly
1				5					10					15	

Leu	Ser	Ala	Leu	Val	Met	Val	Ser	Ile	Val	Gly	Cys	Lys	Ser	Asn	Ala
			20					25					30		

Asp	Asp	Lys	Pro	Lys	Glu	Gln	Ser	Ser	Leu	Ser	Gln	Ser	Val	Gln	Lys
		35					40					45			

Gly	Ala	Phe	Val	Ile	Leu	Glu	Glu	Gln	Lys	Asp	Lys	Ser	Tyr	Lys	Val
	50					55					60				

Val	Glu	Glu	Tyr	Pro	Ser	Ser	Arg	Thr	His	Ile	Ile	Val	Arg	Asp	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65		70		75		80									
Gln	Gly	Asn	Glu	Arg	Val	Leu	Ser	Asn	Glu	Glu	Ile	Gln	Lys	Leu	Ile
				85					90					95	
Lys	Glu	Glu	Glu	Ala	Lys	Ile	Asp	Asn	Gly	Thr	Ser	Lys	Leu	Val	Gln
			100					105					110		
Pro	Asn	Asn	Gly	Gly	Ser	Asn	Glu	Ser	Ser	Gly	Phe	Gly	Leu	Gly	Ser
		115					120					125			
Ala	Ile	Leu	Gly	Ser	Ala	Ala	Gly	Ala	Ile	Leu	Gly	Ser	Tyr	Ile	Gly
	130					135					140				
Asn	Lys	Leu	Phe	Asn	Asn	Pro	Asn	Tyr	Gln	Gln	Asn	Ala	Gln	Arg	Thr
145					150					155					160
Tyr	Lys	Ser	Pro	Gln	Ala	Tyr	Gln	Arg	Ser	Gln	Asn	Ser	Phe	Ser	Lys
				165					170					175	
Ser	Ala	Pro	Ser	Ala	Ser	Ser	Met	Gly	Gly	Ala	Ser	Lys	Gly	Gln	Ser
			180					185					190		
Gly	Phe	Phe	Gly	Ser	Ser	Arg	Pro	Thr	Ser	Ser	Pro	Ala	Val	Ser	Ser
		195					200					205			
Gly	Thr	Arg	Gly	Phe	Asn	Ser									
	210					215									

<210> 191  
 <211> 879  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(879)

<400>	191														
ttg	ttt	tta	gtc	aaa	mmm	mta	ggc	gtg	ata	gta	gtg	gtt	tta	ata	ggc
Leu	Phe	Leu	Val	Lys	Xaa	Xaa	Gly	Val	Ile	Val	Val	Val	Leu	Ile	Gly
1				5					10					15	

ttt cta gct tgc tcg caa gag agg ttt atc caa ttg caa aaa aaa gcc Phe Leu Ala Cys Ser Gln Glu Arg Phe Ile Gln Leu Gln Lys Lys Ala 20 25 30	96
caa gag caa gaa aat gac ggc tct aaa cgc cct agc tat gtg gat tcg Gln Glu Gln Glu Asn Asp Gly Ser Lys Arg Pro Ser Tyr Val Asp Ser 35 40 45	144
gat tat gaa gtc ttt agc gaa acg att ttt tta caa aac atg gtg tat Asp Tyr Glu Val Phe Ser Glu Thr Ile Phe Leu Gln Asn Met Val Tyr 50 55 60	192
cag cct ata gaa gaa aga gat tct ttc gcc caa ctg act aaa gat gga Gln Pro Ile Glu Glu Arg Asp Ser Phe Ala Gln Leu Thr Lys Asp Gly 65 70 75 80	240
gac gat tct ttt aac ccc gaa act tcg gtg att tta ttg aat gag cca Asp Asp Ser Phe Asn Pro Glu Thr Ser Val Ile Leu Leu Asn Glu Pro 85 90 95	288
agc gat aac gat aca aaa aac ccg ccc tta tac cca aat gag tct aat Ser Asp Asn Asp Thr Lys Asn Pro Pro Leu Tyr Pro Asn Glu Ser Asn 100 105 110	336
act aac act gcc aat aac gat aca aaa aac ccg ttc ctt tac aaa ccg Thr Asn Thr Ala Asn Asn Asp Thr Lys Asn Pro Phe Leu Tyr Lys Pro 115 120 125	384
aaa aga aaa aca aaa aat cca aaa ctc att gaa tat tcc caa caa aat Lys Arg Lys Thr Lys Asn Pro Lys Leu Ile Glu Tyr Ser Gln Gln Asn 130 135 140	432
ttc tac ccc cta aag gat ggg gat att atc atg agt aaa gaa ggg gat Phe Tyr Pro Leu Lys Asp Gly Asp Ile Ile Met Ser Lys Glu Gly Asp 145 150 155 160	480
caa tgg ttg gta gaa atc aaa tcc aaa gcc ttg aag cgt ttt tta aaa Gln Trp Leu Val Glu Ile Lys Ser Lys Ala Leu Lys Arg Phe Leu Lys 165 170 175	528
gat caa aac gat aaa gat cgc cag atc caa act ttt act ttt aat gac Asp Gln Asn Asp Lys Asp Arg Gln Ile Gln Thr Phe Thr Phe Asn Asp 180 185 190	576
act aaa acg caa att gcg caa ttt aag ggc aaa att tct tcg tat gtt Thr Lys Thr Gln Ile Ala Gln Phe Lys Gly Lys Ile Ser Ser Tyr Val 195 200 205	624
tat acc acc aat aac agc gat ttg agt tta agg cct ttt tat gaa tcg Tyr Thr Thr Asn Asn Ser Asp Leu Ser Leu Arg Pro Phe Tyr Glu Ser 210 215 220	672
ttt ttg tta gaa aaa aag agc gat gat ctt tat atg ata ggg gat aag Phe Leu Leu Glu Lys Lys Ser Asp Asp Leu Tyr Met Ile Gly Asp Lys 225 230 235 240	720



gct tta gac gcc att gag att tca aag tgt caa atg gtg tta aaa aag	768
Ala Leu Asp Ala Ile Glu Ile Ser Lys Cys Gln Met Val Leu Lys Lys	
245 250 255	
cat tca acc gat aaa tta gac agc cag cat aaa gcc atc agt att gat	816
His Ser Thr Asp Lys Leu Asp Ser Gln His Lys Ala Ile Ser Ile Asp	
260 265 270	
ttg gac ttt aaa aaa gag cgc ttt aag agc gat acg gaa ctt ttt tta	864
Leu Asp Phe Lys Lys Glu Arg Phe Lys Ser Asp Thr Glu Leu Phe Leu	
275 280 285	
gaa tgc caa agt tag	879
Glu Cys Gln Ser	
290	

<210> 192  
 <211> 292  
 <212> PRT  
 <213> Helicobacter pylori  
  
 <220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> The 'Xaa' at location 6 stands for Lys, Asn, Thr, Gln, His, or Pro.  
  
 <220>  
 <221> misc\_feature  
 <222> (7)..(7)  
 <223> The 'Xaa' at location 7 stands for Ile, or Leu.  
  
 <400> 192

Leu Phe Leu Val Lys Xaa Xaa Gly Val Ile Val Val Val Leu Ile Gly	
1 5 10 15	
Phe Leu Ala Cys Ser Gln Glu Arg Phe Ile Gln Leu Gln Lys Lys Ala	
20 25 30	
Gln Glu Gln Glu Asn Asp Gly Ser Lys Arg Pro Ser Tyr Val Asp Ser	
35 40 45	
Asp Tyr Glu Val Phe Ser Glu Thr Ile Phe Leu Gln Asn Met Val Tyr	
50 55 60	
Gln Pro Ile Glu Glu Arg Asp Ser Phe Ala Gln Leu Thr Lys Asp Gly	
65 70 75 80	

Asp	Asp	Ser	Phe	Asn	Pro	Glu	Thr	Ser	Val	Ile	Leu	Leu	Asn	Glu	Pro	
				85					90					95		
Ser	Asp	Asn	Asp	Thr	Lys	Asn	Pro	Pro	Leu	Tyr	Pro	Asn	Glu	Ser	Asn	
			100					105					110			
Thr	Asn	Thr	Ala	Asn	Asn	Asp	Thr	Lys	Asn	Pro	Phe	Leu	Tyr	Lys	Pro	
		115					120					125				
Lys	Arg	Lys	Thr	Lys	Asn	Pro	Lys	Leu	Ile	Glu	Tyr	Ser	Gln	Gln	Asn	
	130					135					140					
Phe	Tyr	Pro	Leu	Lys	Asp	Gly	Asp	Ile	Ile	Met	Ser	Lys	Glu	Gly	Asp	
145					150					155					160	
Gln	Trp	Leu	Val	Glu	Ile	Lys	Ser	Lys	Ala	Leu	Lys	Arg	Phe	Leu	Lys	
				165					170					175		
Asp	Gln	Asn	Asp	Lys	Asp	Arg	Gln	Ile	Gln	Thr	Phe	Thr	Phe	Asn	Asp	
			180					185						190		
Thr	Lys	Thr	Gln	Ile	Ala	Gln	Phe	Lys	Gly	Lys	Ile	Ser	Ser	Tyr	Val	
		195					200						205			
Tyr	Thr	Thr	Asn	Asn	Ser	Asp	Leu	Ser	Leu	Arg	Pro	Phe	Tyr	Glu	Ser	
	210					215					220					
Phe	Leu	Leu	Glu	Lys	Lys	Ser	Asp	Asp	Leu	Tyr	Met	Ile	Gly	Asp	Lys	
225					230					235					240	
Ala	Leu	Asp	Ala	Ile	Glu	Ile	Ser	Lys	Cys	Gln	Met	Val	Leu	Lys	Lys	
				245					250					255		
His	Ser	Thr	Asp	Lys	Leu	Asp	Ser	Gln	His	Lys	Ala	Ile	Ser	Ile	Asp	
			260					265					270			
Leu	Asp	Phe	Lys	Lys	Glu	Arg	Phe	Lys	Ser	Asp	Thr	Glu	Leu	Phe	Leu	
		275					280					285				
Glu	Cys	Gln	Ser													
	290															

<210> 193  
 <211> 1131  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1131)

<400> 193

atg aat ttt ttt aaa atc ctt tta atg gaa tta agg gct att gtt tct	48
Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val Ser	
1 5 10 15	
cat att ggc gtt tta tta atc ctt ata ggc gct cct tta atc tat ggc	96
His Ile Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr Gly	
20 25 30	
ttg tta tac cct ttg cct tat tta aaa gac atc gta acg cag caa aaa	144
Leu Leu Tyr Pro Leu Pro Tyr Leu Lys Asp Ile Val Thr Gln Gln Lys	
35 40 45	
atc gcc ctt gta gat gaa gac aat tcc ttc ctt tct agg caa tta gcc	192
Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu Ala	
50 55 60	
ttc atg gcg caa agc tcc aac gag tta gaa atc gct ttt ttt agc ccc	240
Phe Met Ala Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser Pro	
65 70 75 80	
tct atg ctg gaa gcc aaa aag ctt tta aaa gaa gaa aaa att tat ggg	288
Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr Gly	
85 90 95	
atc ttg cat atc cct tcg tat ttt gaa gcc aat atc cat aag cag gtg	336
Ile Leu His Ile Pro Ser Tyr Phe Glu Ala Asn Ile His Lys Gln Val	
100 105 110	
cct gta acg ata gat ttt tat gcg aat tcc aat tac ttt ttg att tat	384
Pro Val Thr Ile Asp Phe Tyr Ala Asn Ser Asn Tyr Phe Leu Ile Tyr	
115 120 125	
ggc acc tta gcg aat gcg gtg gtg gag agc atc aac gct tta aat gat	432
Gly Thr Leu Ala Asn Ala Val Val Glu Ser Ile Asn Ala Leu Asn Asp	
130 135 140	
gag ata aga ttc aaa cgc aac gcc caa ata gaa gaa gct gaa tta ggg	480
Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu Leu Gly	
145 150 155 160	
aca gac ggg att aaa atc agg cct atc gct ttg tat aac cct agt gag	528
Thr Asp Gly Ile Lys Ile Arg Pro Ile Ala Leu Tyr Asn Pro Ser Glu	

165					170					175						
ggg	tat	ttg	aat	tac	gcg	ctc	tct	agc	gtg	ttt	att	ttc	atc	tta	cac	576
Gly	Tyr	Leu	Asn	Tyr	Ala	Leu	Ser	Ser	Val	Phe	Ile	Phe	Ile	Leu	His	
			180					185					190			
cag	gtg	atg	ctc	att	gca	agc	agc	atg	ttt	act	agc	tct	agg	cgt	ttg	624
Gln	Val	Met	Leu	Ile	Ala	Ser	Ser	Met	Phe	Thr	Ser	Ser	Arg	Arg	Leu	
		195					200					205				
gaa	tta	gcc	ctt	tta	gat	aaa	aag	caa	atc	gct	tta	agg	ctg	tgc	gca	672
Glu	Leu	Ala	Leu	Leu	Asp	Lys	Lys	Gln	Ile	Ala	Leu	Arg	Leu	Cys	Ala	
	210					215					220					
aga	ctc	ttg	gtg	ttt	atg	gca	gcg	ttt	agc	gtt	ttt	gtt	ttg	ttg	tat	720
Arg	Leu	Leu	Val	Phe	Met	Ala	Ala	Phe	Ser	Val	Phe	Val	Leu	Leu	Tyr	
225					230					235					240	
ttt	ggg	gcg	ctg	ttt	tct	ttt	tat	ggg	atc	gaa	cgg	cat	gcg	agt	gct	768
Phe	Gly	Ala	Leu	Phe	Ser	Phe	Tyr	Gly	Ile	Glu	Arg	His	Ala	Ser	Ala	
				245					250					255		
tta	atg	gtg	ttt	ttg	aat	agc	tcc	ata	ttc	atg	ctt	gca	acc	ttg	agt	816
Leu	Met	Val	Phe	Leu	Asn	Ser	Ser	Ile	Phe	Met	Leu	Ala	Thr	Leu	Ser	
			260					265					270			
ttg	ggg	tcg	ttt	tta	ggc	gca	tgg	atc	aaa	aat	gaa	gcc	cac	acc	act	864
Leu	Gly	Ser	Phe	Leu	Gly	Ala	Trp	Ile	Lys	Asn	Glu	Ala	His	Thr	Thr	
		275					280					285				
caa	atc	gtt	ttg	att	tct	tct	ttg	ccc	ttg	att	ttt	atg	atg	ggt	ttt	912
Gln	Ile	Val	Leu	Ile	Ser	Ser	Leu	Pro	Leu	Ile	Phe	Met	Met	Gly	Phe	
	290					295					300					
gtg	tgg	cct	ttt	gaa	tcc	ttg	ccc	tct	tat	ttg	cag	gtt	ttc	gtt	caa	960
Val	Trp	Pro	Phe	Glu	Ser	Leu	Pro	Ser	Tyr	Leu	Gln	Val	Phe	Val	Gln	
305					310					315					320	
ata	gtg	cct	gct	tat	cat	ggg	atc	agt	ttg	tta	ggg	cga	ttg	aat	caa	1008
Ile	Val	Pro	Ala	Tyr	His	Gly	Ile	Ser	Leu	Leu	Gly	Arg	Leu	Asn	Gln	
				325					330					335		
atg	cat	gcg	gaa	ttt	ata	gat	gtt	tct	gtc	cat	ttt	tat	gcg	ctt	att	1056
Met	His	Ala	Glu	Phe	Ile	Asp	Val	Ser	Val	His	Phe	Tyr	Ala	Leu	Ile	
			340					345					350			
gcg	att	ttt	att	gcg	agt	ttt	ata	ggg	agt	gtc	ttt	aaa	ctc	agc	tct	1104
Ala	Ile	Phe	Ile	Ala	Ser	Phe	Ile	Gly	Ser	Val	Phe	Lys	Leu	Ser	Ser	
		355					360					365				
tta	aag	aaa	gct	tgt	gaa	aac	gct	taa								1131
Leu	Lys	Lys	Ala	Cys	Glu	Asn	Ala									
	370					375										

<210> 194  
 <211> 376  
 <212> PRT  
 <213> Helicobacter pylori

<400> 194

Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val Ser  
 1 5 10 15

His Ile Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr Gly  
 20 25 30

Leu Leu Tyr Pro Leu Pro Tyr Leu Lys Asp Ile Val Thr Gln Gln Lys  
 35 40 45

Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu Ala  
 50 55 60

Phe Met Ala Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser Pro  
 65 70 75 80

Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr Gly  
 85 90 95

Ile Leu His Ile Pro Ser Tyr Phe Glu Ala Asn Ile His Lys Gln Val  
 100 105 110

Pro Val Thr Ile Asp Phe Tyr Ala Asn Ser Asn Tyr Phe Leu Ile Tyr  
 115 120 125

Gly Thr Leu Ala Asn Ala Val Val Glu Ser Ile Asn Ala Leu Asn Asp  
 130 135 140

Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu Leu Gly  
 145 150 155 160

Thr Asp Gly Ile Lys Ile Arg Pro Ile Ala Leu Tyr Asn Pro Ser Glu  
 165 170 175

Gly Tyr Leu Asn Tyr Ala Leu Ser Ser Val Phe Ile Phe Ile Leu His  
 180 185 190

Gln Val Met Leu Ile Ala Ser Ser Met Phe Thr Ser Ser Arg Arg Leu  
195 200 205

Glu Leu Ala Leu Leu Asp Lys Lys Gln Ile Ala Leu Arg Leu Cys Ala  
210 215 220

Arg Leu Leu Val Phe Met Ala Ala Phe Ser Val Phe Val Leu Leu Tyr  
225 230 235 240

Phe Gly Ala Leu Phe Ser Phe Tyr Gly Ile Glu Arg His Ala Ser Ala  
245 250 255

Leu Met Val Phe Leu Asn Ser Ser Ile Phe Met Leu Ala Thr Leu Ser  
260 265 270

Leu Gly Ser Phe Leu Gly Ala Trp Ile Lys Asn Glu Ala His Thr Thr  
275 280 285

Gln Ile Val Leu Ile Ser Ser Leu Pro Leu Ile Phe Met Met Gly Phe  
290 295 300

Val Trp Pro Phe Glu Ser Leu Pro Ser Tyr Leu Gln Val Phe Val Gln  
305 310 315 320

Ile Val Pro Ala Tyr His Gly Ile Ser Leu Leu Gly Arg Leu Asn Gln  
325 330 335

Met His Ala Glu Phe Ile Asp Val Ser Val His Phe Tyr Ala Leu Ile  
340 345 350

Ala Ile Phe Ile Ala Ser Phe Ile Gly Ser Val Phe Lys Leu Ser Ser  
355 360 365

Leu Lys Lys Ala Cys Glu Asn Ala  
370 375

<210> 195

<211> 1068

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1068)

<400> 195

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Val	Arg	Leu	Phe	Arg	Phe	Val	Gly	Trp	Tyr	Tyr	Phe	Lys	Tyr	Phe	Leu	
1				5					10					15		

atc	gtg	ctt	ttg	gct	ttg	gaa	ttg	ttt	ttt	gta	ggc	att	gac	agc	ttg	96
Ile	Val	Leu	Leu	Ala	Leu	Glu	Leu	Phe	Phe	Val	Gly	Ile	Asp	Ser	Leu	
			20					25					30			

aaa	tac	gcc	gat	aaa	atg	cct	gat	tct	gcg	aac	atg	atc	att	tta	ttt	144
Lys	Tyr	Ala	Asp	Lys	Met	Pro	Asp	Ser	Ala	Asn	Met	Ile	Ile	Leu	Phe	
		35					40					45				

ttc	acc	tat	gat	att	tta	ttc	gcc	ctc	aat	tac	acc	ttg	ccc	att	tcc	192
Phe	Thr	Tyr	Asp	Ile	Leu	Phe	Ala	Leu	Asn	Tyr	Thr	Leu	Pro	Ile	Ser	
	50					55					60					

ttg	ctt	ttg	gcg	atg	gtt	tta	ttt	tac	atc	acc	ttc	att	aaa	tcc	aac	240
Leu	Leu	Leu	Ala	Met	Val	Leu	Phe	Tyr	Ile	Thr	Phe	Ile	Lys	Ser	Asn	
65					70					75					80	

caa	tac	acc	gcc	ctg	ctc	tcc	att	ggc	ttt	tcc	aaa	tgc	cag	att	tta	288
Gln	Tyr	Thr	Ala	Leu	Leu	Ser	Ile	Gly	Phe	Ser	Lys	Cys	Gln	Ile	Leu	
				85					90					95		

agc	cct	att	ttt	ttg	att	agc	tta	ttt	ttc	acg	gct	gtt	tat	gtg	ggg	336
Ser	Pro	Ile	Phe	Leu	Ile	Ser	Leu	Phe	Phe	Thr	Ala	Val	Tyr	Val	Gly	
			100					105					110			

ttg	aac	gcg	act	cct	ttt	gtg	tat	atg	gaa	gaa	aaa	acg	caa	aat	tta	384
Leu	Asn	Ala	Thr	Pro	Phe	Val	Tyr	Met	Glu	Glu	Lys	Thr	Gln	Asn	Leu	
		115					120					125				

att	tat	aaa	gac	aat	tct	ttg	agc	gtt	tca	gag	cat	ttg	tta	gtg	aaa	432
Ile	Tyr	Lys	Asp	Asn	Ser	Leu	Ser	Val	Ser	Glu	His	Leu	Leu	Val	Lys	
	130					135					140					

tat	aac	gat	gat	tac	gtg	tat	ttt	gat	aag	att	aat	ccc	tta	ttg	caa	480
Tyr	Asn	Asp	Asp	Tyr	Val	Tyr	Phe	Asp	Lys	Ile	Asn	Pro	Leu	Leu	Gln	
145					150					155					160	

aaa	gcc	caa	aat	atc	aag	gtt	ttt	cgc	cta	aaa	gat	aag	act	ttg	gaa	528
Lys	Ala	Gln	Asn	Ile	Lys	Val	Phe	Arg	Leu	Lys	Asp	Lys	Thr	Leu	Glu	
				165					170					175		

tct	tat	gct	gaa	gct	aaa	gaa	gct	ttt	ttt	gaa	gac	aag	tat	tgg	atc	576
Ser	Tyr	Ala	Glu	Ala	Lys	Glu	Ala	Phe	Phe	Glu	Asp	Lys	Tyr	Trp	Ile	
			180					185					190			

ttg	cat	gac	act	act	atc	tat	gag	atg	ccc	tta	aat	ttt	gaa	ctg	ggt	624
Leu	His	Asp	Thr	Thr	Ile	Tyr	Glu	Met	Pro	Leu	Asn	Phe	Glu	Leu	Gly	
		195					200					205				

gca aac gct tta aac acc acg cgt tta aaa acc ttt aaa acg ctc aaa Ala Asn Ala Leu Asn Thr Thr Arg Leu Lys Thr Phe Lys Thr Leu Lys 210 215 220	672
aat ttc cgc cct aaa gtt tta gac acc att tat caa aac aag cct gcg Asn Phe Arg Pro Lys Val Leu Asp Thr Ile Tyr Gln Asn Lys Pro Ala 225 230 235 240	720
gtt tct atc aca gac gct ctt tta tcc ttg cat gct tta gtg cgc caa Val Ser Ile Thr Asp Ala Leu Leu Ser Leu His Ala Leu Val Arg Gln 245 250 255	768
aac gcg gac acg aaa aaa gtg cgc tcg ttt ttg tat gtg ttt gcg att Asn Ala Asp Thr Lys Lys Val Arg Ser Phe Leu Tyr Val Phe Ala Ile 260 265 270	816
ttg ccc ttt ttt gtg ccg ttt tta agc gtt tta atc gct tat ttt tcg Leu Pro Phe Phe Val Pro Phe Leu Ser Val Leu Ile Ala Tyr Phe Ser 275 280 285	864
ccc agt ctc gcc cgc tat gaa aac ctg gct ctt tta ggg cta aag ttt Pro Ser Leu Ala Arg Tyr Glu Asn Leu Ala Leu Leu Gly Leu Lys Phe 290 295 300	912
atc att atc acg ctc gtt gtt tgg ggg cta ttc ttt gct tta ggg aag Ile Ile Ile Thr Leu Val Val Trp Gly Leu Phe Phe Ala Leu Gly Lys 305 310 315 320	960
ttc agc att tca ggg ata ctc att cct gaa ata ggc gtt cta tcg ccc Phe Ser Ile Ser Gly Ile Leu Ile Pro Glu Ile Gly Val Leu Ser Pro 325 330 335	1008
ttt ttc gta ttc tta gcc ctc agt ctt tgg tat ttt aaa aag ctt aat Phe Phe Val Phe Leu Ala Leu Ser Leu Trp Tyr Phe Lys Lys Leu Asn 340 345 350	1056
aag agg ttg tag Lys Arg Leu 355	1068

<210> 196  
 <211> 355  
 <212> PRT  
 <213> Helicobacter pylori

<400> 196

Val Arg Leu Phe Arg Phe Val Gly Trp Tyr Tyr Phe Lys Tyr Phe Leu 1 5 10 15
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Ile Val Leu Leu Ala Leu Glu Leu Phe Phe Val Gly Ile Asp Ser Leu 20 25 30
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Lys Tyr Ala Asp Lys Met Pro Asp Ser Ala Asn Met Ile Ile Leu Phe  
35 40 45

Phe Thr Tyr Asp Ile Leu Phe Ala Leu Asn Tyr Thr Leu Pro Ile Ser  
50 55 60

Leu Leu Leu Ala Met Val Leu Phe Tyr Ile Thr Phe Ile Lys Ser Asn  
65 70 75 80

Gln Tyr Thr Ala Leu Leu Ser Ile Gly Phe Ser Lys Cys Gln Ile Leu  
85 90 95

Ser Pro Ile Phe Leu Ile Ser Leu Phe Phe Thr Ala Val Tyr Val Gly  
100 105 110

Leu Asn Ala Thr Pro Phe Val Tyr Met Glu Glu Lys Thr Gln Asn Leu  
115 120 125

Ile Tyr Lys Asp Asn Ser Leu Ser Val Ser Glu His Leu Leu Val Lys  
130 135 140

Tyr Asn Asp Asp Tyr Val Tyr Phe Asp Lys Ile Asn Pro Leu Leu Gln  
145 150 155 160

Lys Ala Gln Asn Ile Lys Val Phe Arg Leu Lys Asp Lys Thr Leu Glu  
165 170 175

Ser Tyr Ala Glu Ala Lys Glu Ala Phe Phe Glu Asp Lys Tyr Trp Ile  
180 185 190

Leu His Asp Thr Thr Ile Tyr Glu Met Pro Leu Asn Phe Glu Leu Gly  
195 200 205

Ala Asn Ala Leu Asn Thr Thr Arg Leu Lys Thr Phe Lys Thr Leu Lys  
210 215 220

Asn Phe Arg Pro Lys Val Leu Asp Thr Ile Tyr Gln Asn Lys Pro Ala  
225 230 235 240

Val Ser Ile Thr Asp Ala Leu Leu Ser Leu His Ala Leu Val Arg Gln

	245		250		255										
Asn	Ala	Asp	Thr	Lys	Lys	Val	Arg	Ser	Phe	Leu	Tyr	Val	Phe	Ala	Ile
			260					265					270		
Leu	Pro	Phe	Phe	Val	Pro	Phe	Leu	Ser	Val	Leu	Ile	Ala	Tyr	Phe	Ser
		275					280					285			
Pro	Ser	Leu	Ala	Arg	Tyr	Glu	Asn	Leu	Ala	Leu	Leu	Gly	Leu	Lys	Phe
	290					295					300				
Ile	Ile	Ile	Thr	Leu	Val	Val	Trp	Gly	Leu	Phe	Phe	Ala	Leu	Gly	Lys
305					310					315					320
Phe	Ser	Ile	Ser	Gly	Ile	Leu	Ile	Pro	Glu	Ile	Gly	Val	Leu	Ser	Pro
				325					330					335	
Phe	Phe	Val	Phe	Leu	Ala	Leu	Ser	Leu	Trp	Tyr	Phe	Lys	Lys	Leu	Asn
			340					345					350		
Lys	Arg	Leu													
		355													

<210> 197  
 <211> 1533  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1533)

<400>	197															
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Met	Lys	Lys	Thr	Thr	Leu	Phe	Val	Leu	Gly	Leu	Leu	Phe	Asn	Ser	Ser	
1				5					10					15		
tta	agc	gct	gtt	gat	gga	gtt	cct	aaa	acc	gag	cct	tct	tct	ttg	aat	96
Leu	Ser	Ala	Val	Asp	Gly	Val	Pro	Lys	Thr	Glu	Pro	Ser	Ser	Leu	Asn	
			20					25					30			
ttg	gct	gaa	gac	agc	aca	ccc	ttg	aac	cat	tct	aac	gct	caa	aaa	ctt	144
Leu	Ala	Glu	Asp	Ser	Thr	Pro	Leu	Asn	His	Ser	Asn	Ala	Gln	Lys	Leu	
		35					40					45				
tct	tta	aaa	aac	gca	tgg	aat	agg	gtg	tta	tcc	aac	cat	gaa	ggc	ttg	192

Ser	Leu	Lys	Asn	Ala	Trp	Asn	Arg	Val	Leu	Ser	Asn	His	Glu	Gly	Leu	
50						55					60					
cat	gcg	caa	gaa	tac	gcc	att	aaa	aga	gcg	agt	aaa	atg	aaa	tta	gcg	240
His	Ala	Gln	Glu	Tyr	Ala	Ile	Lys	Arg	Ala	Ser	Lys	Met	Lys	Leu	Ala	
65					70					75					80	
gct	aag	ctt	tct	ttt	ttg	cct	caa	att	gat	ttg	agc	gct	ttt	tat	gtg	288
Ala	Lys	Leu	Ser	Phe	Leu	Pro	Gln	Ile	Asp	Leu	Ser	Ala	Phe	Tyr	Val	
				85					90					95		
tac	ctc	tct	aac	cct	att	aaa	atg	gat	ttt	gcc	agc	caa	aaa	caa	ccg	336
Tyr	Leu	Ser	Asn	Pro	Ile	Lys	Met	Asp	Phe	Ala	Ser	Gln	Lys	Gln	Pro	
			100					105					110			
ggc	gtg	caa	aaa	gcc	acc	aac	cag	atc	cat	caa	ggc	ttg	caa	agc	att	384
Gly	Val	Gln	Lys	Ala	Thr	Asn	Gln	Ile	His	Gln	Gly	Leu	Gln	Ser	Ile	
		115					120					125				
cag	caa	aat	atc	ccc	cct	caa	gtc	cta	acc	cct	caa	atc	caa	gcg	ggc	432
Gln	Gln	Asn	Ile	Pro	Pro	Gln	Val	Leu	Thr	Pro	Gln	Ile	Gln	Ala	Gly	
		130				135					140					
atg	caa	ggg	gtg	atg	caa	ggg	ttt	ggg	gct	ttg	agc	agc	act	tta	gaa	480
Met	Gln	Gly	Val	Met	Gln	Gly	Phe	Gly	Ala	Leu	Ser	Ser	Thr	Leu	Glu	
145					150					155					160	
gcc	ccc	tta	ttg	ttt	tct	aag	caa	aat	gtg	gtg	att	ggg	gct	ttg	agc	528
Ala	Pro	Leu	Leu	Phe	Ser	Lys	Gln	Asn	Val	Val	Ile	Gly	Ala	Leu	Ser	
				165					170					175		
att	att	tat	ccc	ctt	tat	atg	ggt	ggg	gca	aga	ttc	acg	atg	gtg	cgc	576
Ile	Ile	Tyr	Pro	Leu	Tyr	Met	Gly	Gly	Ala	Arg	Phe	Thr	Met	Val	Arg	
			180					185					190			
att	gcg	gat	ttg	atg	caa	aaa	gac	gcc	aat	gaa	gtg	tat	cgc	ttg	aaa	624
Ile	Ala	Asp	Leu	Met	Gln	Lys	Asp	Ala	Asn	Glu	Val	Tyr	Arg	Leu	Lys	
		195					200					205				
aag	ctt	tcc	act	ttt	caa	gag	ctt	gtg	agc	gtg	tat	tat	ggc	atg	gtg	672
Lys	Leu	Ser	Thr	Phe	Gln	Glu	Leu	Val	Ser	Val	Tyr	Tyr	Gly	Met	Val	
		210				215					220					
tta	aac	gca	gaa	gtg	gct	gaa	act	tta	gaa	gag	gta	gaa	aaa	ggc	cat	720
Leu	Asn	Ala	Glu	Val	Ala	Glu	Thr	Leu	Glu	Glu	Val	Glu	Lys	Gly	His	
225					230					235					240	
tat	aag	cat	ttc	caa	aac	gct	ttg	aaa	atg	caa	aaa	gta	ggg	caa	atc	768
Tyr	Lys	His	Phe	Gln	Asn	Ala	Leu	Lys	Met	Gln	Lys	Val	Gly	Gln	Ile	
				245				250						255		
gct	agg	gta	gaa	acc	tta	ggc	gct	caa	gtg	gct	tat	gat	aag	gcc	cat	816
Ala	Arg	Val	Glu	Thr	Leu	Gly	Ala	Gln	Val	Ala	Tyr	Asp	Lys	Ala	His	
			260					265					270			

atc gct agc gtt aag gct aaa gac gtg tta gaa gtt tcg caa ctc tcg Ile Ala Ser Val Lys Ala Lys Asp Val Leu Glu Val Ser Gln Leu Ser 275 280 285	864
ttc aat tct att tta tct agc aag gac gat tta gcg cct tca agc aaa Phe Asn Ser Ile Leu Ser Ser Lys Asp Asp Leu Ala Pro Ser Ser Lys 290 295 300	912
tta gag atc cac acc gag aaa aat ctg ccc gat ttg agc ttt ttt gtt Leu Glu Ile His Thr Glu Lys Asn Leu Pro Asp Leu Ser Phe Phe Val 305 310 315 320	960
tct tcc acg ctc aat tcc tac ccg gct tta aag act tta gaa aat cag Ser Ser Thr Leu Asn Ser Tyr Pro Ala Leu Lys Thr Leu Glu Asn Gln 325 330 335	1008
gtt caa att tct aaa gaa aac acg aaa cta cag atc gct aaa ttc ttg Val Gln Ile Ser Lys Glu Asn Thr Lys Leu Gln Ile Ala Lys Phe Leu 340 345 350	1056
ccc caa gtg agt ttt ttt ggc tct tat atc atg aag caa aac aat tcg Pro Gln Val Ser Phe Phe Gly Ser Tyr Ile Met Lys Gln Asn Asn Ser 355 360 365	1104
gtg ttt gaa gac atg atc cct agt tgg ttt gtg ggc gtm gct ggg cgc Val Phe Glu Asp Met Ile Pro Ser Trp Phe Val Gly Xaa Ala Gly Arg 370 375 380	1152
atg cst att ctt tct ccc aca ggg cgt atc caa aaa tac caa gcg agc Met Xaa Ile Leu Ser Pro Thr Gly Arg Ile Gln Lys Tyr Gln Ala Ser 385 390 395 400	1200
aaa tta gcg gag ttg caa gct aat agc gaa caa atc caa gct aaa aaa Lys Leu Ala Glu Leu Gln Ala Asn Ser Glu Gln Ile Gln Ala Lys Lys 405 410 415	1248
aac atg gaa ttg tta gtg aat aag act tat aaa gag acg ctt tct tat Asn Met Glu Leu Leu Val Asn Lys Thr Tyr Lys Glu Thr Leu Ser Tyr 420 425 430	1296
ttg aaa gaa tac aaa agc ttg ctt tct agc gtg gaa tta gcc aag gaa Leu Lys Glu Tyr Lys Ser Leu Leu Ser Ser Val Glu Leu Ala Lys Glu 435 440 445	1344
aac tta aaa ctc caa gag cag gct ttt tta caa ggc tta agc acg aac Asn Leu Lys Leu Gln Glu Gln Ala Phe Leu Gln Gly Leu Ser Thr Asn 450 455 460	1392
gct caa gtc att gat gcg agg aac acg ctt tct tct atc atc gtg gag Ala Gln Val Ile Asp Ala Arg Asn Thr Leu Ser Ser Ile Ile Val Glu 465 470 475 480	1440
caa aaa agc gtg gct tat aaa tac atc gtt tca tta gcg aat tta atg Gln Lys Ser Val Ala Tyr Lys Tyr Ile Val Ser Leu Ala Asn Leu Met 485 490 495	1488

gcg tta agc gat cat att gat tta ttt tat gaa ttt gtt tat taa 1533  
Ala Leu Ser Asp His Ile Asp Leu Phe Tyr Glu Phe Val Tyr  
500 505 510

<210> 198  
<211> 510  
<212> PRT  
<213> Helicobacter pylori

<220>  
<221> misc\_feature  
<222> (381)..(381)  
<223> The 'Xaa' at location 381 stands for Val.

<220>  
<221> misc\_feature  
<222> (386)..(386)  
<223> The 'Xaa' at location 386 stands for Arg, or Pro.

<400> 198

Met Lys Lys Thr Thr Leu Phe Val Leu Gly Leu Leu Phe Asn Ser Ser  
1 5 10 15

Leu Ser Ala Val Asp Gly Val Pro Lys Thr Glu Pro Ser Ser Leu Asn  
20 25 30

Leu Ala Glu Asp Ser Thr Pro Leu Asn His Ser Asn Ala Gln Lys Leu  
35 40 45

Ser Leu Lys Asn Ala Trp Asn Arg Val Leu Ser Asn His Glu Gly Leu  
50 55 60

His Ala Gln Glu Tyr Ala Ile Lys Arg Ala Ser Lys Met Lys Leu Ala  
65 70 75 80

Ala Lys Leu Ser Phe Leu Pro Gln Ile Asp Leu Ser Ala Phe Tyr Val  
85 90 95

Tyr Leu Ser Asn Pro Ile Lys Met Asp Phe Ala Ser Gln Lys Gln Pro  
100 105 110

Gly Val Gln Lys Ala Thr Asn Gln Ile His Gln Gly Leu Gln Ser Ile  
115 120 125

Gln Gln Asn Ile Pro Pro Gln Val Leu Thr Pro Gln Ile Gln Ala Gly  
 130 135 140

Met Gln Gly Val Met Gln Gly Phe Gly Ala Leu Ser Ser Thr Leu Glu  
 145 150 155 160

Ala Pro Leu Leu Phe Ser Lys Gln Asn Val Val Ile Gly Ala Leu Ser  
 165 170 175

Ile Ile Tyr Pro Leu Tyr Met Gly Gly Ala Arg Phe Thr Met Val Arg  
 180 185 190

Ile Ala Asp Leu Met Gln Lys Asp Ala Asn Glu Val Tyr Arg Leu Lys  
 195 200 205

Lys Leu Ser Thr Phe Gln Glu Leu Val Ser Val Tyr Tyr Gly Met Val  
 210 215 220

Leu Asn Ala Glu Val Ala Glu Thr Leu Glu Glu Val Glu Lys Gly His  
 225 230 235 240

Tyr Lys His Phe Gln Asn Ala Leu Lys Met Gln Lys Val Gly Gln Ile  
 245 250 255

Ala Arg Val Glu Thr Leu Gly Ala Gln Val Ala Tyr Asp Lys Ala His  
 260 265 270

Ile Ala Ser Val Lys Ala Lys Asp Val Leu Glu Val Ser Gln Leu Ser  
 275 280 285

Phe Asn Ser Ile Leu Ser Ser Lys Asp Asp Leu Ala Pro Ser Ser Lys  
 290 295 300

Leu Glu Ile His Thr Glu Lys Asn Leu Pro Asp Leu Ser Phe Phe Val  
 305 310 315 320

Ser Ser Thr Leu Asn Ser Tyr Pro Ala Leu Lys Thr Leu Glu Asn Gln  
 325 330 335

Val Gln Ile Ser Lys Glu Asn Thr Lys Leu Gln Ile Ala Lys Phe Leu  
 340 345 350

Pro Gln Val Ser Phe Phe Gly Ser Tyr Ile Met Lys Gln Asn Asn Ser  
 355 360 365

Val Phe Glu Asp Met Ile Pro Ser Trp Phe Val Gly Xaa Ala Gly Arg  
 370 375 380

Met Xaa Ile Leu Ser Pro Thr Gly Arg Ile Gln Lys Tyr Gln Ala Ser  
 385 390 395 400

Lys Leu Ala Glu Leu Gln Ala Asn Ser Glu Gln Ile Gln Ala Lys Lys  
 405 410 415

Asn Met Glu Leu Leu Val Asn Lys Thr Tyr Lys Glu Thr Leu Ser Tyr  
 420 425 430

Leu Lys Glu Tyr Lys Ser Leu Leu Ser Ser Val Glu Leu Ala Lys Glu  
 435 440 445

Asn Leu Lys Leu Gln Glu Gln Ala Phe Leu Gln Gly Leu Ser Thr Asn  
 450 455 460

Ala Gln Val Ile Asp Ala Arg Asn Thr Leu Ser Ser Ile Ile Val Glu  
 465 470 475 480

Gln Lys Ser Val Ala Tyr Lys Tyr Ile Val Ser Leu Ala Asn Leu Met  
 485 490 495

Ala Leu Ser Asp His Ile Asp Leu Phe Tyr Glu Phe Val Tyr  
 500 505 510

<210> 199  
 <211> 516  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(516)

<400> 199  
 atg gtg tta gtt aaa atg gtg tta ggg ttt ttg atc ctt tta agc cct  
 Met Val Leu Val Lys Met Val Leu Gly Phe Leu Ile Leu Leu Ser Pro  
 1 5 10 15

ttg tac gct act gga ttg gat att vma caa acg gac att ata gag cgt	96
Leu Tyr Ala Thr Gly Leu Asp Ile Xaa Gln Thr Asp Ile Ile Glu Arg	
20 25 30	
tct tta aat ttc ctc tta ttt gcg ggg att ttg tgg tat ttt ttg gct	144
Ser Leu Asn Phe Leu Leu Phe Ala Gly Ile Leu Trp Tyr Phe Leu Ala	
35 40 45	
aaa aaa ctg cgt tca ttt tta cgc tcc aaa agc ctt gaa atc tcc aaa	192
Lys Lys Leu Arg Ser Phe Leu Arg Ser Lys Ser Leu Glu Ile Ser Lys	
50 55 60	
cga tta gaa gag att caa gcc caa ctc aaa gtg agt aaa gaa aat aag	240
Arg Leu Glu Glu Ile Gln Ala Gln Leu Lys Val Ser Lys Glu Asn Lys	
65 70 75 80	
aaa aaa ctc tta aaa gaa tta gag caa gcc aaa gaa aaa gct gaa tta	288
Lys Lys Leu Leu Lys Glu Leu Glu Gln Ala Lys Glu Lys Ala Glu Leu	
85 90 95	
att att tct gat gcg aat aaa gaa gct tac acg atc acg caa aaa tac	336
Ile Ile Ser Asp Ala Asn Lys Glu Ala Tyr Thr Ile Thr Gln Lys Tyr	
100 105 110	
gaa ttg caa acc aaa atg gat gtg gaa aat ttg atc aaa aat tct aag	384
Glu Leu Gln Thr Lys Met Asp Val Glu Asn Leu Ile Lys Asn Ser Lys	
115 120 125	
gcg ttg atg gat tta gaa gtt aaa aag atc aaa aga gag ctg gtt gar	432
Ala Leu Met Asp Leu Glu Val Lys Lys Ile Lys Arg Glu Leu Val Glu	
130 135 140	
agc gtt ttt raa gat cta aga gag agc aaa ara gtc tct ttc aat gcg	480
Ser Val Phe Xaa Asp Leu Arg Glu Ser Lys Xaa Val Ser Phe Asn Ala	
145 150 155 160	
caa gat tgc gtg aat att ttg ava cav agg ctt taa	516
Gln Asp Cys Val Asn Ile Leu Xaa Xaa Arg Leu	
165 170	

<210> 200

<211> 171

<212> PRT

<213> Helicobacter pylori

<220>

<221> misc\_feature

<222> (25)..(25)

<223> The 'Xaa' at location 25 stands for Lys, Thr, Glu, Ala, Gln, or Pro.

<220>

<221> misc\_feature



<222> (148)..(148)  
 <223> The 'Xaa' at location 148 stands for Glu, or Lys.

<220>  
 <221> misc\_feature  
 <222> (155)..(155)  
 <223> The 'Xaa' at location 155 stands for Arg, or Lys.

<220>  
 <221> misc\_feature  
 <222> (168)..(168)  
 <223> The 'Xaa' at location 168 stands for Lys, Arg, or Thr.

<220>  
 <221> misc\_feature  
 <222> (169)..(169)  
 <223> The 'Xaa' at location 169 stands for Gln, or His.

<400> 200

Met	Val	Leu	Val	Lys	Met	Val	Leu	Gly	Phe	Leu	Ile	Leu	Leu	Ser	Pro
1				5					10					15	
Leu	Tyr	Ala	Thr	Gly	Leu	Asp	Ile	Xaa	Gln	Thr	Asp	Ile	Ile	Glu	Arg
			20					25					30		
Ser	Leu	Asn	Phe	Leu	Leu	Phe	Ala	Gly	Ile	Leu	Trp	Tyr	Phe	Leu	Ala
		35					40					45			
Lys	Lys	Leu	Arg	Ser	Phe	Leu	Arg	Ser	Lys	Ser	Leu	Glu	Ile	Ser	Lys
	50					55					60				
Arg	Leu	Glu	Glu	Ile	Gln	Ala	Gln	Leu	Lys	Val	Ser	Lys	Glu	Asn	Lys
65					70					75				80	
Lys	Lys	Leu	Leu	Lys	Glu	Leu	Glu	Gln	Ala	Lys	Glu	Lys	Ala	Glu	Leu
				85					90					95	
Ile	Ile	Ser	Asp	Ala	Asn	Lys	Glu	Ala	Tyr	Thr	Ile	Thr	Gln	Lys	Tyr
			100					105					110		
Glu	Leu	Gln	Thr	Lys	Met	Asp	Val	Glu	Asn	Leu	Ile	Lys	Asn	Ser	Lys
		115					120					125			
Ala	Leu	Met	Asp	Leu	Glu	Val	Lys	Lys	Ile	Lys	Arg	Glu	Leu	Val	Glu
		130				135					140				

Ser Val Phe Xaa Asp Leu Arg Glu Ser Lys Xaa Val Ser Phe Asn Ala  
145 150 155 160

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<210> 201
<211> 565
<212> DNA
<213> Helicobacter pylori
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<400>	201															
atg	ctc	gct	tcc	att	att	gaa	ttt	tcc	tta	cgc	cag	cga	ata	atc	gtg	48
Met	Leu	Ala	Ser	Ile	Ile	Glu	Phe	Ser	Leu	Arg	Gln	Arg	Ile	Ile	Val	
1				5					10					15		
att	gtt	ggc	gcg	att	ctt	att	ttg	ttt	ttt	ggg	act	tat	agt	ttt	atc	96
Ile	Val	Gly	Ala	Ile	Leu	Ile	Leu	Phe	Phe	Gly	Thr	Tyr	Ser	Phe	Ile	
			20					25					30			
cac	act	cca	gta	gat	gct	ttc	ccg	gat	att	tcg	ccc	act	caa	gtc	aaa	144
His	Thr	Pro	Val	Asp	Ala	Phe	Pro	Asp	Ile	Ser	Pro	Thr	Gln	Val	Lys	
		35					40					45				
atc	att	tta	aaa	ctc	ccc	ggt	tct	agc	cct	gaa	gaa	atg	gaa	aat	aac	192
Ile	Ile	Leu	Lys	Leu	Pro	Gly	Ser	Ser	Pro	Glu	Glu	Met	Glu	Asn	Asn	
	50					55					60					
atc	gtg	cgc	cct	tta	gaa	ttg	gag	ctt	tta	ggc	ttg	aaa	ggg	caa	aaa	240
Ile	Val	Arg	Pro	Leu	Glu	Leu	Glu	Leu	Leu	Gly	Leu	Lys	Gly	Gln	Lys	
65					70					75					80	
tct	tta	aga	agt	att	tca	aaa	tat	tct	att	tca	gac	atc	acg	ata	gat	288
Ser	Leu	Arg	Ser	Ile	Ser	Lys	Tyr	Ser	Ile	Ser	Asp	Ile	Thr	Ile	Asp	
				85					90					95		
ttt	gat	gac	agc	gtg	gat	att	tat	tta	gcg	aga	aac	att	gtt	aat	gag	336
Phe	Asp	Asp	Ser	Val	Asp	Ile	Tyr	Leu	Ala	Arg	Asn	Ile	Val	Asn	Glu	
			100					105					110			
cgc	ttg	agc	agc	gtg	atg	aaa	gat	tta	ccc	gtg	ggg	gtt	gaa	ggg	ggc	384
Arg	Leu	Ser	Ser	Val	Met	Lys	Asp	Leu	Pro	Val	Gly	Val	Glu	Gly	Gly	
		115					120					125				
atg	gcg	ccc	att	gtt	acg	ccg	cta	tca	gat	atc	ttt	atg	ttc	act	att	432
Met	Ala	Pro	Ile	Val	Thr	Pro	Leu	Ser	Asp	Ile	Phe	Met	Phe	Thr	Ile	
	130					135					140					

gat	ggc	aat	atc	act	gag	ata	gaa	aaa	cga	cag	ctt	tta	gac	ttt	gtg	480
Asp	Gly	Asn	Ile	Thr	Glu	Ile	Glu	Lys	Arg	Gln	Leu	Leu	Asp	Phe	Val	
145					150					155					160	

atc	cgc	ccg	caa	tta	aga	atg	att	agc	ggc	gtg	gcg	gat	gtc	aat	tct	528
Ile	Arg	Pro	Gln	Leu	Arg	Met	Ile	Ser	Gly	Val	Ala	Asp	Val	Asn	Ser	
			165						170					175		

att	gga	ggc	ttt	agc	agg	gcg	ttt	tgt	gat	cgt	gcc	g				565
Ile	Gly	Gly	Phe	Ser	Arg	Ala	Phe	Cys	Asp	Arg	Ala					
			180					185								

<210> 202  
 <211> 188  
 <212> PRT  
 <213> Helicobacter pylori

<400> 202

Met	Leu	Ala	Ser	Ile	Ile	Glu	Phe	Ser	Leu	Arg	Gln	Arg	Ile	Ile	Val
1				5					10					15	

Ile	Val	Gly	Ala	Ile	Leu	Ile	Leu	Phe	Phe	Gly	Thr	Tyr	Ser	Phe	Ile
			20					25					30		

His	Thr	Pro	Val	Asp	Ala	Phe	Pro	Asp	Ile	Ser	Pro	Thr	Gln	Val	Lys
		35					40					45			

Ile	Ile	Leu	Lys	Leu	Pro	Gly	Ser	Ser	Pro	Glu	Glu	Met	Glu	Asn	Asn
	50					55					60				

Ile	Val	Arg	Pro	Leu	Glu	Leu	Glu	Leu	Leu	Gly	Leu	Lys	Gly	Gln	Lys
65					70					75					80

Ser	Leu	Arg	Ser	Ile	Ser	Lys	Tyr	Ser	Ile	Ser	Asp	Ile	Thr	Ile	Asp
				85					90					95	

Phe	Asp	Asp	Ser	Val	Asp	Ile	Tyr	Leu	Ala	Arg	Asn	Ile	Val	Asn	Glu
			100					105					110		

Arg	Leu	Ser	Ser	Val	Met	Lys	Asp	Leu	Pro	Val	Gly	Val	Glu	Gly	Gly
		115					120					125			

Met	Ala	Pro	Ile	Val	Thr	Pro	Leu	Ser	Asp	Ile	Phe	Met	Phe	Thr	Ile
	130					135					140				

Asp Gly Asn Ile Thr Glu Ile Glu Lys Arg Gln Leu Leu Asp Phe Val  
 145 150 155 160

Ile Arg Pro Gln Leu Arg Met Ile Ser Gly Val Ala Asp Val Asn Ser  
 165 170 175

Ile Gly Gly Phe Ser Arg Ala Phe Cys Asp Arg Ala  
 180 185

<210> 203  
 <211> 663  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(663)

<400> 203  
 atg gct gaa aat tct ttc aaa aat gtt tcc aca caa ccc aaa cca ttt 48  
 Met Ala Glu Asn Ser Phe Lys Asn Val Ser Thr Gln Pro Lys Pro Phe  
 1 5 10 15  
 ttc tta tta cca gtt aaa acc ctg ttt ctt tta gga ggc gtt ttt agc 96  
 Phe Leu Leu Pro Val Lys Thr Leu Phe Leu Leu Gly Gly Val Phe Ser  
 20 25 30  
 gcg ttt ttt atc ctt gtt gct ggc ttg gtt ttt ttt aat tac act aat 144  
 Ala Phe Phe Ile Leu Val Ala Gly Leu Val Phe Phe Asn Tyr Thr Asn  
 35 40 45  
 tca atg gac cat gcg att ttt aac ttg atg cgt tca aac tct tct aac 192  
 Ser Met Asp His Ala Ile Phe Asn Leu Met Arg Ser Asn Ser Ser Asn  
 50 55 60  
 cct att tta gat caa acg ctc cga cgc gtt gtt ttt tta ggc tct tct 240  
 Pro Ile Leu Asp Gln Thr Leu Arg Arg Val Val Phe Leu Gly Ser Ser  
 65 70 75 80  
 caa ttc gtg ttg cct ttg agc ttg tta gtg ggg gtg ttt tta agc ttg 288  
 Gln Phe Val Leu Pro Leu Ser Leu Leu Val Gly Val Phe Leu Ser Leu  
 85 90 95  
 tat cgt aaa aat tta gca ctt ggg gtg tgg ttt gtg cta agc gtg atc 336  
 Tyr Arg Lys Asn Leu Ala Leu Gly Val Trp Phe Val Leu Ser Val Ile  
 100 105 110  
 tta ttt gaa gcc ctt tta gaa tct tta aaa cac ctt ttg gca cac tcc 384  
 Leu Phe Glu Ala Leu Leu Glu Ser Leu Lys His Leu Leu Ala His Ser

115					120					125						
att	caa	tgg	ttt	tcg	cac	agc	gct	aat	ttc	cct	agc	act	atc	gcg	ctt	432
Ile	Gln	Trp	Phe	Ser	His	Ser	Ala	Asn	Phe	Pro	Ser	Thr	Ile	Ala	Leu	
	130						135				140					
tct	ttg	acg	cat	ttt	tat	ggg	ttg	ctt	gtt	tta	tta	ata	ccc	cat	ttg	480
Ser	Leu	Thr	His	Phe	Tyr	Gly	Leu	Leu	Val	Leu	Leu	Ile	Pro	His	Leu	
	145					150				155					160	
atc	acg	cat	caa	ata	ttt	caa	aac	att	ctt	cct	tat	agt	ttg	ctt	gkt	528
Ile	Thr	His	Gln	Ile	Phe	Gln	Asn	Ile	Leu	Pro	Tyr	Ser	Leu	Leu	Xaa	
				165					170					175		
ttg	att	ctt	tta	att	ggg	tta	gcg	ctg	att	gtt	tta	ggg	gtg	tct	ttt	576
Leu	Ile	Leu	Leu	Ile	Gly	Leu	Ala	Leu	Ile	Val	Leu	Gly	Val	Ser	Phe	
			180					185					190			
agc	agt	gtt	tta	gga	ggg	ttt	tgt	tta	ggg	gcg	tca	ggg	gct	tgt	ttt	624
Ser	Ser	Val	Leu	Gly	Gly	Phe	Cys	Leu	Gly	Ala	Ser	Gly	Ala	Cys	Phe	
		195					200					205				
tcc	ata	ggg	att	tat	ttg	agc	gtg	ttt	caa	aag	atc	taa				663
Ser	Ile	Gly	Ile	Tyr	Leu	Ser	Val	Phe	Gln	Lys	Ile					
	210					215					220					

<210> 204

<211> 220

<212> PRT

<213> Helicobacter pylori

<220>

<221> misc\_feature

<222> (176)..(176)

<223> The 'Xaa' at location 176 stands for Gly, or Val.

<400> 204

Met	Ala	Glu	Asn	Ser	Phe	Lys	Asn	Val	Ser	Thr	Gln	Pro	Lys	Pro	Phe
1				5					10					15	

Phe	Leu	Leu	Pro	Val	Lys	Thr	Leu	Phe	Leu	Leu	Gly	Gly	Val	Phe	Ser
			20					25					30		

Ala	Phe	Phe	Ile	Leu	Val	Ala	Gly	Leu	Val	Phe	Phe	Asn	Tyr	Thr	Asn
		35					40					45			

Ser	Met	Asp	His	Ala	Ile	Phe	Asn	Leu	Met	Arg	Ser	Asn	Ser	Ser	Asn
	50					55					60				

Pro Ile Leu Asp Gln Thr Leu Arg Arg Val Val Phe Leu Gly Ser Ser  
65 70 75 80

Gln Phe Val Leu Pro Leu Ser Leu Leu Val Gly Val Phe Leu Ser Leu  
85 90 95

Tyr Arg Lys Asn Leu Ala Leu Gly Val Trp Phe Val Leu Ser Val Ile  
100 105 110

Leu Phe Glu Ala Leu Leu Glu Ser Leu Lys His Leu Leu Ala His Ser  
115 120 125

Ile Gln Trp Phe Ser His Ser Ala Asn Phe Pro Ser Thr Ile Ala Leu  
130 135 140

Ser Leu Thr His Phe Tyr Gly Leu Leu Val Leu Leu Ile Pro His Leu  
145 150 155 160

Ile Thr His Gln Ile Phe Gln Asn Ile Leu Pro Tyr Ser Leu Leu Xaa  
165 170 175

Leu Ile Leu Leu Ile Gly Leu Ala Leu Ile Val Leu Gly Val Ser Phe  
180 185 190

Ser Ser Val Leu Gly Gly Phe Cys Leu Gly Ala Ser Gly Ala Cys Phe  
195 200 205

Ser Ile Gly Ile Tyr Leu Ser Val Phe Gln Lys Ile  
210 215 220

<210> 205  
<211> 454  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(453)

<400> 205  
atg ggt aat cat ttt tct aaa tta gga ttt gtt tta gcc gca tta ggg  
Met Gly Asn His Phe Ser Lys Leu Gly Phe Val Leu Ala Ala Leu Gly  
1 5 10 15

48

agc gcg ata ggt tta ggg cat atc tgg cgt ttc ccc tac atg act ggg	96
Ser Ala Ile Gly Leu Gly His Ile Trp Arg Phe Pro Tyr Met Thr Gly	
20 25 30	
gtg agt ggt ggg ggt gct ttt gtt tta ttg ttt tta ttt tta tct tta	144
Val Ser Gly Gly Gly Ala Phe Val Leu Leu Phe Leu Phe Leu Ser Leu	
35 40 45	
agc gtt ggc gcg gcg atg ttt atc gct gaa atg cta tta ggg caa agc	192
Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu Gly Gln Ser	
50 55 60	
acg caa aaa aat gta ata gaa gcc ttt aaa gag ctt gac ctt aac cct	240
Thr Gln Lys Asn Val Ile Glu Ala Phe Lys Glu Leu Asp Leu Asn Pro	
65 70 75 80	
aaa aaa cgc tgg aaa tac gca ggg att ttg ctt att tct ggg cca tta	288
Lys Lys Arg Trp Lys Tyr Ala Gly Ile Leu Leu Ile Ser Gly Pro Leu	
85 90 95	
ata ctg act ttt tac ggc acg att tta ggc tgg gtg ctt tat tat ttg	336
Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu Tyr Tyr Leu	
100 105 110	
gtg agt gtt agt ttt aat ttg cct aac aat atc caa gaa tct gaa caa	384
Val Ser Val Ser Phe Asn Leu Pro Asn Asn Ile Gln Glu Ser Glu Gln	
115 120 125	
att ttt act caa act ttg cag tct ata ggg tta caa tcc ata ggg ctt	432
Ile Phe Thr Gln Thr Leu Gln Ser Ile Gly Leu Gln Ser Ile Gly Leu	
130 135 140	
ttg agc gtt tta ttg ata acc g	454
Leu Ser Val Leu Leu Ile Thr	
145 150	

<210> 206  
 <211> 151  
 <212> PRT  
 <213> Helicobacter pylori

<400> 206

Met Gly Asn His Phe Ser Lys Leu Gly Phe Val Leu Ala Ala Leu Gly	
1 5 10 15	
Ser Ala Ile Gly Leu Gly His Ile Trp Arg Phe Pro Tyr Met Thr Gly	
20 25 30	
Val Ser Gly Gly Gly Ala Phe Val Leu Leu Phe Leu Phe Leu Ser Leu	
35 40 45	

Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu Gly Gln Ser  
50 55 60

Thr Gln Lys Asn Val Ile Glu Ala Phe Lys Glu Leu Asp Leu Asn Pro  
65 70 75 80

Lys Lys Arg Trp Lys Tyr Ala Gly Ile Leu Leu Ile Ser Gly Pro Leu  
85 90 95

Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu Tyr Tyr Leu  
100 105 110

Val Ser Val Ser Phe Asn Leu Pro Asn Asn Ile Gln Glu Ser Glu Gln  
115 120 125

Ile Phe Thr Gln Thr Leu Gln Ser Ile Gly Leu Gln Ser Ile Gly Leu  
130 135 140

Leu Ser Val Leu Leu Ile Thr  
145 150

<210> 207  
<211> 921  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(921)

<400> 207  
atg aaa aag att att ctt gca tgc ctt atg gct ttt gtg ggt gcc aat 48  
Met Lys Lys Ile Ile Leu Ala Cys Leu Met Ala Phe Val Gly Ala Asn  
1 5 10 15  
  
tta agc gca gag cct aag tgg tat agc aag gcc tat aac aaa aca aac 96  
Leu Ser Ala Glu Pro Lys Trp Tyr Ser Lys Ala Tyr Asn Lys Thr Asn  
20 25 30  
  
acc caa aaa ggc tat ctt tat ggg agt ggt tca gcc act tct aaa gag 144  
Thr Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr Ser Lys Glu  
35 40 45  
  
gct tct aaa caa aaa gcg tta gcg gat tta gtg gcg tct att agc gtg 192  
Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser Ile Ser Val  
50 55 60



gtg gtt aat tcc cag atc cat atc caa aaa agt cgt gtg gat aat aag	240
Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val Asp Asn Lys	
65 70 75 80	
tta aaa tcc agt gat tcg caa acg att aac tta aaa acc gat gac ttg	288
Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr Asp Asp Leu	
85 90 95	
gaa ttg aat aat gta gaa att gtc aat caa gaa gcg caa aaa ggg atc	336
Glu Leu Asn Asn Val Glu Ile Val Asn Gln Glu Ala Gln Lys Gly Ile	
100 105 110	
tac tac acc aga gta agg att aat caa aac ttg ttt ttg cag ggt tta	384
Tyr Tyr Thr Arg Val Arg Ile Asn Gln Asn Leu Phe Leu Gln Gly Leu	
115 120 125	
agg gat aag tat aac gct ctt tat ggg cag ttt tcc acc tta atg cct	432
Arg Asp Lys Tyr Asn Ala Leu Tyr Gly Gln Phe Ser Thr Leu Met Pro	
130 135 140	
aag gtt tgt aaa ggg gtt ttt tta cag caa tct aaa agc atg ggg gat	480
Lys Val Cys Lys Gly Val Phe Leu Gln Gln Ser Lys Ser Met Gly Asp	
145 150 155 160	
tta ttg gct aaa gcg atg cct ata gaa agg att tta aaa gcg tat tct	528
Leu Leu Ala Lys Ala Met Pro Ile Glu Arg Ile Leu Lys Ala Tyr Ser	
165 170 175	
gtc ccg gtg agt tcg tta gaa aat tat gaa aaa atc tat tat caa aac	576
Val Pro Val Ser Ser Leu Glu Asn Tyr Glu Lys Ile Tyr Tyr Gln Asn	
180 185 190	
gct ttc aaa cct aaa gtg caa atc act ttt gat aac aac agc gat aca	624
Ala Phe Lys Pro Lys Val Gln Ile Thr Phe Asp Asn Asn Ser Asp Thr	
195 200 205	
gag gat aca gag att aaa aac gct ctc ata agt gct tat gcc aga gtg	672
Glu Asp Thr Glu Ile Lys Asn Ala Leu Ile Ser Ala Tyr Ala Arg Val	
210 215 220	
cta acc cct agc gat gaa gaa aaa ctc tat caa atc aaa aat gaa gtt	720
Leu Thr Pro Ser Asp Glu Glu Lys Leu Tyr Gln Ile Lys Asn Glu Val	
225 230 235 240	
ttc aca gac agc gct aat ggc atc aca cgc att aga gtg gtt gtt agc	768
Phe Thr Asp Ser Ala Asn Gly Ile Thr Arg Ile Arg Val Val Val Ser	
245 250 255	
gca agc gat tgt caa ggc acg cct gta ttg aat aga agc ctt gaa gtg	816
Ala Ser Asp Cys Gln Gly Thr Pro Val Leu Asn Arg Ser Leu Glu Val	
260 265 270	
gat gaa aag aat aag aat ttt gct atc acg cgc ttg caa tct ttg ctt	864
Asp Glu Lys Asn Lys Asn Phe Ala Ile Thr Arg Leu Gln Ser Leu Leu	

275	280	285	
tat aaa gaa ttg aaa gat	tat gcc aat aaa gaa ggg	caa ggc aat acg	912
Tyr Lys Glu Leu Lys Asp	Tyr Ala Asn Lys Glu Gly	Gln Gly Asn Thr	
290	295	300	
ggg tta taa			921
Gly Leu			
305			
<210> 208			
<211> 306			
<212> PRT			
<213> Helicobacter pylori			
<400> 208			
Met Lys Lys Ile Ile Leu Ala Cys Leu Met Ala Phe Val Gly Ala Asn			
1	5	10	15
Leu Ser Ala Glu Pro Lys Trp Tyr Ser Lys Ala Tyr Asn Lys Thr Asn			
	20	25	30
Thr Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr Ser Lys Glu			
	35	40	45
Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser Ile Ser Val			
	50	55	60
Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val Asp Asn Lys			
65	70	75	80
Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr Asp Asp Leu			
	85	90	95
Glu Leu Asn Asn Val Glu Ile Val Asn Gln Glu Ala Gln Lys Gly Ile			
	100	105	110
Tyr Tyr Thr Arg Val Arg Ile Asn Gln Asn Leu Phe Leu Gln Gly Leu			
	115	120	125
Arg Asp Lys Tyr Asn Ala Leu Tyr Gly Gln Phe Ser Thr Leu Met Pro			
	130	135	140

Lys Val Cys Lys Gly Val Phe Leu Gln Gln Ser Lys Ser Met Gly Asp  
 145 150 155 160

Leu Leu Ala Lys Ala Met Pro Ile Glu Arg Ile Leu Lys Ala Tyr Ser  
 165 170 175

Val Pro Val Ser Ser Leu Glu Asn Tyr Glu Lys Ile Tyr Tyr Gln Asn  
 180 185 190

Ala Phe Lys Pro Lys Val Gln Ile Thr Phe Asp Asn Asn Ser Asp Thr  
 195 200 205

Glu Asp Thr Glu Ile Lys Asn Ala Leu Ile Ser Ala Tyr Ala Arg Val  
 210 215 220

Leu Thr Pro Ser Asp Glu Glu Lys Leu Tyr Gln Ile Lys Asn Glu Val  
 225 230 235 240

Phe Thr Asp Ser Ala Asn Gly Ile Thr Arg Ile Arg Val Val Val Ser  
 245 250 255

Ala Ser Asp Cys Gln Gly Thr Pro Val Leu Asn Arg Ser Leu Glu Val  
 260 265 270

Asp Glu Lys Asn Lys Asn Phe Ala Ile Thr Arg Leu Gln Ser Leu Leu  
 275 280 285

Tyr Lys Glu Leu Lys Asp Tyr Ala Asn Lys Glu Gly Gln Gly Asn Thr  
 290 295 300

Gly Leu  
 305

<210> 209  
 <211> 1572  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1572)  
 <400> 209

atg gca tta agg gta ttg tta ttc ttt tgt ttt ttg ttt tta caa gca	48
Met Ala Leu Arg Val Leu Leu Phe Phe Cys Phe Leu Phe Leu Gln Ala	
1 5 10 15	
gaa gat aaa agc caa gag cta ttg tcc ata caa aaa caa atg gct ttg	96
Glu Asp Lys Ser Gln Glu Leu Leu Ser Ile Gln Lys Gln Met Ala Leu	
20 25 30	
gtg gat aaa aaa ctc gcc aaa gac gat aac gtg tgg ttg aaa aaa ttt	144
Val Asp Lys Lys Leu Ala Lys Asp Asp Asn Val Trp Leu Lys Lys Phe	
35 40 45	
gaa aac tat aag atc tac aac caa att tat acc gaa aaa gag agc gtg	192
Glu Asn Tyr Lys Ile Tyr Asn Gln Ile Tyr Thr Glu Lys Glu Ser Val	
50 55 60	
agg cag gaa tta agg cgt tta aaa aat aaa aaa agc aag gat tta tta	240
Arg Gln Glu Leu Arg Arg Leu Lys Asn Lys Lys Ser Lys Asp Leu Leu	
65 70 75 80	
aag att agc acc tta gag cac acc tta aag gct tta gaa tcc cag caa	288
Lys Ile Ser Thr Leu Glu His Thr Leu Lys Ala Leu Glu Ser Gln Gln	
85 90 95	
aaa atg ttt gaa agc tat ggg gtc aat cct ttt aag gat ttg ata gag	336
Lys Met Phe Glu Ser Tyr Gly Val Asn Pro Phe Lys Asp Leu Ile Glu	
100 105 110	
cgc ccc aat atc ccc aat atc cct aat atc gct aac cct att gca atc	384
Arg Pro Asn Ile Pro Asn Ile Pro Asn Ile Ala Asn Pro Ile Ala Ile	
115 120 125	
att gat ggc att tct ttc att aaa agc atg cat tta aag cat gaa agt	432
Ile Asp Gly Ile Ser Phe Ile Lys Ser Met His Leu Lys His Glu Ser	
130 135 140	
ctt aaa aaa aac caa act tct tta gaa gaa gtt tta aag ctt cta gat	480
Leu Lys Lys Asn Gln Thr Ser Leu Glu Glu Val Leu Lys Leu Leu Asp	
145 150 155 160	
caa aaa cac cag ctt tta aat gag tgg cac gcc ttg gat aaa agc gtg	528
Gln Lys His Gln Leu Leu Asn Glu Trp His Ala Leu Asp Lys Ser Val	
165 170 175	
aaa cta agc gat gag att tat caa act caa gcc aaa cgc tta gaa ttg	576
Lys Leu Ser Asp Glu Ile Tyr Gln Thr Gln Ala Lys Arg Leu Glu Leu	
180 185 190	
caa ggg gct caa aac att tta aaa acc acg att ggg att ttc caa aaa	624
Gln Gly Ala Gln Asn Ile Leu Lys Thr Thr Ile Gly Ile Phe Gln Lys	
195 200 205	
gac agc gat gaa gct ata agc att gtt aaa tct caa gtt aaa aac cag	672
Asp Ser Asp Glu Ala Ile Ser Ile Val Lys Ser Gln Val Lys Asn Gln	
210 215 220	

ctt ttt aaa ttg att tat gtg ttt tta gca gcc ctt ttg agc gtg gtg	720
Leu Phe Lys Leu Ile Tyr Val Phe Leu Ala Ala Leu Leu Ser Val Val	
225 230 235 240	
ttt gct tgg att tta aaa atc att tcc agt aaa tac att gaa aat aat	768
Phe Ala Trp Ile Leu Lys Ile Ile Ser Ser Lys Tyr Ile Glu Asn Asn	
245 250 255	
gag cgc gtc tat acc gtg aat aaa gcc att aac ttc gtg aat gtg agc	816
Glu Arg Val Tyr Thr Val Asn Lys Ala Ile Asn Phe Val Asn Val Ser	
260 265 270	
gtg atc att tta atc ttt ctt ttt tct tat tta gag aat gtt act tac	864
Val Ile Ile Leu Ile Phe Leu Phe Ser Tyr Leu Glu Asn Val Thr Tyr	
275 280 285	
ttg gtc acg gtt tta ggc ttt gcg agc gct ggc tta gcg att gcg atg	912
Leu Val Thr Val Leu Gly Phe Ala Ser Ala Gly Leu Ala Ile Ala Met	
290 295 300	
aaa gat tta ttc atg agc ttg ctc ggg tgg ttt att att ttg att ggg	960
Lys Asp Leu Phe Met Ser Leu Leu Gly Trp Phe Ile Ile Leu Ile Gly	
305 310 315 320	
ggg agc gtg cat gtg ggc gat agg gtg cgt atc gct aag ggg acg gat	1008
Gly Ser Val His Val Gly Asp Arg Val Arg Ile Ala Lys Gly Thr Asp	
325 330 335	
att ttt att ggc gat gtg ttg gat att tct atg ttg cac att acg att	1056
Ile Phe Ile Gly Asp Val Leu Asp Ile Ser Met Leu His Ile Thr Ile	
340 345 350	
tta gaa gat gta acc ttt acc act tac acg aac aac agg aga gcg ggc	1104
Leu Glu Asp Val Thr Phe Thr Thr Tyr Thr Asn Asn Arg Arg Ala Gly	
355 360 365	
cgg att att ttt gtg cct aat aat tat att ttc acc acc atg ttt gct	1152
Arg Ile Ile Phe Val Pro Asn Asn Tyr Ile Phe Thr Thr Met Phe Ala	
370 375 380	
aat tac agc cat ttt ggg atg aaa acg gtt tgg gat ggc gtg gat ttt	1200
Asn Tyr Ser His Phe Gly Met Lys Thr Val Trp Asp Gly Val Asp Phe	
385 390 395 400	
tgc gtt aca ttt gat tct gat ttt aaa aaa gct tct aaa att gcg ctc	1248
Cys Val Thr Phe Asp Ser Asp Phe Lys Lys Ala Ser Lys Ile Ala Leu	
405 410 415	
aat atc gct acg gaa ttg tct aaa gaa tac acg gat att acc tat aaa	1296
Asn Ile Ala Thr Glu Leu Ser Lys Glu Tyr Thr Asp Ile Thr Tyr Lys	
420 425 430	
cag ctc aat aaa atg cgc gac cgg tat tct tta agg agt ttg agt gtg	1344
Gln Leu Asn Lys Met Arg Asp Arg Tyr Ser Leu Arg Ser Leu Ser Val	

435					440					445							
aag	cct	cga	tgc	ttt	ttg	atg	cct	gaa	aat	aac	ggg	ata	aaa	atc	tcg	1392	
Lys	Pro	Arg	Cys	Phe	Leu	Met	Pro	Glu	Asn	Asn	Gly	Ile	Lys	Ile	Ser		
450					455					460							
gtg	tgg	tat	caa	acc	aat	tcg	tat	gcg	acc	atg	tct	tta	agg	agc	aag	1440	
Val	Trp	Tyr	Gln	Thr	Asn	Ser	Tyr	Ala	Thr	Met	Ser	Leu	Arg	Ser	Lys		
465					470					475					480		
att	gtg	gct	gaa	atc	gtt	gaa	gct	ttt	ttg	aaa	gaa	gaa	aat	atc	cat	1488	
Ile	Val	Ala	Glu	Ile	Val	Glu	Ala	Phe	Leu	Lys	Glu	Glu	Asn	Ile	His		
485					490					495							
atc	gct	tat	acg	acc	agc	aag	ttg	ctt	aaa	gtg	gat	gct	gat	ttt	tta	1536	
Ile	Ala	Tyr	Thr	Thr	Ser	Lys	Leu	Leu	Lys	Val	Asp	Ala	Asp	Phe	Leu		
500					505					510							
ggc	gat	ggg	ttt	ggg	aat	aaa	agg	gaa	caa	aaa	tga					1572	
Gly	Asp	Gly	Phe	Gly	Asn	Lys	Arg	Glu	Gln	Lys							
515					520												

<210> 210  
 <211> 523  
 <212> PRT  
 <213> Helicobacter pylori

<400> 210

Met	Ala	Leu	Arg	Val	Leu	Leu	Phe	Phe	Cys	Phe	Leu	Phe	Leu	Gln	Ala
1				5					10					15	
Glu	Asp	Lys	Ser	Gln	Glu	Leu	Leu	Ser	Ile	Gln	Lys	Gln	Met	Ala	Leu
			20					25					30		
Val	Asp	Lys	Lys	Leu	Ala	Lys	Asp	Asp	Asn	Val	Trp	Leu	Lys	Lys	Phe
		35					40					45			
Glu	Asn	Tyr	Lys	Ile	Tyr	Asn	Gln	Ile	Tyr	Thr	Glu	Lys	Glu	Ser	Val
	50					55					60				
Arg	Gln	Glu	Leu	Arg	Arg	Leu	Lys	Asn	Lys	Lys	Ser	Lys	Asp	Leu	Leu
65					70					75				80	
Lys	Ile	Ser	Thr	Leu	Glu	His	Thr	Leu	Lys	Ala	Leu	Glu	Ser	Gln	Gln
				85					90					95	

Lys Met Phe Glu Ser Tyr Gly Val Asn Pro Phe Lys Asp Leu Ile Glu  
 100 105 110

Arg Pro Asn Ile Pro Asn Ile Pro Asn Ile Ala Asn Pro Ile Ala Ile  
 115 120 125

Ile Asp Gly Ile Ser Phe Ile Lys Ser Met His Leu Lys His Glu Ser  
 130 135 140

Leu Lys Lys Asn Gln Thr Ser Leu Glu Glu Val Leu Lys Leu Leu Asp  
 145 150 155 160

Gln Lys His Gln Leu Leu Asn Glu Trp His Ala Leu Asp Lys Ser Val  
 165 170 175

Lys Leu Ser Asp Glu Ile Tyr Gln Thr Gln Ala Lys Arg Leu Glu Leu  
 180 185 190

Gln Gly Ala Gln Asn Ile Leu Lys Thr Thr Ile Gly Ile Phe Gln Lys  
 195 200 205

Asp Ser Asp Glu Ala Ile Ser Ile Val Lys Ser Gln Val Lys Asn Gln  
 210 215 220

Leu Phe Lys Leu Ile Tyr Val Phe Leu Ala Ala Leu Leu Ser Val Val  
 225 230 235 240

Phe Ala Trp Ile Leu Lys Ile Ile Ser Ser Lys Tyr Ile Glu Asn Asn  
 245 250 255

Glu Arg Val Tyr Thr Val Asn Lys Ala Ile Asn Phe Val Asn Val Ser  
 260 265 270

Val Ile Ile Leu Ile Phe Leu Phe Ser Tyr Leu Glu Asn Val Thr Tyr  
 275 280 285

Leu Val Thr Val Leu Gly Phe Ala Ser Ala Gly Leu Ala Ile Ala Met  
 290 295 300

Lys Asp Leu Phe Met Ser Leu Leu Gly Trp Phe Ile Ile Leu Ile Gly  
 305 310 315 320

Gly Ser Val His Val Gly Asp Arg Val Arg Ile Ala Lys Gly Thr Asp  
325 330 335

Ile Phe Ile Gly Asp Val Leu Asp Ile Ser Met Leu His Ile Thr Ile  
340 345 350

Leu Glu Asp Val Thr Phe Thr Thr Tyr Thr Asn Asn Arg Arg Ala Gly  
355 360 365

Arg Ile Ile Phe Val Pro Asn Asn Tyr Ile Phe Thr Thr Met Phe Ala  
370 375 380

Asn Tyr Ser His Phe Gly Met Lys Thr Val Trp Asp Gly Val Asp Phe  
385 390 395 400

Cys Val Thr Phe Asp Ser Asp Phe Lys Lys Ala Ser Lys Ile Ala Leu  
405 410 415

Asn Ile Ala Thr Glu Leu Ser Lys Glu Tyr Thr Asp Ile Thr Tyr Lys  
420 425 430

Gln Leu Asn Lys Met Arg Asp Arg Tyr Ser Leu Arg Ser Leu Ser Val  
435 440 445

Lys Pro Arg Cys Phe Leu Met Pro Glu Asn Asn Gly Ile Lys Ile Ser  
450 455 460

Val Trp Tyr Gln Thr Asn Ser Tyr Ala Thr Met Ser Leu Arg Ser Lys  
465 470 475 480

Ile Val Ala Glu Ile Val Glu Ala Phe Leu Lys Glu Glu Asn Ile His  
485 490 495

Ile Ala Tyr Thr Thr Ser Lys Leu Leu Lys Val Asp Ala Asp Phe Leu  
500 505 510

Gly Asp Gly Phe Gly Asn Lys Arg Glu Gln Lys  
515 520

<210> 211

<211> 966



<212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(966)

<400> 211

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Met Pro Glu Asn Ser Lys Leu Gln Pro Ala Lys Leu Gly Lys Asn Phe	
1 5 10 15	
gac cct gtg gat cat tct aac agg aat ttt ttc ttt tct ctc att ctg	96
Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Phe Ser Leu Ile Leu	
20 25 30	
tct gta ttg tta cac tgg ttg att tat ttt tta ttt gaa cac aga gaa	144
Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu His Arg Glu	
35 40 45	
gat ttt ttt cct tca aaa ccc aag ctt gtt aaa tta aat cct gaa aat	192
Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn Pro Glu Asn	
50 55 60	
tta ttg gtt tta aaa aga ggc cat tcg caa gat ccc agt aaa aac acc	240
Leu Leu Val Leu Lys Arg Gly His Ser Gln Asp Pro Ser Lys Asn Thr	
65 70 75 80	
cag ggc gct cct aaa ccc acg ctg gct ggc ccc caa aaa ccc ccc act	288
Gln Gly Ala Pro Lys Pro Thr Leu Ala Gly Pro Gln Lys Pro Pro Thr	
85 90 95	
cca ccc aca ccc cca att ccg cca acc ccg cca aaa cct ata gaa aag	336
Pro Pro Thr Pro Pro Ile Pro Pro Thr Pro Pro Lys Pro Ile Glu Lys	
100 105 110	
cct aaa cct gag cct aaa cct aag cca aaa cca gaa ccc aaa aag ccc	384
Pro Lys Pro Glu Pro Lys Pro Lys Pro Lys Pro Glu Pro Lys Lys Pro	
115 120 125	
aac cac aaa cat aag gct ctt aaa aaa gtg gaa aaa gtg gaa gag aaa	432
Asn His Lys His Lys Ala Leu Lys Lys Val Glu Lys Val Glu Glu Lys	
130 135 140	
aaa ata gta gag gag aaa aaa gaa gag aaa aaa atc gta gag cag aaa	480
Lys Ile Val Glu Glu Lys Lys Glu Glu Lys Lys Ile Val Glu Gln Lys	
145 150 155 160	
gta gaa caa aaa gta gag cag aaa aaa ata gaa gag aaa aaa cct gtc	528
Val Glu Gln Lys Val Glu Gln Lys Lys Ile Glu Glu Lys Lys Pro Val	
165 170 175	
aaa aaa gaa ttt gac cct aac cag ctt tct ttc ttg cct aaa gaa gtt	576
Lys Lys Glu Phe Asp Pro Asn Gln Leu Ser Phe Leu Pro Lys Glu Val	

180								185				190				
gcg	cca	ccc	aga	aaa	gaa	aat	aat	aaa	ggc	tta	gat	aac	caa	acc	aga	624
Ala	Pro	Pro	Arg	Lys	Glu	Asn	Asn	Lys	Gly	Leu	Asp	Asn	Gln	Thr	Arg	
		195					200					205				
agg	gat	att	gat	gaa	ttg	tat	ggc	gaa	gaa	ttt	ggg	gat	tta	ggc	aca	672
Arg	Asp	Ile	Asp	Glu	Leu	Tyr	Gly	Glu	Glu	Phe	Gly	Asp	Leu	Gly	Thr	
	210					215					220					
gcc	gaa	aaa	gat	ttc	atc	agg	aat	aat	tta	agg	gat	att	ggg	cgc	atc	720
Ala	Glu	Lys	Asp	Phe	Ile	Arg	Asn	Asn	Leu	Arg	Asp	Ile	Gly	Arg	Ile	
225					230					235					240	
acg	caa	aaa	tat	tta	gaa	tac	cct	caa	gta	gcg	gct	tat	tta	ggg	cag	768
Thr	Gln	Lys	Tyr	Leu	Glu	Tyr	Pro	Gln	Val	Ala	Ala	Tyr	Leu	Gly	Gln	
				245					250					255		
gac	ggg	acg	aat	gcg	gta	gag	ttt	tac	ttg	cac	cct	aac	ggc	gat	att	816
Asp	Gly	Thr	Asn	Ala	Val	Glu	Phe	Tyr	Leu	His	Pro	Asn	Gly	Asp	Ile	
			260					265					270			
acc	gat	ctt	aaa	atc	atc	att	ggc	tct	gaa	tat	aaa	atg	ctt	gat	gac	864
Thr	Asp	Leu	Lys	Ile	Ile	Ile	Gly	Ser	Glu	Tyr	Lys	Met	Leu	Asp	Asp	
		275					280					285				
aac	act	tta	aag	acc	att	cag	atc	gct	tat	aag	gat	tac	cca	cgc	cct	912
Asn	Thr	Leu	Lys	Thr	Ile	Gln	Ile	Ala	Tyr	Lys	Asp	Tyr	Pro	Arg	Pro	
	290					295					300					
aaa	act	aaa	acc	ctc	att	cgc	atc	aga	gtg	cgt	tat	tac	ttg	gga	ggc	960
Lys	Thr	Lys	Thr	Leu	Ile	Arg	Ile	Arg	Val	Arg	Tyr	Tyr	Leu	Gly	Gly	
305					310					315					320	
aat	taa															966
Asn																

<210> 212  
 <211> 321  
 <212> PRT  
 <213> Helicobacter pylori

<400> 212

Met	Pro	Glu	Asn	Ser	Lys	Leu	Gln	Pro	Ala	Lys	Leu	Gly	Lys	Asn	Phe
1				5					10					15	

Asp	Pro	Val	Asp	His	Ser	Asn	Arg	Asn	Phe	Phe	Phe	Ser	Leu	Ile	Leu
		20					25						30		

Ser	Val	Leu	Leu	His	Trp	Leu	Ile	Tyr	Phe	Leu	Phe	Glu	His	Arg	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn Pro Glu Asn 50 55 60		
Leu Leu Val Leu Lys Arg Gly His Ser Gln Asp Pro Ser Lys Asn Thr 65 70 75 80		
Gln Gly Ala Pro Lys Pro Thr Leu Ala Gly Pro Gln Lys Pro Pro Thr 85 90 95		
Pro Pro Thr Pro Pro Ile Pro Pro Thr Pro Pro Lys Pro Ile Glu Lys 100 105 110		
Pro Lys Pro Glu Pro Lys Pro Lys Pro Lys Pro Glu Pro Lys Lys Pro 115 120 125		
Asn His Lys His Lys Ala Leu Lys Lys Val Glu Lys Val Glu Glu Lys 130 135 140		
Lys Ile Val Glu Glu Lys Lys Glu Glu Lys Lys Ile Val Glu Gln Lys 145 150 155 160		
Val Glu Gln Lys Val Glu Gln Lys Lys Ile Glu Glu Lys Lys Pro Val 165 170 175		
Lys Lys Glu Phe Asp Pro Asn Gln Leu Ser Phe Leu Pro Lys Glu Val 180 185 190		
Ala Pro Pro Arg Lys Glu Asn Asn Lys Gly Leu Asp Asn Gln Thr Arg 195 200 205		
Arg Asp Ile Asp Glu Leu Tyr Gly Glu Glu Phe Gly Asp Leu Gly Thr 210 215 220		
Ala Glu Lys Asp Phe Ile Arg Asn Asn Leu Arg Asp Ile Gly Arg Ile 225 230 235 240		
Thr Gln Lys Tyr Leu Glu Tyr Pro Gln Val Ala Ala Tyr Leu Gly Gln 245 250 255		

Asp Gly Thr Asn Ala Val Glu Phe Tyr Leu His Pro Asn Gly Asp Ile  
 260 265 270

Thr Asp Leu Lys Ile Ile Ile Gly Ser Glu Tyr Lys Met Leu Asp Asp  
 275 280 285

Asn Thr Leu Lys Thr Ile Gln Ile Ala Tyr Lys Asp Tyr Pro Arg Pro  
 290 295 300

Lys Thr Lys Thr Leu Ile Arg Ile Arg Val Arg Tyr Tyr Leu Gly Gly  
 305 310 315 320

Asn

<210> 213  
 <211> 812  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(810)

<400> 213  
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 Met Lys Thr Asn Gly Leu Phe Lys Met Trp Gly Leu Phe Leu Val Leu  
 1 5 10 15  
 atc gct tta gtc ttt aac gca tgc tct gat agc cat aaa gaa aaa aag 96  
 Ile Ala Leu Val Phe Asn Ala Cys Ser Asp Ser His Lys Glu Lys Lys  
 20 25 30  
 gac gct tta gaa gtc att aaa caa aga ggg gtt tta aaa gtg ggg gtt 144  
 Asp Ala Leu Glu Val Ile Lys Gln Arg Gly Val Leu Lys Val Gly Val  
 35 40 45  
 ttt agc gat aag cct cct ttt gga tct gtg gat tct aaa ggg aaa tat 192  
 Phe Ser Asp Lys Pro Pro Phe Gly Ser Val Asp Ser Lys Gly Lys Tyr  
 50 55 60  
 caa ggc tat gat gtg atc atc gct aaa cgc atg gcc ctt gat tta ttg 240  
 Gln Gly Tyr Asp Val Ile Ile Ala Lys Arg Met Ala Leu Asp Leu Leu  
 65 70 75 80  
 ggc gat gaa aat aag att gag ttt att ccc gta gaa gct tca gct agg 288  
 Gly Asp Glu Asn Lys Ile Glu Phe Ile Pro Val Glu Ala Ser Ala Arg  
 85 90 95

gtg gaa ttt tta aaa gcc aat aaa gtg gat att atc atg gct aat ttc	336
Val Glu Phe Leu Lys Ala Asn Lys Val Asp Ile Ile Met Ala Asn Phe	
100 105 110	
acg cgc act aaa gaa aga gaa aaa gtc gtg gat ttc gct aat ccg tat	384
Thr Arg Thr Lys Glu Arg Glu Lys Val Val Asp Phe Ala Asn Pro Tyr	
115 120 125	
atg aaa gtc gct tkg ggg gtg att tct aaa gat ggg gtc att aaa aat	432
Met Lys Val Ala Xaa Gly Val Ile Ser Lys Asp Gly Val Ile Lys Asn	
130 135 140	
ata gaa gag ttg aag gat aaa gag ttg att gtg aat aaa ggc acg aca	480
Ile Glu Glu Leu Lys Asp Lys Glu Leu Ile Val Asn Lys Gly Thr Thr	
145 150 155 160	
gcg gaw ttt tat ttc act aaa aat tac ccc aat atc aaa ctt ttg aaa	528
Ala Xaa Phe Tyr Phe Thr Lys Asn Tyr Pro Asn Ile Lys Leu Leu Lys	
165 170 175	
ttt gta caa aac aca gag act ttt tta gcc ctt tta aat aat aag gcc	576
Phe Val Gln Asn Thr Glu Thr Phe Leu Ala Leu Leu Asn Asn Lys Ala	
180 185 190	
acc gct cta gcc cat gac aac act tta ttg ctc gct tgg gcg aaa caa	624
Thr Ala Leu Ala His Asp Asn Thr Leu Leu Leu Ala Trp Ala Lys Gln	
195 200 205	
cac cct gaa ttt aaa tta ggc att aca agc ctt ggc gat aaa gat gtg	672
His Pro Glu Phe Lys Leu Gly Ile Thr Ser Leu Gly Asp Lys Asp Val	
210 215 220	
atc gct cca gcg att aaa aaa ggc aac cct aag ctt tta gaa tgg ttg	720
Ile Ala Pro Ala Ile Lys Lys Gly Asn Pro Lys Leu Leu Glu Trp Leu	
225 230 235 240	
aat aac gag att gat tcc ctc att tct agc gac ttt tta aaa gaa gct	768
Asn Asn Glu Ile Asp Ser Leu Ile Ser Ser Asp Phe Leu Lys Glu Ala	
245 250 255	
tat caa gaa act tta gag cct gtt tat ggc gat gaa atc aaa cc	812
Tyr Gln Glu Thr Leu Glu Pro Val Tyr Gly Asp Glu Ile Lys	
260 265 270	

<210> 214

<211> 270

<212> PRT

<213> Helicobacter pylori

<220>

<221> misc\_feature

<222> (133)..(133)

<223> The 'Xaa' at location 133 stands for Trp, or Leu.

<220>

<221> misc\_feature

<222> (162)..(162)

<223> The 'Xaa' at location 162 stands for Glu, or Asp.

<400> 214

Met Lys Thr Asn Gly Leu Phe Lys Met Trp Gly Leu Phe Leu Val Leu  
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Ile Ala Leu Val Phe Asn Ala Cys Ser Asp Ser His Lys Glu Lys Lys  
20 25 30

Asp Ala Leu Glu Val Ile Lys Gln Arg Gly Val Leu Lys Val Gly Val  
35 40 45

Phe Ser Asp Lys Pro Pro Phe Gly Ser Val Asp Ser Lys Gly Lys Tyr  
50 55 60

Gln Gly Tyr Asp Val Ile Ile Ala Lys Arg Met Ala Leu Asp Leu Leu  
65 70 75 80

Gly Asp Glu Asn Lys Ile Glu Phe Ile Pro Val Glu Ala Ser Ala Arg  
85 90 95

Val Glu Phe Leu Lys Ala Asn Lys Val Asp Ile Ile Met Ala Asn Phe  
100 105 110

Thr Arg Thr Lys Glu Arg Glu Lys Val Val Asp Phe Ala Asn Pro Tyr  
115 120 125

Met Lys Val Ala Xaa Gly Val Ile Ser Lys Asp Gly Val Ile Lys Asn  
130 135 140

Ile Glu Glu Leu Lys Asp Lys Glu Leu Ile Val Asn Lys Gly Thr Thr  
145 150 155 160

Ala Xaa Phe Tyr Phe Thr Lys Asn Tyr Pro Asn Ile Lys Leu Leu Lys  
165 170 175

Phe Val Gln Asn Thr Glu Thr Phe Leu Ala Leu Leu Asn Asn Lys Ala  
180 185 190

Thr Ala Leu Ala His Asp Asn Thr Leu Leu Leu Ala Trp Ala Lys Gln  
195 200 205

His Pro Glu Phe Lys Leu Gly Ile Thr Ser Leu Gly Asp Lys Asp Val  
210 215 220

Ile Ala Pro Ala Ile Lys Lys Gly Asn Pro Lys Leu Leu Glu Trp Leu  
225 230 235 240

Asn Asn Glu Ile Asp Ser Leu Ile Ser Ser Asp Phe Leu Lys Glu Ala  
245 250 255

Tyr Gln Glu Thr Leu Glu Pro Val Tyr Gly Asp Glu Ile Lys  
260 265 270

<210> 215  
<211> 1268  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(1266)

<400> 215  
atg aaa aac acc aat aca aaa gag ata aag aat aca aga atg gaa aaa 48  
Met Lys Asn Thr Asn Thr Lys Glu Ile Lys Asn Thr Arg Met Glu Lys  
1 5 10 15  
ggt tat agt caa tac cac gca ctc aaa aaa ggg ctt tta aaa acc gct 96  
Gly Tyr Ser Gln Tyr His Ala Leu Lys Lys Gly Leu Leu Lys Thr Ala  
20 25 30  
ttg ctt ttt agc ctt cct tta agc atg gcg tta gct gaa gac gat ggc 144  
Leu Leu Phe Ser Leu Pro Leu Ser Met Ala Leu Ala Glu Asp Asp Gly  
35 40 45  
ttt tat atg gga gtg ggc tat caa atc ggc ggt gcg caa caa aat atc 192  
Phe Tyr Met Gly Val Gly Tyr Gln Ile Gly Gly Ala Gln Gln Asn Ile  
50 55 60  
aat aac aaa ggc agc acc cta agg aat aat gtc att gat gat ttc cgc 240  
Asn Asn Lys Gly Ser Thr Leu Arg Asn Asn Val Ile Asp Asp Phe Arg  
65 70 75 80  
caa gtg ggc gtg ggt atg gca ggg ggt aat ggg ctt tta gcc tta gcg 288  
Gln Val Gly Val Gly Met Ala Gly Gly Asn Gly Leu Leu Ala Leu Ala

85								90				95				
aca Thr	aac Asn	acg Thr	acc Thr 100	atg Met	gac Asp	gct Ala	ctt Leu 105	tta Leu 105	ggg Gly	ata Ile	ggc Gly	aat Asn	caa Gln 110	att Ile	ttc Phe	336
aat Asn	act Thr	aat Asn 115	aca Thr	act Thr	gtt Val	ggc Gly	aac Asn 120	aac Asn	aac Asn	gca Ala	gaa Glu	tta Leu 125	acc Thr	cag Gln	ttt Phe	384
aaa Lys 130	aaa Lys	ata Ile	ctc Leu	ccc Pro	caa Gln	att Ile 135	gag Glu	caa Gln	cgc Arg	ttt Phe	gaa Glu 140	gcg Ala	aat Asn	aaa Lys	aac Asn	432
gct Ala 145	tat Tyr	agc Ser	gtt Val	caa Gln	gcc Ala 150	ttg Leu	caa Gln	gtg Val	tat Tyr	ttg Leu 155	agt Ser	aat Asn	gtg Val	ctt Leu	tat Tyr 160	480
aac Asn	ttg Leu	gtt Val	aat Asn 165	aat Asn	agt Ser	aat Asn	aat Asn	ggc Gly 170	agc Ser	aat Asn	aat Asn	gga Gly	gtc Val 175	gtt Val 175	cct Pro	528
gaa Glu	tat Tyr	gta Val	ggg Gly 180	att Ile	ata Ile	aaa Lys	gtt Val 185	ctc Leu 185	tat Tyr	ggg Gly	tct Ser	caa Gln	aat Asn 190	gaa Glu	ttc Phe	576
agt Ser	ctc Leu	tta Leu 195	gcc Ala	acg Thr	gag Glu	agt Ser	gtg Val 200	gcg Ala	ctt Leu	cta Leu	aac Asn	gcg Ala 205	ctt Leu	aca Thr	agg Arg	624
gtg Val	aat Asn 210	ctg Leu	gat Asp	agc Ser	aat Asn	tcg Ser 215	gtg Val	ttt Phe	tta Leu	aaa Lys	ggg Gly 220	cwa Xaa	tta Leu	gcc Ala	caa Gln	672
atg Met 225	cag Gln	ctt Leu	ttt Phe	aat Asn	gac Asp 230	act Thr	tct Ser	gca Ala	gca Ala	aag Lys 235	cta Leu	ggc Gly	cag Gln	atc Ile	gca Ala 240	720
gaa Glu	agc Ser	ttg Leu	aat Asn	aag Lys 245	agc Ser	ggg Gly	ggg Gly	gca Ala	ggg Gly 250	gcc Ala	atg Met	ctt Leu	caa Gln	aag Lys 255	gat Asp	768
gtg Val	aaa Lys	acc Thr	atc Ile 260	tcg Ser	gat Asp	cga Arg	atc Ile	gct Ala 265	act Thr	tac Tyr	caa Gln	gag Glu	aat Asn 270	cta Leu	aaa Lys	816
cag Gln	cta Leu	gga Gly 275	ggg Gly	atg Met	cta Leu	aag Lys	aat Asn 280	tac Tyr	gat Asp	gag Glu	cca Pro	tac Tyr 285	cta Leu	ccc Pro	caa Gln	864
ttt Phe 290	ggg Gly	cma Xaa	ggc Gly	aca Thr	agc Ser	tct Ser 295	cag Gln	cat His	ggg Gly	gtt Val 300	att Ile	aat Asn	ggc Gly	ttt Phe	ggc Gly	912
att	caa	atg	ggc	tat	aag	caa	ttt	ttt	ggg	aac	aag	agg	aat	ata	ggc	960



Ile	Gln	Met	Gly	Tyr	Lys	Gln	Phe	Phe	Gly	Asn	Lys	Arg	Asn	Ile	Gly	
305					310					315					320	
tta	cgg	tat	tac	gct	ttc	ttt	gat	tac	ggc	ttt	acg	caa	ttg	ggc	agt	1008
Leu	Arg	Tyr	Tyr	Ala	Phe	Phe	Asp	Tyr	Gly	Phe	Thr	Gln	Leu	Gly	Ser	
				325					330					335		
ctt	agc	agc	gct	ggt	aaa	gcg	aac	atc	ttt	act	tat	ggg	gct	ggc	acg	1056
Leu	Ser	Ser	Ala	Val	Lys	Ala	Asn	Ile	Phe	Thr	Tyr	Gly	Ala	Gly	Thr	
			340					345					350			
gac	ttt	tta	tgg	aat	atc	ttt	aga	agg	ggt	ttt	agc	gat	cag	tcc	ttg	1104
Asp	Phe	Leu	Trp	Asn	Ile	Phe	Arg	Arg	Val	Phe	Ser	Asp	Gln	Ser	Leu	
		355					360					365				
aat	gtg	ggg	gtg	ttt	gga	ggc	att	caa	ata	gcg	ggg	aac	act	tgg	gat	1152
Asn	Val	Gly	Val	Phe	Gly	Gly	Ile	Gln	Ile	Ala	Gly	Asn	Thr	Trp	Asp	
	370					375					380					
agc	tct	tta	aga	ggg	caa	att	gag	aat	tcg	ttt	aaa	gaa	tac	ccc	act	1200
Ser	Ser	Leu	Arg	Gly	Gln	Ile	Glu	Asn	Ser	Phe	Lys	Glu	Tyr	Pro	Thr	
385					390					395				400		
ccc	aca	aat	ttc	caa	ttt	tta	ttt	aat	ttg	ggc	tta	agg	gct	cat	ttt	1248
Pro	Thr	Asn	Phe	Gln	Phe	Leu	Phe	Asn	Leu	Gly	Leu	Arg	Ala	His	Phe	
			405						410					415		
gcc	agc	acc	atg	cac	cgc	cg										1268
Ala	Ser	Thr	Met	His	Arg											
			420													

<210> 216  
 <211> 422  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <221> misc\_feature  
 <222> (221)..(221)  
 <223> The 'Xaa' at location 221 stands for Gln, or Leu.

<220>  
 <221> misc\_feature  
 <222> (291)..(291)  
 <223> The 'Xaa' at location 291 stands for Gln, or Pro.

<400> 216

Met	Lys	Asn	Thr	Asn	Thr	Lys	Glu	Ile	Lys	Asn	Thr	Arg	Met	Glu	Lys
1				5					10					15	

Gly	Tyr	Ser	Gln	Tyr	His	Ala	Leu	Lys	Lys	Gly	Leu	Leu	Lys	Thr	Ala
			20					25					30		

Leu Leu Phe Ser Leu Pro Leu Ser Met Ala Leu Ala Glu Asp Asp Gly  
 35 40 45

Phe Tyr Met Gly Val Gly Tyr Gln Ile Gly Gly Ala Gln Gln Asn Ile  
 50 55 60

Asn Asn Lys Gly Ser Thr Leu Arg Asn Asn Val Ile Asp Asp Phe Arg  
 65 70 75 80

Gln Val Gly Val Gly Met Ala Gly Gly Asn Gly Leu Leu Ala Leu Ala  
 85 90 95

Thr Asn Thr Thr Met Asp Ala Leu Leu Gly Ile Gly Asn Gln Ile Phe  
 100 105 110

Asn Thr Asn Thr Thr Val Gly Asn Asn Asn Ala Glu Leu Thr Gln Phe  
 115 120 125

Lys Lys Ile Leu Pro Gln Ile Glu Gln Arg Phe Glu Ala Asn Lys Asn  
 130 135 140

Ala Tyr Ser Val Gln Ala Leu Gln Val Tyr Leu Ser Asn Val Leu Tyr  
 145 150 155 160

Asn Leu Val Asn Asn Ser Asn Asn Gly Ser Asn Asn Gly Val Val Pro  
 165 170 175

Glu Tyr Val Gly Ile Ile Lys Val Leu Tyr Gly Ser Gln Asn Glu Phe  
 180 185 190

Ser Leu Leu Ala Thr Glu Ser Val Ala Leu Leu Asn Ala Leu Thr Arg  
 195 200 205

Val Asn Leu Asp Ser Asn Ser Val Phe Leu Lys Gly Xaa Leu Ala Gln  
 210 215 220

Met Gln Leu Phe Asn Asp Thr Ser Ala Ala Lys Leu Gly Gln Ile Ala  
 225 230 235 240

Glu Ser Leu Asn Lys Ser Gly Gly Ala Gly Ala Met Leu Gln Lys Asp

245								250				255			
Val	Lys	Thr	Ile	Ser	Asp	Arg	Ile	Ala	Thr	Tyr	Gln	Glu	Asn	Leu	Lys
			260					265					270		
Gln	Leu	Gly	Gly	Met	Leu	Lys	Asn	Tyr	Asp	Glu	Pro	Tyr	Leu	Pro	Gln
		275					280					285			
Phe	Gly	Xaa	Gly	Thr	Ser	Ser	Gln	His	Gly	Val	Ile	Asn	Gly	Phe	Gly
	290					295					300				
Ile	Gln	Met	Gly	Tyr	Lys	Gln	Phe	Phe	Gly	Asn	Lys	Arg	Asn	Ile	Gly
305					310					315					320
Leu	Arg	Tyr	Tyr	Ala	Phe	Phe	Asp	Tyr	Gly	Phe	Thr	Gln	Leu	Gly	Ser
				325					330					335	
Leu	Ser	Ser	Ala	Val	Lys	Ala	Asn	Ile	Phe	Thr	Tyr	Gly	Ala	Gly	Thr
			340					345					350		
Asp	Phe	Leu	Trp	Asn	Ile	Phe	Arg	Arg	Val	Phe	Ser	Asp	Gln	Ser	Leu
		355					360					365			
Asn	Val	Gly	Val	Phe	Gly	Gly	Ile	Gln	Ile	Ala	Gly	Asn	Thr	Trp	Asp
	370					375					380				
Ser	Ser	Leu	Arg	Gly	Gln	Ile	Glu	Asn	Ser	Phe	Lys	Glu	Tyr	Pro	Thr
385					390					395					400
Pro	Thr	Asn	Phe	Gln	Phe	Leu	Phe	Asn	Leu	Gly	Leu	Arg	Ala	His	Phe
				405					410					415	
Ala	Ser	Thr	Met	His	Arg										
			420												

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 <211> 312  
 <212> DNA  
 <213> Helicobacter pylori

<220>

<221> CDS  
 <222> (1)..(312)

<400> 217  
 ttt aca aag att atg aag aga gtt aga ggg ctt gtg aaa aaa cac ccc 48  
 Phe Thr Lys Ile Met Lys Arg Val Arg Gly Leu Val Lys Lys His Pro  
 1 5 10 15  
 aag aaa agc aag gcg gca tta gta gta ttg acc cat gtt gcg tgc aag 96  
 Lys Lys Ser Lys Ala Ala Leu Val Val Leu Thr His Val Ala Cys Lys  
 20 25 30  
 aaa gcg aaa gaa ttg gac gat aaa gtc cag gat aaa tcc aaa caa gct 144  
 Lys Ala Lys Glu Leu Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala  
 35 40 45  
 gaa aaa gaa aat caa atc aat tgg tgg aaa tat tca gga tta aca ata 192  
 Glu Lys Glu Asn Gln Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile  
 50 55 60  
 gcg aca agt tta tta tta gcc gct tgt agt gct ggt gat att gat aaa 240  
 Ala Thr Ser Leu Leu Leu Ala Ala Cys Ser Ala Gly Asp Ile Asp Lys  
 65 70 75 80  
 caa ata gag tta gaa caa gaa aaa caa aag aca gaa caa gaa caa cag 288  
 Gln Ile Glu Leu Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Gln Gln  
 85 90 95  
 aaa aca gaa caa gaa aga caa aaa 312  
 Lys Thr Glu Gln Glu Arg Gln Lys  
 100

<210> 218  
 <211> 104  
 <212> PRT  
 <213> Helicobacter pylori

<400> 218  
 Phe Thr Lys Ile Met Lys Arg Val Arg Gly Leu Val Lys Lys His Pro  
 1 5 10 15  
 Lys Lys Ser Lys Ala Ala Leu Val Val Leu Thr His Val Ala Cys Lys  
 20 25 30  
 Lys Ala Lys Glu Leu Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala  
 35 40 45  
 Glu Lys Glu Asn Gln Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile  
 50 55 60

Ala Thr Ser Leu Leu Leu Ala Ala Cys Ser Ala Gly Asp Ile Asp Lys  
65 70 75 80

Gln Ile Glu Leu Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Gln Gln  
85 90 95

Lys Thr Glu Gln Glu Arg Gln Lys  
100

<210> 219  
<211> 1290  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(1290)

<400> 219  
atg cca tac gcc tta aga aaa aga ttt ttc aaa cgc ctt gcg ctg att 48  
Met Pro Tyr Ala Leu Arg Lys Arg Phe Phe Lys Arg Leu Ala Leu Ile  
1 5 10 15  
ggt tcc act ttt tgc gcg ata agc ttg aac gct aaa agc tat ctg ttt 96  
Val Ser Thr Phe Cys Ala Ile Ser Leu Asn Ala Lys Ser Tyr Leu Phe  
20 25 30  
tcc ccc ttg ccc cca gcg cac caa caa atc att aag aca gag cct tgc 144  
Ser Pro Leu Pro Pro Ala His Gln Gln Ile Ile Lys Thr Glu Pro Cys  
35 40 45  
tct ttg gaa tgc ttg aaa gac ttg atg ttg caa aat caa atc ttt tct 192  
Ser Leu Glu Cys Leu Lys Asp Leu Met Leu Gln Asn Gln Ile Phe Ser  
50 55 60  
ttt gtt tct caa tac gat aac aac aac caa gat gag agc ctt aaa act 240  
Phe Val Ser Gln Tyr Asp Asn Asn Asn Gln Asp Glu Ser Leu Lys Thr  
65 70 75 80  
tat tat cat gac ata ctc aat aaa ctc aac cct gca ttc atc gct tct 288  
Tyr Tyr His Asp Ile Leu Asn Lys Leu Asn Pro Ala Phe Ile Ala Ser  
85 90 95  
caa act cca gct aaa gac agc tat gag cct aag att gaa tta gcg gtt 336  
Gln Thr Pro Ala Lys Asp Ser Tyr Glu Pro Lys Ile Glu Leu Ala Val  
100 105 110  
tta ctg cct aaa aag gtg gtg ggg cgt tat gcc att tcg gtg atg aac 384  
Leu Leu Pro Lys Lys Val Val Gly Arg Tyr Ala Ile Ser Val Met Asn  
115 120 125

acc ctt tta gcg tat ttg aac acc aga aac aac gat ttc aat atc caa	432
Thr Leu Leu Ala Tyr Leu Asn Thr Arg Asn Asn Asp Phe Asn Ile Gln	
130 135 140	
gtc ttt gac agc gat gaa gag agt cct gaa aaa tta gag caa acc tat	480
Val Phe Asp Ser Asp Glu Glu Ser Pro Glu Lys Leu Glu Gln Thr Tyr	
145 150 155 160	
aaa gaa att gaa aaa gaa aaa ttc cct ttt gtg ata gcc tta tta acc	528
Lys Glu Ile Glu Lys Glu Lys Phe Pro Phe Val Ile Ala Leu Leu Thr	
165 170 175	
aaa gag ggc gtg gaa aat ttg ctc caa aac acc acg att agc acc cct	576
Lys Glu Gly Val Glu Asn Leu Leu Gln Asn Thr Thr Ile Ser Thr Pro	
180 185 190	
act tat gtg cct acg gtg aat aga acg caa tta gaa aat caa act gag	624
Thr Tyr Val Pro Thr Val Asn Arg Thr Gln Leu Glu Asn Gln Thr Glu	
195 200 205	
cgt tct tta agc gag cgc ttg tat ttt ggg ggg att gac tat aaa gag	672
Arg Ser Leu Ser Glu Arg Leu Tyr Phe Gly Gly Ile Asp Tyr Lys Glu	
210 215 220	
caa tta agc atg ctc acg gct ttc att agc cct aat tcg ccc gtg att	720
Gln Leu Ser Met Leu Thr Ala Phe Ile Ser Pro Asn Ser Pro Val Ile	
225 230 235 240	
gaa tac gat gat gat ggc cta ata gga gaa cgc ttg agg caa atc acg	768
Glu Tyr Asp Asp Asp Gly Leu Ile Gly Glu Arg Leu Arg Gln Ile Thr	
245 250 255	
gag tct tta agc att gaa gtc aaa cac caa gaa aat att tct tac aaa	816
Glu Ser Leu Ser Ile Glu Val Lys His Gln Glu Asn Ile Ser Tyr Lys	
260 265 270	
caa gcc acc agt ttt tct aaa aat ttt aga aaa aac gat gcg ttt ttt	864
Gln Ala Thr Ser Phe Ser Lys Asn Phe Arg Lys Asn Asp Ala Phe Phe	
275 280 285	
aaa aat tct att ttg att tta aac acc cct acc act aaa agc ggc ctt	912
Lys Asn Ser Ile Leu Ile Leu Asn Thr Pro Thr Thr Lys Ser Gly Leu	
290 295 300	
atc ctt tct caa ata ggg ctt tta gaa tac aag ccc ttt aaa atc ctt	960
Ile Leu Ser Gln Ile Gly Leu Leu Glu Tyr Lys Pro Phe Lys Ile Leu	
305 310 315 320	
tcc aca caa atc aat ttc aac ctc tct tta ctc tta ctc acc cag cct	1008
Ser Thr Gln Ile Asn Phe Asn Leu Ser Leu Leu Leu Leu Thr Gln Pro	
325 330 335	
aaa gac aga aag aat tta ttc atc gtc aat gcc ttg caa aat agc gat	1056
Lys Asp Arg Lys Asn Leu Phe Ile Val Asn Ala Leu Gln Asn Ser Asp	

340					345					350						
gaa	acg	ctt	ata	gaa	tac	gcc	tcc	tta	ttg	gag	agc	gat	tta	agg	cat	1104
Glu	Thr	Leu	Ile	Glu	Tyr	Ala	Ser	Leu	Leu	Glu	Ser	Asp	Leu	Arg	His	
		355					360					365				
gat	tgg	gtg	aat	tat	tcc	agt	gca	att	ggg	cta	gag	gtg	ttt	tta	aac	1152
Asp	Trp	Val	Asn	Tyr	Ser	Ser	Ala	Ile	Gly	Leu	Glu	Val	Phe	Leu	Asn	
	370					375					380					
aca	cta	gat	ccg	cat	ttt	aaa	aaa	tct	ttt	caa	gaa	agt	tta	gaa	gac	1200
Thr	Leu	Asp	Pro	His	Phe	Lys	Lys	Ser	Phe	Gln	Glu	Ser	Leu	Glu	Asp	
385					390					395					400	
aat	caa	gtc	cgt	tac	cac	aat	caa	att	tat	cag	gct	tta	ggg	tat	tct	1248
Asn	Gln	Val	Arg	Tyr	His	Asn	Gln	Ile	Tyr	Gln	Ala	Leu	Gly	Tyr	Ser	
				405					410					415		
ttt	gag	ccg	ata	aaa	aat	gaa	agc	gga	aca	aaa	aaa	gaa	taa			1290
Phe	Glu	Pro	Ile	Lys	Asn	Glu	Ser	Gly	Thr	Lys	Lys	Glu				
			420					425								

<210> 220  
 <211> 429  
 <212> PRT  
 <213> Helicobacter pylori

<400> 220

Met	Pro	Tyr	Ala	Leu	Arg	Lys	Arg	Phe	Phe	Lys	Arg	Leu	Ala	Leu	Ile
1				5					10					15	

Val	Ser	Thr	Phe	Cys	Ala	Ile	Ser	Leu	Asn	Ala	Lys	Ser	Tyr	Leu	Phe
			20					25					30		

Ser	Pro	Leu	Pro	Pro	Ala	His	Gln	Gln	Ile	Ile	Lys	Thr	Glu	Pro	Cys
		35					40					45			

Ser	Leu	Glu	Cys	Leu	Lys	Asp	Leu	Met	Leu	Gln	Asn	Gln	Ile	Phe	Ser
	50					55					60				

Phe	Val	Ser	Gln	Tyr	Asp	Asn	Asn	Asn	Gln	Asp	Glu	Ser	Leu	Lys	Thr
65					70					75				80	

Tyr	Tyr	His	Asp	Ile	Leu	Asn	Lys	Leu	Asn	Pro	Ala	Phe	Ile	Ala	Ser
				85					90					95	

Gln	Thr	Pro	Ala	Lys	Asp	Ser	Tyr	Glu	Pro	Lys	Ile	Glu	Leu	Ala	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100						105						110					
Leu	Leu	Pro	Lys	Lys	Val	Val	Gly	Arg	Tyr	Ala	Ile	Ser	Val	Met	Asn		
		115					120						125				
Thr	Leu	Leu	Ala	Tyr	Leu	Asn	Thr	Arg	Asn	Asn	Asp	Phe	Asn	Ile	Gln		
	130						135				140						
Val	Phe	Asp	Ser	Asp	Glu	Glu	Ser	Pro	Glu	Lys	Leu	Glu	Gln	Thr	Tyr		
145					150					155					160		
Lys	Glu	Ile	Glu	Lys	Glu	Lys	Phe	Pro	Phe	Val	Ile	Ala	Leu	Leu	Thr		
				165					170					175			
Lys	Glu	Gly	Val	Glu	Asn	Leu	Leu	Gln	Asn	Thr	Thr	Ile	Ser	Thr	Pro		
			180					185					190				
Thr	Tyr	Val	Pro	Thr	Val	Asn	Arg	Thr	Gln	Leu	Glu	Asn	Gln	Thr	Glu		
		195					200						205				
Arg	Ser	Leu	Ser	Glu	Arg	Leu	Tyr	Phe	Gly	Gly	Ile	Asp	Tyr	Lys	Glu		
		210					215				220						
Gln	Leu	Ser	Met	Leu	Thr	Ala	Phe	Ile	Ser	Pro	Asn	Ser	Pro	Val	Ile		
225					230					235					240		
Glu	Tyr	Asp	Asp	Asp	Gly	Leu	Ile	Gly	Glu	Arg	Leu	Arg	Gln	Ile	Thr		
				245					250					255			
Glu	Ser	Leu	Ser	Ile	Glu	Val	Lys	His	Gln	Glu	Asn	Ile	Ser	Tyr	Lys		
			260					265					270				
Gln	Ala	Thr	Ser	Phe	Ser	Lys	Asn	Phe	Arg	Lys	Asn	Asp	Ala	Phe	Phe		
		275					280						285				
Lys	Asn	Ser	Ile	Leu	Ile	Leu	Asn	Thr	Pro	Thr	Thr	Lys	Ser	Gly	Leu		
	290						295				300						
Ile	Leu	Ser	Gln	Ile	Gly	Leu	Leu	Glu	Tyr	Lys	Pro	Phe	Lys	Ile	Leu		
305					310					315					320		



Ser Thr Gln Ile Asn Phe Asn Leu Ser Leu Leu Leu Leu Thr Gln Pro  
325 330 335

Lys Asp Arg Lys Asn Leu Phe Ile Val Asn Ala Leu Gln Asn Ser Asp  
340 345 350

Glu Thr Leu Ile Glu Tyr Ala Ser Leu Leu Glu Ser Asp Leu Arg His  
355 360 365

Asp Trp Val Asn Tyr Ser Ser Ala Ile Gly Leu Glu Val Phe Leu Asn  
370 375 380

Thr Leu Asp Pro His Phe Lys Lys Ser Phe Gln Glu Ser Leu Glu Asp  
385 390 395 400

Asn Gln Val Arg Tyr His Asn Gln Ile Tyr Gln Ala Leu Gly Tyr Ser  
405 410 415

Phe Glu Pro Ile Lys Asn Glu Ser Gly Thr Lys Lys Glu  
420 425

<210> 221  
<211> 471  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(471)

<400> 221  
atg tca aat agc atg ttg gat aaa aat aaa gcg att ctt aca ggg ggt 48  
Met Ser Asn Ser Met Leu Asp Lys Asn Lys Ala Ile Leu Thr Gly Gly  
1 5 10 15  
ggg gct tta tta tta ggg cta atc gtg ctt ttt tat tta gct tat cgc 96  
Gly Ala Leu Leu Leu Gly Leu Ile Val Leu Phe Tyr Leu Ala Tyr Arg  
20 25 30  
cct aag gct gaa gtg ctg caa ggg ttt ttg gaa gcc aga gaa tac agc 144  
Pro Lys Ala Glu Val Leu Gln Gly Phe Leu Glu Ala Arg Glu Tyr Ser  
35 40 45  
gtg agt tcc aaa gtc cct ggc cgc att gaa aag gtg ttt gtt aaa aaa 192  
Val Ser Ser Lys Val Pro Gly Arg Ile Glu Lys Val Phe Val Lys Lys  
50 55 60

ggc gat cgc att aaa aag ggc gat ttg gtt ttt agc att tct agc cct	240
Gly Asp Arg Ile Lys Lys Gly Asp Leu Val Phe Ser Ile Ser Ser Pro	
65 70 75 80	

gaa tta gaa gcc aaa ctc gct caa gct gaa gcc ggg cat aaa gcc gct	288
Glu Leu Glu Ala Lys Leu Ala Gln Ala Glu Ala Gly His Lys Ala Ala	
85 90 95	

aaa gcg ctt agc gat gaa gtc aaa aga ggc tca aga gac gaa acg atc	336
Lys Ala Leu Ser Asp Glu Val Lys Arg Gly Ser Arg Asp Glu Thr Ile	
100 105 110	

aat tct gca aga gat gtt tgg caa gcg gca aaa tcc caa gcg act cta	384
Asn Ser Ala Arg Asp Val Trp Gln Ala Ala Lys Ser Gln Ala Thr Leu	
115 120 125	

gcc aaa gag act tat aag cgc gtt caa gat ttg tat gat aac ggc gtg	432
Ala Lys Glu Thr Tyr Lys Arg Val Gln Asp Leu Tyr Asp Asn Gly Val	
130 135 140	

gcg agc ttg caa aag cgc gat aaa gcc tat gca gct tat	471
Ala Ser Leu Gln Lys Arg Asp Lys Ala Tyr Ala Ala Tyr	
145 150 155	

<210> 222

<211> 157

<212> PRT

<213> Helicobacter pylori

<400> 222

Met Ser Asn Ser Met Leu Asp Lys Asn Lys Ala Ile Leu Thr Gly Gly
1 5 10 15

Gly Ala Leu Leu Leu Gly Leu Ile Val Leu Phe Tyr Leu Ala Tyr Arg
20 25 30

Pro Lys Ala Glu Val Leu Gln Gly Phe Leu Glu Ala Arg Glu Tyr Ser
35 40 45

Val Ser Ser Lys Val Pro Gly Arg Ile Glu Lys Val Phe Val Lys Lys
50 55 60

Gly Asp Arg Ile Lys Lys Gly Asp Leu Val Phe Ser Ile Ser Ser Pro
65 70 75 80

Glu Leu Glu Ala Lys Leu Ala Gln Ala Glu Ala Gly His Lys Ala Ala  
85 90 95

Lys Ala Leu Ser Asp Glu Val Lys Arg Gly Ser Arg Asp Glu Thr Ile  
100 105 110

Asn Ser Ala Arg Asp Val Trp Gln Ala Ala Lys Ser Gln Ala Thr Leu  
115 120 125

Ala Lys Glu Thr Tyr Lys Arg Val Gln Asp Leu Tyr Asp Asn Gly Val  
130 135 140

Ala Ser Leu Gln Lys Arg Asp Lys Ala Tyr Ala Ala Tyr  
145 150 155

<210> 223  
<211> 186  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(186)

<400> 223  
atg aaa att tta agt tta tgg tta ggg gtg ttt tgt ttc ctt aag gct 48  
Met Lys Ile Leu Ser Leu Trp Leu Gly Val Phe Cys Phe Leu Lys Ala  
1 5 10 15  
acg cct tat tta tac ttg ggc gaa gag cct aaa tat aag gag aat ttc 96  
Thr Pro Tyr Leu Tyr Leu Gly Glu Glu Pro Lys Tyr Lys Glu Asn Phe  
20 25 30  
acg cat ttt gaa tac gct aac cct aac gct aga aag ggc ggt gtt ttg 144  
Thr His Phe Glu Tyr Ala Asn Pro Asn Ala Arg Lys Gly Gly Val Leu  
35 40 45  
agg aat gac gcc ata ggg act ttt gat agc ctt aac cct tga 186  
Arg Asn Asp Ala Ile Gly Thr Phe Asp Ser Leu Asn Pro  
50 55 60

<210> 224  
<211> 61  
<212> PRT  
<213> Helicobacter pylori

<400> 224

Met Lys Ile Leu Ser Leu Trp Leu Gly Val Phe Cys Phe Leu Lys Ala  
1 5 10 15

Thr Pro Tyr Leu Tyr Leu Gly Glu Glu Pro Lys Tyr Lys Glu Asn Phe  
20 25 30

Thr His Phe Glu Tyr Ala Asn Pro Asn Ala Arg Lys Gly Gly Val Leu  
35 40 45

Arg Asn Asp Ala Ile Gly Thr Phe Asp Ser Leu Asn Pro  
50 55 60

<210> 225

<211> 1096

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(1095)

<400> 225

atg aaa act tat tta tat aac cat ttt tta ttt ttc tgc ttt att ctg 48  
Met Lys Thr Tyr Leu Tyr Asn His Phe Leu Phe Phe Cys Phe Ile Leu  
1 5 10 15

gga gcg ttt tta tta ggt ttg ctt agt cca gct tat gct ttg agt gtt 96  
Gly Ala Phe Leu Leu Gly Leu Leu Ser Pro Ala Tyr Ala Leu Ser Val  
20 25 30

atc acc act aaa gaa att aac gct aat ttg cct aat gga gcg ata gaa 144  
Ile Thr Thr Lys Glu Ile Asn Ala Asn Leu Pro Asn Gly Ala Ile Glu  
35 40 45

agc agg gtg gtg tta ggc aag agg gtg ttt aaa gta gaa gct cat ggg 192  
Ser Arg Val Val Leu Gly Lys Arg Val Phe Lys Val Glu Ala His Gly  
50 55 60

ttt tat ttt aga aac aac gca act aac agc ata gac ata gaa atc acc 240  
Phe Tyr Phe Arg Asn Asn Ala Thr Asn Ser Ile Asp Ile Glu Ile Thr  
65 70 75 80

agt ctt tta aga gac aat caa tcg ttt cct ttg act agc cct gct aaa 288  
Ser Leu Leu Arg Asp Asn Gln Ser Phe Pro Leu Thr Ser Pro Ala Lys  
85 90 95

acc agt tta aaa ata cct tct aac gcc aag att aaa aaa tcc act ctc 336  
Thr Ser Leu Lys Ile Pro Ser Asn Ala Lys Ile Lys Lys Ser Thr Leu  
100 105 110

ctt gtt tta aag ggc gag aat gct gaa gaa gtg gct aag att tta ggc Leu Val Leu Lys Gly Glu Asn Ala Glu Glu Val Ala Lys Ile Leu Gly 115 120 125	384
att agc aaa gaa gaa tac caa aag cta gaa aac acc gct caa acc aac Ile Ser Lys Glu Glu Tyr Gln Lys Leu Glu Asn Thr Ala Gln Thr Asn 130 135 140	432
gct acc aat gac cct atg tat gcc aac acg cct ttt agt aat ggc tct Ala Thr Asn Asp Pro Met Tyr Ala Asn Thr Pro Phe Ser Asn Gly Ser 145 150 155 160	480
gat agt tcc gct tac gat aac aat cct aat agc cct aac aat aac gct Asp Ser Ser Ala Tyr Asp Asn Asn Pro Asn Ser Pro Asn Asn Ala 165 170 175	528
atc aat ggt aaa gat ggc gca aat ggg agt aat ggc tat ggg gta aat Ile Asn Gly Lys Asp Gly Ala Asn Gly Ser Asn Gly Tyr Gly Val Asn 180 185 190	576
ggc aac gat ggg ata aat ggg agc agt ggg agt aat gga aat aat tca Gly Asn Asp Gly Ile Asn Gly Ser Ser Gly Ser Asn Gly Asn Asn Ser 195 200 205	624
aat aat aat gcc gtg ggc agt ggt att gat aca gat ggc gtg ttg ggt Asn Asn Asn Ala Val Gly Ser Gly Ile Asp Thr Asp Gly Val Leu Gly 210 215 220	672
gtg gat gga gtg aat gga tct aac tct tca agc ggt ggc tct gta ggg Val Asp Gly Val Asn Gly Ser Asn Ser Ser Ser Gly Gly Ser Val Gly 225 230 235 240	720
ggt tat gag aat aat ttc act aat cat ggc tct act agc aat aac aca Gly Tyr Glu Asn Asn Phe Thr Asn His Gly Ser Thr Ser Asn Asn Thr 245 250 255	768
gga ggg tat gac aat ttt aat aat aat agc tca agt ggt ggg ggg tta Gly Gly Tyr Asp Asn Phe Asn Asn Asn Ser Ser Ser Gly Gly Gly Leu 260 265 270	816
ggg aat ggg ggg ctt ttc cct att cct ttt ggt aat ggt ggc aca aac Gly Asn Gly Gly Leu Phe Pro Ile Pro Phe Gly Asn Gly Gly Thr Asn 275 280 285	864
aat tcc aat aat cct act aac acc act agc cca act aat ggc agt agt Asn Ser Asn Asn Pro Thr Asn Thr Thr Ser Pro Thr Asn Gly Ser Ser 290 295 300	912
tcc aat agc gcc act aat cct aac tcg caa gaa aac aat tac tcc agc Ser Asn Ser Ala Thr Asn Pro Asn Ser Gln Glu Asn Asn Tyr Ser Ser 305 310 315 320	960
cag tat tgt aaa gcg ccc aar tta agc cct aac aac acg atg aaa cta Gln Tyr Cys Lys Ala Pro Lys Leu Ser Pro Asn Asn Thr Met Lys Leu 325 330 335	1008

gat	gtt	atc	gct	aaa	gat	ggc	tct	tgt	att	tct	atg	aac	gct	tta	aga	1056
Asp	Val	Ile	Ala	Lys	Asp	Gly	Ser	Cys	Ile	Ser	Met	Asn	Ala	Leu	Arg	
			340					345					350			

gat	gac	act	aaa	tgt	gct	tat	aga	tac	gat	ttt	gaa	gcc	g			1096
Asp	Asp	Thr	Lys	Cys	Ala	Tyr	Arg	Tyr	Asp	Phe	Glu	Ala				
		355					360					365				

<210> 226  
 <211> 365  
 <212> PRT  
 <213> Helicobacter pylori

<400> 226

Met	Lys	Thr	Tyr	Leu	Tyr	Asn	His	Phe	Leu	Phe	Phe	Cys	Phe	Ile	Leu
1				5					10					15	

Gly	Ala	Phe	Leu	Leu	Gly	Leu	Leu	Ser	Pro	Ala	Tyr	Ala	Leu	Ser	Val
			20					25					30		

Ile	Thr	Thr	Lys	Glu	Ile	Asn	Ala	Asn	Leu	Pro	Asn	Gly	Ala	Ile	Glu
		35					40					45			

Ser	Arg	Val	Val	Leu	Gly	Lys	Arg	Val	Phe	Lys	Val	Glu	Ala	His	Gly
	50					55					60				

Phe	Tyr	Phe	Arg	Asn	Asn	Ala	Thr	Asn	Ser	Ile	Asp	Ile	Glu	Ile	Thr
65					70					75					80

Ser	Leu	Leu	Arg	Asp	Asn	Gln	Ser	Phe	Pro	Leu	Thr	Ser	Pro	Ala	Lys
				85					90					95	

Thr	Ser	Leu	Lys	Ile	Pro	Ser	Asn	Ala	Lys	Ile	Lys	Lys	Ser	Thr	Leu
			100					105					110		

Leu	Val	Leu	Lys	Gly	Glu	Asn	Ala	Glu	Glu	Val	Ala	Lys	Ile	Leu	Gly
			115				120					125			

Ile	Ser	Lys	Glu	Glu	Tyr	Gln	Lys	Leu	Glu	Asn	Thr	Ala	Gln	Thr	Asn
	130					135					140				

Ala	Thr	Asn	Asp	Pro	Met	Tyr	Ala	Asn	Thr	Pro	Phe	Ser	Asn	Gly	Ser
145					150					155					160

Asp Ser Ser Ala Tyr Asp Asn Asn Pro Asn Ser Pro Asn Asn Asn Ala  
165 170 175

Ile Asn Gly Lys Asp Gly Ala Asn Gly Ser Asn Gly Tyr Gly Val Asn  
180 185 190

Gly Asn Asp Gly Ile Asn Gly Ser Ser Gly Ser Asn Gly Asn Asn Ser  
195 200 205

Asn Asn Asn Ala Val Gly Ser Gly Ile Asp Thr Asp Gly Val Leu Gly  
210 215 220

Val Asp Gly Val Asn Gly Ser Asn Ser Ser Ser Gly Gly Ser Val Gly  
225 230 235 240

Gly Tyr Glu Asn Asn Phe Thr Asn His Gly Ser Thr Ser Asn Asn Thr  
245 250 255

Gly Gly Tyr Asp Asn Phe Asn Asn Asn Ser Ser Ser Gly Gly Gly Leu  
260 265 270

Gly Asn Gly Gly Leu Phe Pro Ile Pro Phe Gly Asn Gly Gly Thr Asn  
275 280 285

Asn Ser Asn Asn Pro Thr Asn Thr Thr Ser Pro Thr Asn Gly Ser Ser  
290 295 300

Ser Asn Ser Ala Thr Asn Pro Asn Ser Gln Glu Asn Asn Tyr Ser Ser  
305 310 315 320

Gln Tyr Cys Lys Ala Pro Lys Leu Ser Pro Asn Asn Thr Met Lys Leu  
325 330 335

Asp Val Ile Ala Lys Asp Gly Ser Cys Ile Ser Met Asn Ala Leu Arg  
340 345 350

Asp Asp Thr Lys Cys Ala Tyr Arg Tyr Asp Phe Glu Ala  
355 360 365

<210> 227

<211> 1722  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(1722)

<400> 227

ttg tct aaa ggt ttg agt atc ggt aat aaa atc ata ttg tgg gtg gcg	48
Leu Ser Lys Gly Leu Ser Ile Gly Asn Lys Ile Ile Leu Trp Val Ala	
1 5 10 15	
ttg att gtg atc gtg tgc gtg agc att tta ggg gtg tcc ttg aac agc	96
Leu Ile Val Ile Val Cys Val Ser Ile Leu Gly Val Ser Leu Asn Ser	
20 25 30	
agg gtg aaa gag att tta aaa gaa agc gct ctg cat tct atg caa gat	144
Arg Val Lys Glu Ile Leu Lys Glu Ser Ala Leu His Ser Met Gln Asp	
35 40 45	
agt ttg cat ttc aag gtt aag gaa gtg caa ggg gtt ctt gaa aac act	192
Ser Leu His Phe Lys Val Lys Glu Val Gln Gly Val Leu Glu Asn Thr	
50 55 60	
tat acg agc atg ggc att gtc aaa gaa atg ctc cct aaa gac acc aaa	240
Tyr Thr Ser Met Gly Ile Val Lys Glu Met Leu Pro Lys Asp Thr Lys	
65 70 75 80	
aga gaa atc aaa atc cgc ttg ttg aaa aac ttc att tta gcc aat tcg	288
Arg Glu Ile Lys Ile Arg Leu Leu Lys Asn Phe Ile Leu Ala Asn Ser	
85 90 95	
cat gtc gct ggg gcg agc gtg ttt ttt aaa gac aga gaa gat tta gga	336
His Val Ala Gly Ala Ser Val Phe Phe Lys Asp Arg Glu Asp Leu Gly	
100 105 110	
tta acg ctt tta agg gat aac gat acg att aaa gtg atg gaa aac ccg	384
Leu Thr Leu Leu Arg Asp Asn Asp Thr Ile Lys Val Met Glu Asn Pro	
115 120 125	
tca tta ggg aat aac cct tta gcg caa aaa gcg atg aaa aat aaa gaa	432
Ser Leu Gly Asn Asn Pro Leu Ala Gln Lys Ala Met Lys Asn Lys Glu	
130 135 140	
att tct aaa agc ttg cct tat tat agg aaa atg cct aat ggg gcg gaa	480
Ile Ser Lys Ser Leu Pro Tyr Tyr Arg Lys Met Pro Asn Gly Ala Glu	
145 150 155 160	
gtt tat ggg gtt gat att ctt tta cct tta ttg aat gag aac gct caa	528
Val Tyr Gly Val Asp Ile Leu Leu Pro Leu Leu Asn Glu Asn Ala Gln	
165 170 175	
gag gtt gta ggg gct ttg atg gtt ttt ctt tcc att gac agc ttc agc	576



Glu	Val	Val	Gly	Ala	Leu	Met	Val	Phe	Leu	Ser	Ile	Asp	Ser	Phe	Ser	
			180					185					190			
aat	gaa	atc	act	aaa	aac	agg	agc	gat	ttg	ttt	tta	att	ggt	gtt	aag	624
Asn	Glu	Ile	Thr	Lys	Asn	Arg	Ser	Asp	Leu	Phe	Leu	Ile	Gly	Val	Lys	
		195					200					205				
ggt	aaa	gtg	ctt	ttg	agc	gcg	aat	aag	agt	ttg	caa	gac	aaa	tct	atc	672
Gly	Lys	Val	Leu	Leu	Ser	Ala	Asn	Lys	Ser	Leu	Gln	Asp	Lys	Ser	Ile	
	210					215					220					
gca	gaa	att	tat	aag	agc	gtg	cct	aaa	gcc	acc	aac	gaa	gtg	ctg	gct	720
Ala	Glu	Ile	Tyr	Lys	Ser	Val	Pro	Lys	Ala	Thr	Asn	Glu	Val	Leu	Ala	
225					230				235						240	
att	tta	gaa	aac	ggc	tct	aaa	gcg	act	tta	gaa	tat	ttg	gat	ccc	ttt	768
Ile	Leu	Glu	Asn	Gly	Ser	Lys	Ala	Thr	Leu	Glu	Tyr	Leu	Asp	Pro	Phe	
				245					250					255		
agc	cat	aag	gaa	aat	ttc	tta	gcc	gtt	gaa	ccc	ttt	aaa	atg	cta	ggc	816
Ser	His	Lys	Glu	Asn	Phe	Leu	Ala	Val	Glu	Pro	Phe	Lys	Met	Leu	Gly	
			260					265					270			
aaa	aca	gaa	agt	aaa	gac	awt	ctt	aat	tgg	atg	atc	gct	tta	atc	att	864
Lys	Thr	Glu	Ser	Lys	Asp	Xaa	Leu	Asn	Trp	Met	Ile	Ala	Leu	Ile	Ile	
		275					280					285				
gaa	aaa	gac	aag	gtc	tat	gag	caa	gtg	ggc	tcg	gtg	cgt	ttt	gtg	gtg	912
Glu	Lys	Asp	Lys	Val	Tyr	Glu	Gln	Val	Gly	Ser	Val	Arg	Phe	Val	Val	
	290					295					300					
atc	ata	gcg	agc	gcg	atc	atg	gtg	tta	gcc	ttg	att	ata	gcg	atc	act	960
Ile	Ile	Ala	Ser	Ala	Ile	Met	Val	Leu	Ala	Leu	Ile	Ile	Ala	Ile	Thr	
305					310					315					320	
ctt	tta	atg	cga	gcg	att	gtg	agc	aat	cgt	ttg	gaa	gcc	gtt	tct	agc	1008
Leu	Leu	Met	Arg	Ala	Ile	Val	Ser	Asn	Arg	Leu	Glu	Ala	Val	Ser	Ser	
				325					330					335		
acc	ttg	tct	cat	ttc	ttt	aaa	tta	ttg	aac	aat	caa	gcc	cat	tct	agc	1056
Thr	Leu	Ser	His	Phe	Phe	Lys	Leu	Leu	Asn	Asn	Gln	Ala	His	Ser	Ser	
			340					345					350			
gat	att	aaa	ttg	att	gaa	gca	aaa	tcc	aat	gac	gaa	tta	ggg	cgc	atg	1104
Asp	Ile	Lys	Leu	Ile	Glu	Ala	Lys	Ser	Asn	Asp	Glu	Leu	Gly	Arg	Met	
		355					360					365				
caa	aca	gcg	atc	aat	aaa	aat	atc	ttg	caa	acc	caa	aaa	acc	atg	caa	1152
Gln	Thr	Ala	Ile	Asn	Lys	Asn	Ile	Leu	Gln	Thr	Gln	Lys	Thr	Met	Gln	
	370					375					380					
gaa	gac	agg	caa	gcc	gtc	caa	gac	acc	att	aaa	gtg	gtt	tca	gac	gtg	1200
Glu	Asp	Arg	Gln	Ala	Val	Gln	Asp	Thr	Ile	Lys	Val	Val	Ser	Asp	Val	
385					390					395					400	

aaa gca ggg aat ttt gcg gtg cgc atc aca gct gat ccc gca agc cct	1248
Lys Ala Gly Asn Phe Ala Val Arg Ile Thr Ala Asp Pro Ala Ser Pro	
405 410 415	
gat ttg aaa gaa ttg agg gac gcg cta aat ggg atc atg gat tat ttg	1296
Asp Leu Lys Glu Leu Arg Asp Ala Leu Asn Gly Ile Met Asp Tyr Leu	
420 425 430	
caa gaa agc gta ggg act cac atg cca agc att ttc aaa atc ttt gaa	1344
Gln Glu Ser Val Gly Thr His Met Pro Ser Ile Phe Lys Ile Phe Glu	
435 440 445	
agc tat tct ggt ttg gat ttt aga ggc cga atc caa aac gct tcg ggt	1392
Ser Tyr Ser Gly Leu Asp Phe Arg Gly Arg Ile Gln Asn Ala Ser Gly	
450 455 460	
agg gtg gaa ttg gtt act aac gct tta ggg caa gaa atc caa aaa atg	1440
Arg Val Glu Leu Val Thr Asn Ala Leu Gly Gln Glu Ile Gln Lys Met	
465 470 475 480	
cta gaa act tcg tct aat ttt gcc aaa gat tta gcg aac gat agc gcg	1488
Leu Glu Thr Ser Ser Asn Phe Ala Lys Asp Leu Ala Asn Asp Ser Ala	
485 490 495	
aat tta aaa gaa tgc gtg caa aat tta gaa aag gct tca aac tcc caa	1536
Asn Leu Lys Glu Cys Val Gln Asn Leu Glu Lys Ala Ser Asn Ser Gln	
500 505 510	
cac aaa agc ttg atg gaa act tct aaa acg ata gag aat atc acc act	1584
His Lys Ser Leu Met Glu Thr Ser Lys Thr Ile Glu Asn Ile Thr Thr	
515 520 525	
tcc att caa ggc gtg agc tct caa agt gaa gcc atg att gaa caa ggg	1632
Ser Ile Gln Gly Val Ser Ser Gln Ser Glu Ala Met Ile Glu Gln Gly	
530 535 540	
caa gac att aaa agc att gta gaa atc att aga gac atc gct gat caa	1680
Gln Asp Ile Lys Ser Ile Val Glu Ile Ile Arg Asp Ile Ala Asp Gln	
545 550 555 560	
acc aat cta tta gcc cta aac gcc gct att gaa gcc gca agg	1722
Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala Arg	
565 570	

<210> 228

<211> 574

<212> PRT

<213> Helicobacter pylori

<220>

<221> misc\_feature

<222> (279)..(279)

<223> The 'Xaa' at location 279 stands for Asn, or Ile.

<400> 228

Leu Ser Lys Gly Leu Ser Ile Gly Asn Lys Ile Ile Leu Trp Val Ala  
1 5 10 15

Leu Ile Val Ile Val Cys Val Ser Ile Leu Gly Val Ser Leu Asn Ser  
20 25 30

Arg Val Lys Glu Ile Leu Lys Glu Ser Ala Leu His Ser Met Gln Asp  
35 40 45

Ser Leu His Phe Lys Val Lys Glu Val Gln Gly Val Leu Glu Asn Thr  
50 55 60

Tyr Thr Ser Met Gly Ile Val Lys Glu Met Leu Pro Lys Asp Thr Lys  
65 70 75 80

Arg Glu Ile Lys Ile Arg Leu Leu Lys Asn Phe Ile Leu Ala Asn Ser  
85 90 95

His Val Ala Gly Ala Ser Val Phe Phe Lys Asp Arg Glu Asp Leu Gly  
100 105 110

Leu Thr Leu Leu Arg Asp Asn Asp Thr Ile Lys Val Met Glu Asn Pro  
115 120 125

Ser Leu Gly Asn Asn Pro Leu Ala Gln Lys Ala Met Lys Asn Lys Glu  
130 135 140

Ile Ser Lys Ser Leu Pro Tyr Tyr Arg Lys Met Pro Asn Gly Ala Glu  
145 150 155 160

Val Tyr Gly Val Asp Ile Leu Leu Pro Leu Leu Asn Glu Asn Ala Gln  
165 170 175

Glu Val Val Gly Ala Leu Met Val Phe Leu Ser Ile Asp Ser Phe Ser  
180 185 190

Asn Glu Ile Thr Lys Asn Arg Ser Asp Leu Phe Leu Ile Gly Val Lys  
195 200 205

Gly Lys Val Leu Leu Ser Ala Asn Lys Ser Leu Gln Asp Lys Ser Ile

210		215		220
Ala Glu Ile Tyr Lys Ser Val Pro Lys Ala Thr Asn Glu Val Leu Ala				
225		230		235 240
Ile Leu Glu Asn Gly Ser Lys Ala Thr Leu Glu Tyr Leu Asp Pro Phe				
	245		250	255
Ser His Lys Glu Asn Phe Leu Ala Val Glu Pro Phe Lys Met Leu Gly				
	260		265	270
Lys Thr Glu Ser Lys Asp Xaa Leu Asn Trp Met Ile Ala Leu Ile Ile				
	275		280	285
Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val Arg Phe Val Val				
	290		295	300
Ile Ile Ala Ser Ala Ile Met Val Leu Ala Leu Ile Ile Ala Ile Thr				
305		310		315 320
Leu Leu Met Arg Ala Ile Val Ser Asn Arg Leu Glu Ala Val Ser Ser				
	325		330	335
Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln Ala His Ser Ser				
	340		345	350
Asp Ile Lys Leu Ile Glu Ala Lys Ser Asn Asp Glu Leu Gly Arg Met				
	355		360	365
Gln Thr Ala Ile Asn Lys Asn Ile Leu Gln Thr Gln Lys Thr Met Gln				
	370		375	380
Glu Asp Arg Gln Ala Val Gln Asp Thr Ile Lys Val Val Ser Asp Val				
385		390		395 400
Lys Ala Gly Asn Phe Ala Val Arg Ile Thr Ala Asp Pro Ala Ser Pro				
	405		410	415
Asp Leu Lys Glu Leu Arg Asp Ala Leu Asn Gly Ile Met Asp Tyr Leu				
	420		425	430

Gln Glu Ser Val Gly Thr His Met Pro Ser Ile Phe Lys Ile Phe Glu  
435 440 445

Ser Tyr Ser Gly Leu Asp Phe Arg Gly Arg Ile Gln Asn Ala Ser Gly  
450 455 460

Arg Val Glu Leu Val Thr Asn Ala Leu Gly Gln Glu Ile Gln Lys Met  
465 470 475 480

Leu Glu Thr Ser Ser Asn Phe Ala Lys Asp Leu Ala Asn Asp Ser Ala  
485 490 495

Asn Leu Lys Glu Cys Val Gln Asn Leu Glu Lys Ala Ser Asn Ser Gln  
500 505 510

His Lys Ser Leu Met Glu Thr Ser Lys Thr Ile Glu Asn Ile Thr Thr  
515 520 525

Ser Ile Gln Gly Val Ser Ser Gln Ser Glu Ala Met Ile Glu Gln Gly  
530 535 540

Gln Asp Ile Lys Ser Ile Val Glu Ile Ile Arg Asp Ile Ala Asp Gln  
545 550 555 560

Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala Arg  
565 570

<210> 229  
<211> 273  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(273)

<400> 229  
gtg gcg gtg aaa aaa atc gtt gtg ggt tgg tgt gtg gcg ttg gct ttt 48  
Val Ala Val Lys Lys Ile Val Val Gly Trp Cys Val Ala Leu Ala Phe  
1 5 10 15

tta agc gca aat cca gcg caa gcc gat aaa gcg atc agt aat gcg gat 96  
Leu Ser Ala Asn Pro Ala Gln Ala Asp Lys Ala Ile Ser Asn Ala Asp  
20 25 30

ttg att aaa gaa ata agg gac tta aaa aaa atc atc agc gcg caa aac	144
Leu Ile Lys Glu Ile Arg Asp Leu Lys Lys Ile Ile Ser Ala Gln Asn	
35 40 45	

act gag atc aac aat tta aga aga gtg caa gaa gtc ttg tct ggg caa	192
Thr Glu Ile Asn Asn Leu Arg Arg Val Gln Glu Val Leu Ser Gly Gln	
50 55 60	

tta ggg gat atg cgt aag gat ata tta agc act aga gat tat tgc att	240
Leu Gly Asp Met Arg Lys Asp Ile Leu Ser Thr Arg Asp Tyr Cys Ile	
65 70 75 80	

agc tta agg cct tat atc tat aat tgg cgc tag	273
Ser Leu Arg Pro Tyr Ile Tyr Asn Trp Arg	
85 90	

<210> 230  
 <211> 90  
 <212> PRT  
 <213> Helicobacter pylori

<400> 230

Val Ala Val Lys Lys Ile Val Val Gly Trp Cys Val Ala Leu Ala Phe
1 5 10 15

Leu Ser Ala Asn Pro Ala Gln Ala Asp Lys Ala Ile Ser Asn Ala Asp
20 25 30

Leu Ile Lys Glu Ile Arg Asp Leu Lys Lys Ile Ile Ser Ala Gln Asn
35 40 45

Thr Glu Ile Asn Asn Leu Arg Arg Val Gln Glu Val Leu Ser Gly Gln
50 55 60

Leu Gly Asp Met Arg Lys Asp Ile Leu Ser Thr Arg Asp Tyr Cys Ile
65 70 75 80

Ser Leu Arg Pro Tyr Ile Tyr Asn Trp Arg
85 90

<210> 231  
 <211> 183  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(183)  
  
 <400> 231  
 atg gta ttt gac aga aca atc agc gta aga gaa aaa aaa gcg gct aaa 48  
 Met Val Phe Asp Arg Thr Ile Ser Val Arg Glu Lys Lys Ala Ala Lys  
 1 5 10 15  
  
 acg ctt ggg att gtg ggg atc gtc ttt ttt att ttg ttt ggc atc gta 96  
 Thr Leu Gly Ile Val Gly Ile Val Phe Phe Ile Leu Phe Gly Ile Val  
 20 25 30  
  
 ata agc ggg gtg gct ttt caa aaa gag tgg gtg caa caa ttg gat tta 144  
 Ile Ser Gly Val Ala Phe Gln Lys Glu Trp Val Gln Gln Leu Asp Leu  
 35 40 45  
  
 ttt ttt ata gac ttg atc cac aac cct gcc ccc att caa 183  
 Phe Phe Ile Asp Leu Ile His Asn Pro Ala Pro Ile Gln  
 50 55 60

<210> 232  
 <211> 61  
 <212> PRT  
 <213> Helicobacter pylori

<400> 232  
  
 Met Val Phe Asp Arg Thr Ile Ser Val Arg Glu Lys Lys Ala Ala Lys  
 1 5 10 15  
  
 Thr Leu Gly Ile Val Gly Ile Val Phe Phe Ile Leu Phe Gly Ile Val  
 20 25 30  
  
 Ile Ser Gly Val Ala Phe Gln Lys Glu Trp Val Gln Gln Leu Asp Leu  
 35 40 45  
  
 Phe Phe Ile Asp Leu Ile His Asn Pro Ala Pro Ile Gln  
 50 55 60

<210> 233  
 <211> 543  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(543)

<400> 233  
 cga tat gat aaa ggg ttt gaa aaa gat aaa aaa gat cta gaa tat tat 48  
 Arg Tyr Asp Lys Gly Phe Glu Lys Asp Lys Lys Asp Leu Glu Tyr Tyr  
 1 5 10 15  
  
 tct aaa gct tgc gag tta aac tat ggc gat ggc tgt gcg att tta ggg 96  
 Ser Lys Ala Cys Glu Leu Asn Tyr Gly Asp Gly Cys Ala Ile Leu Gly  
 20 25 30  
  
 gat att tat cgt aat ggt gaa ggc gta aca caa aat ttt aaa aaa gct 144  
 Asp Ile Tyr Arg Asn Gly Glu Gly Val Thr Gln Asn Phe Lys Lys Ala  
 35 40 45  
  
 ttc aaa tat tac tct aaa gct tgc gaa tta aat aat ggt gaa ggg tgt 192  
 Phe Lys Tyr Tyr Ser Lys Ala Cys Glu Leu Asn Asn Gly Glu Gly Cys  
 50 55 60  
  
 tcc aaa tta gga ggg gat tat ttt ttt ggt gaa agc gta acg caa gat 240  
 Ser Lys Leu Gly Gly Asp Tyr Phe Phe Gly Glu Ser Val Thr Gln Asp  
 65 70 75 80  
  
 ctt aaa aaa gct ttt gga tat tac tct aaa gct tgc gaa tta aac gaa 288  
 Leu Lys Lys Ala Phe Gly Tyr Tyr Ser Lys Ala Cys Glu Leu Asn Glu  
 85 90 95  
  
 gct cta aca tgc acg ctt gta gga gag ttt tat cgt gat ggt gaa ggc 336  
 Ala Leu Thr Cys Thr Leu Val Gly Glu Phe Tyr Arg Asp Gly Glu Gly  
 100 105 110  
  
 gta aca aag gat ctt aaa aaa gct ttt gaa tat tct gct aaa gct tgt 384  
 Val Thr Lys Asp Leu Lys Lys Ala Phe Glu Tyr Ser Ala Lys Ala Cys  
 115 120 125  
  
 gaa ttg aac gat gct aaa ggg tgt tac gct cta gca gcg ttt tat aat 432  
 Glu Leu Asn Asp Ala Lys Gly Cys Tyr Ala Leu Ala Ala Phe Tyr Asn  
 130 135 140  
  
 gag ggt aag ggc gta gca aag gat gaa aaa caa acg aca gaa aac ctt 480  
 Glu Gly Lys Gly Val Ala Lys Asp Glu Lys Gln Thr Thr Glu Asn Leu  
 145 150 155 160  
  
 gaa aag agt tgc aag cta gga tta aaa gaa gca tgc gat att ctc aaa 528  
 Glu Lys Ser Cys Lys Leu Gly Leu Lys Glu Ala Cys Asp Ile Leu Lys  
 165 170 175  
  
 gaa caa aaa caa taa 543  
 Glu Gln Lys Gln  
 180  
  
 <210> 234  
 <211> 180  
 <212> PRT  
 <213> Helicobacter pylori



<400> 234

Arg Tyr Asp Lys Gly Phe Glu Lys Asp Lys Lys Asp Leu Glu Tyr Tyr  
1 5 10 15

Ser Lys Ala Cys Glu Leu Asn Tyr Gly Asp Gly Cys Ala Ile Leu Gly  
20 25 30

Asp Ile Tyr Arg Asn Gly Glu Gly Val Thr Gln Asn Phe Lys Lys Ala  
35 40 45

Phe Lys Tyr Tyr Ser Lys Ala Cys Glu Leu Asn Asn Gly Glu Gly Cys  
50 55 60

Ser Lys Leu Gly Gly Asp Tyr Phe Phe Gly Glu Ser Val Thr Gln Asp  
65 70 75 80

Leu Lys Lys Ala Phe Gly Tyr Tyr Ser Lys Ala Cys Glu Leu Asn Glu  
85 90 95

Ala Leu Thr Cys Thr Leu Val Gly Glu Phe Tyr Arg Asp Gly Glu Gly  
100 105 110

Val Thr Lys Asp Leu Lys Lys Ala Phe Glu Tyr Ser Ala Lys Ala Cys  
115 120 125

Glu Leu Asn Asp Ala Lys Gly Cys Tyr Ala Leu Ala Ala Phe Tyr Asn  
130 135 140

Glu Gly Lys Gly Val Ala Lys Asp Glu Lys Gln Thr Thr Glu Asn Leu  
145 150 155 160

Glu Lys Ser Cys Lys Leu Gly Leu Lys Glu Ala Cys Asp Ile Leu Lys  
165 170 175

Glu Gln Lys Gln  
180

<210> 235

<211> 729

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (1)..(729)

<400> 235

atg	aaa	aaa	ttt	ttt	tct	caa	tct	tta	tta	gct	ttg	att	gtg	tct	atg	48
Met	Lys	Lys	Phe	Phe	Ser	Gln	Ser	Leu	Leu	Ala	Leu	Ile	Val	Ser	Met	
1				5					10					15		

aac	gcg	cta	ctg	gcc	atg	gat	ggc	aat	ggc	ggt	ttt	tta	ggg	gcg	ggt	96
Asn	Ala	Leu	Leu	Ala	Met	Asp	Gly	Asn	Gly	Val	Phe	Leu	Gly	Ala	Gly	
			20					25					30			

tat	ttg	caa	ggg	caa	gcc	caa	atg	cat	gcg	gat	att	aat	tct	caa	aaa	144
Tyr	Leu	Gln	Gly	Gln	Ala	Gln	Met	His	Ala	Asp	Ile	Asn	Ser	Gln	Lys	
		35					40					45				

caa	gcc	act	aac	gct	act	atc	aaa	ggc	ttt	gat	gcg	ctt	tta	ggg	tat	192
Gln	Ala	Thr	Asn	Ala	Thr	Ile	Lys	Gly	Phe	Asp	Ala	Leu	Leu	Gly	Tyr	
	50					55					60					

caa	ttt	ttc	ttt	ggg	aaa	tac	ttt	ggc	tgt	cgt	gct	tat	ggg	ttt	ttt	240
Gln	Phe	Phe	Phe	Gly	Lys	Tyr	Phe	Gly	Cys	Arg	Ala	Tyr	Gly	Phe	Phe	
65					70					75					80	

gac	tac	gct	cat	gcc	aat	tct	att	agg	ctt	aaa	aac	cct	aac	tat	aac	288
Asp	Tyr	Ala	His	Ala	Asn	Ser	Ile	Arg	Leu	Lys	Asn	Pro	Asn	Tyr	Asn	
				85					90					95		

agc	gaa	gtg	gcg	caa	ttg	gcg	ggt	caa	att	ctt	ggg	aaa	caa	gaa	atc	336
Ser	Glu	Val	Ala	Gln	Leu	Ala	Gly	Gln	Ile	Leu	Gly	Lys	Gln	Glu	Ile	
			100					105					110			

aat	cgc	tta	acg	agc	ctt	gct	gat	cct	aaa	acc	ttt	gag	cca	aac	atg	384
Asn	Arg	Leu	Thr	Ser	Leu	Ala	Asp	Pro	Lys	Thr	Phe	Glu	Pro	Asn	Met	
		115					120					125				

ctc	act	tat	ggg	ggg	gct	atg	gat	tta	atg	ggt	aat	gtc	atc	aat	aac	432
Leu	Thr	Tyr	Gly	Gly	Ala	Met	Asp	Leu	Met	Val	Asn	Val	Ile	Asn	Asn	
	130					135					140					

ggt	atc	atc	agt	ttg	ggg	gct	ttt	ggt	ggg	gtg	caa	ttg	gcc	ggc	aat	480
Gly	Ile	Ile	Ser	Leu	Gly	Ala	Phe	Gly	Gly	Val	Gln	Leu	Ala	Gly	Asn	
145					150					155					160	

tca	tgg	ctt	atg	gcg	aca	ccg	agc	ttt	gaa	ggc	att	tta	gtg	gag	caa	528
Ser	Trp	Leu	Met	Ala	Thr	Pro	Ser	Phe	Glu	Gly	Ile	Leu	Val	Glu	Gln	
				165					170					175		

gct	ttg	gtg	agt	aaa	aaa	gcc	act	tct	ttc	caa	ttt	tta	ttc	aat	gtg	576
Ala	Leu	Val	Ser	Lys	Lys	Ala	Thr	Ser	Phe	Gln	Phe	Leu	Phe	Asn	Val	
			180					185					190			

ggg gct cgc tta agg atc tta aag cat tcc agc att gaa gcg ggc gtg	624
Gly Ala Arg Leu Arg Ile Leu Lys His Ser Ser Ile Glu Ala Gly Val	
195 200 205	

aaa ttc ccc atg cta aag aaa aac ccc tat atc act gca aaa aat ttg	672
Lys Phe Pro Met Leu Lys Lys Asn Pro Tyr Ile Thr Ala Lys Asn Leu	
210 215 220	

gat ata ggg ttt agg cgc gtg tat tcg tgg tat gtg aat tat gtg ttc	720
Asp Ile Gly Phe Arg Arg Val Tyr Ser Trp Tyr Val Asn Tyr Val Phe	
225 230 235 240	

act ttc tag	729
Thr Phe	

<210> 236  
 <211> 242  
 <212> PRT  
 <213> Helicobacter pylori  
 <400> 236

Met Lys Lys Phe Phe Ser Gln Ser Leu Leu Ala Leu Ile Val Ser Met
1 5 10 15

Asn Ala Leu Leu Ala Met Asp Gly Asn Gly Val Phe Leu Gly Ala Gly
20 25 30

Tyr Leu Gln Gly Gln Ala Gln Met His Ala Asp Ile Asn Ser Gln Lys
35 40 45

Gln Ala Thr Asn Ala Thr Ile Lys Gly Phe Asp Ala Leu Leu Gly Tyr
50 55 60

Gln Phe Phe Phe Gly Lys Tyr Phe Gly Cys Arg Ala Tyr Gly Phe Phe
65 70 75 80

Asp Tyr Ala His Ala Asn Ser Ile Arg Leu Lys Asn Pro Asn Tyr Asn
85 90 95

Ser Glu Val Ala Gln Leu Ala Gly Gln Ile Leu Gly Lys Gln Glu Ile
100 105 110

Asn Arg Leu Thr Ser Leu Ala Asp Pro Lys Thr Phe Glu Pro Asn Met
115 120 125

Leu Thr Tyr Gly Gly Ala Met Asp Leu Met Val Asn Val Ile Asn Asn  
 130 135 140

Gly Ile Ile Ser Leu Gly Ala Phe Gly Gly Val Gln Leu Ala Gly Asn  
 145 150 155 160

Ser Trp Leu Met Ala Thr Pro Ser Phe Glu Gly Ile Leu Val Glu Gln  
 165 170 175

Ala Leu Val Ser Lys Lys Ala Thr Ser Phe Gln Phe Leu Phe Asn Val  
 180 185 190

Gly Ala Arg Leu Arg Ile Leu Lys His Ser Ser Ile Glu Ala Gly Val  
 195 200 205

Lys Phe Pro Met Leu Lys Lys Asn Pro Tyr Ile Thr Ala Lys Asn Leu  
 210 215 220

Asp Ile Gly Phe Arg Arg Val Tyr Ser Trp Tyr Val Asn Tyr Val Phe  
 225 230 235 240

Thr Phe

<210> 237  
 <211> 540  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(540)

<400> 237  
 atg tta ggg aaa aaa aac gag gaa gtc ttg att gat gaa aat ttg gtt 48  
 Met Leu Gly Lys Lys Asn Glu Glu Val Leu Ile Asp Glu Asn Leu Val  
 1 5 10 15  
 ggg ggt gtg ata gcc ctt gat aga ttg gca aaa ctc aat aag gcc aat 96  
 Gly Gly Val Ile Ala Leu Asp Arg Leu Ala Lys Leu Asn Lys Ala Asn  
 20 25 30  
 agg act ttc aaa agg gct ttt tat ctc tct atg gtg ctc aat gtt gcc 144  
 Arg Thr Phe Lys Arg Ala Phe Tyr Leu Ser Met Val Leu Asn Val Ala

35					40					45						
gct	gta	acg	agt	att	gtg	atg	atg	atg	cct	ttg	aag	aaa	acg	gat	ata	192
Ala	Val	Thr	Ser	Ile	Val	Met	Met	Met	Pro	Leu	Lys	Lys	Thr	Asp	Ile	
50						55					60					
ttt	gtt	tat	ggc	att	gat	cga	tac	aca	gga	gaa	ttt	aaa	att	gtc	aaa	240
Phe	Val	Tyr	Gly	Ile	Asp	Arg	Tyr	Thr	Gly	Glu	Phe	Lys	Ile	Val	Lys	
65					70					75					80	
cgc	tcc	gat	gct	aga	caa	att	gtc	aat	tct	gaa	gct	gtt	gtg	gat	agt	288
Arg	Ser	Asp	Ala	Arg	Gln	Ile	Val	Asn	Ser	Glu	Ala	Val	Val	Asp	Ser	
				85					90					95		
gca	act	tca	aaa	ttt	gtc	tca	ttg	ctg	ttt	ggg	tat	agc	aaa	aat	tct	336
Ala	Thr	Ser	Lys	Phe	Val	Ser	Leu	Leu	Phe	Gly	Tyr	Ser	Lys	Asn	Ser	
			100					105					110			
ttg	agg	gat	cgc	aag	gat	caa	tta	atg	cag	tat	tgc	gat	gtg	agt	ttc	384
Leu	Arg	Asp	Arg	Lys	Asp	Gln	Leu	Met	Gln	Tyr	Cys	Asp	Val	Ser	Phe	
		115					120					125				
caa	acc	caa	gca	atg	aga	atg	ttc	aat	gaa	aat	atc	aga	caa	ttc	gta	432
Gln	Thr	Gln	Ala	Met	Arg	Met	Phe	Asn	Glu	Asn	Ile	Arg	Gln	Phe	Val	
	130					135					140					
gat	aaa	gtc	cga	gca	gaa	gct	atc	att	agc	tct	aac	ata	caa	aga	gaa	480
Asp	Lys	Val	Arg	Ala	Glu	Ala	Ile	Ile	Ser	Ser	Asn	Ile	Gln	Arg	Glu	
145					150					155					160	
aaa	gtc	aaa	aat	agt	ccc	tta	acg	aga	tta	gca	ttt	ttc	att	acc	atc	528
Lys	Val	Lys	Asn	Ser	Pro	Leu	Thr	Arg	Leu	Ala	Phe	Phe	Ile	Thr	Ile	
				165					170					175		
aaa	atc	aca	ccg													540
Lys	Ile	Thr	Pro													
			180													

<210> 238  
 <211> 180  
 <212> PRT  
 <213> Helicobacter pylori

<400> 238

Met	Leu	Gly	Lys	Lys	Asn	Glu	Glu	Val	Leu	Ile	Asp	Glu	Asn	Leu	Val
1				5					10					15	

Gly	Gly	Val	Ile	Ala	Leu	Asp	Arg	Leu	Ala	Lys	Leu	Asn	Lys	Ala	Asn
			20					25					30		

Arg	Thr	Phe	Lys	Arg	Ala	Phe	Tyr	Leu	Ser	Met	Val	Leu	Asn	Val	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Ala Val Thr Ser Ile Val Met Met Met Pro Leu Lys Lys Thr Asp Ile		
50	55	60
Phe Val Tyr Gly Ile Asp Arg Tyr Thr Gly Glu Phe Lys Ile Val Lys		
65	70	75
Arg Ser Asp Ala Arg Gln Ile Val Asn Ser Glu Ala Val Val Asp Ser		
	85	90
Ala Thr Ser Lys Phe Val Ser Leu Leu Phe Gly Tyr Ser Lys Asn Ser		
	100	105
Leu Arg Asp Arg Lys Asp Gln Leu Met Gln Tyr Cys Asp Val Ser Phe		
	115	120
Gln Thr Gln Ala Met Arg Met Phe Asn Glu Asn Ile Arg Gln Phe Val		
	130	135
Asp Lys Val Arg Ala Glu Ala Ile Ile Ser Ser Asn Ile Gln Arg Glu		
145	150	155
Lys Val Lys Asn Ser Pro Leu Thr Arg Leu Ala Phe Phe Ile Thr Ile		
	165	170
		175
Lys Ile Thr Pro		
	180	

<210> 239  
 <211> 864  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(864)

<400> 239	
atg aaa acc ttt aaa aac ctg ctc tgt ttt agc ctg atc gct atg agt	48
Met Lys Thr Phe Lys Asn Leu Leu Cys Phe Ser Leu Ile Ala Met Ser	
1	5
	10
	15
tgg ctc caa gcg gac atg ttg gat aat ttc act agg gcc att aac agc	96

Trp	Leu	Gln	Ala	Asp	Met	Leu	Asp	Asn	Phe	Thr	Arg	Ala	Ile	Asn	Ser	
			20					25					30			
tac	acc	act	aaa	aag	ctt	aat	gaa	atc	aag	gat	caa	gtc	aat	agc	gct	144
Tyr	Thr	Thr	Lys	Lys	Leu	Asn	Glu	Ile	Lys	Asp	Gln	Val	Asn	Ser	Ala	
		35					40					45				
aac	cct	act	aaa	aat	cac	aat	acc	act	tat	aac	gct	aat	ggc	atg	ctc	192
Asn	Pro	Thr	Lys	Asn	His	Asn	Thr	Thr	Tyr	Asn	Ala	Asn	Gly	Met	Leu	
	50					55					60					
att	aac	att	gat	tgt	aaa	gtc	tta	aaa	aat	aac	ttc	tat	tcg	gtg	tgt	240
Ile	Asn	Ile	Asp	Cys	Lys	Val	Leu	Lys	Asn	Asn	Phe	Tyr	Ser	Val	Cys	
65				70					75						80	
tat	tct	agc	gag	tta	aaa	aac	cct	att	tat	ggc	gtg	agc	gtg	ttg	ttt	288
Tyr	Ser	Ser	Glu	Leu	Lys	Asn	Pro	Ile	Tyr	Gly	Val	Ser	Val	Leu	Phe	
			85						90					95		
ggg	gat	tta	gtg	gat	aaa	aat	aat	att	gaa	aaa	cgc	tat	gag	ttt	aaa	336
Gly	Asp	Leu	Val	Asp	Lys	Asn	Asn	Ile	Glu	Lys	Arg	Tyr	Glu	Phe	Lys	
		100						105					110			
aca	gac	act	cga	tta	gcc	aaa	tac	caa	caa	gcc	acg	aca	caa	gat	tac	384
Thr	Asp	Thr	Arg	Leu	Ala	Lys	Tyr	Gln	Gln	Ala	Thr	Thr	Gln	Asp	Tyr	
		115					120						125			
acc	aga	agc	ggc	ttt	gat	agg	ggg	cat	ttt	gtg	gcg	aat	gac	gct	tct	432
Thr	Arg	Ser	Gly	Phe	Asp	Arg	Gly	His	Phe	Val	Ala	Asn	Asp	Ala	Ser	
	130					135					140					
ttt	gat	ttt	gcg	tct	aac	cct	tta	aga	gag	act	tac	aga	atg	act	aat	480
Phe	Asp	Phe	Ala	Ser	Asn	Pro	Leu	Arg	Glu	Thr	Tyr	Arg	Met	Thr	Asn	
145					150					155					160	
atc	acc	cct	gaa	gcc	aaa	aac	acc	aat	agg	cat	tct	ggt	tta	ttg	gta	528
Ile	Thr	Pro	Glu	Ala	Lys	Asn	Thr	Asn	Arg	His	Ser	Val	Leu	Leu	Val	
			165						170					175		
gaa	aaa	gag	ggc	sgt	aat	ttg	gcc	agg	aaa	tac	cat	caa	ggt	ttr	gta	576
Glu	Lys	Glu	Gly	Xaa	Asn	Leu	Ala	Arg	Lys	Tyr	His	Gln	Val	Xaa	Val	
		180						185					190			
gaa	gaa	ctc	acc	atc	atc	aaa	cag	ggc	tat	agg	act	ttt	agc	cct	aaa	624
Glu	Glu	Leu	Thr	Ile	Ile	Lys	Gln	Gly	Tyr	Arg	Thr	Phe	Ser	Pro	Lys	
		195					200					205				
awt	atc	gct	att	cct	agc	ggc	ttt	tgg	tac	cac	tat	gat	aca	agg	cta	672
Xaa	Ile	Ala	Ile	Pro	Ser	Gly	Phe	Trp	Tyr	His	Tyr	Asp	Thr	Arg	Leu	
	210					215					220					
acg	gac	agc	tat	gaa	aac	gct	aaa	agc	gaa	tgc	ttt	tat	atc	cct	aat	720
Thr	Asp	Ser	Tyr	Glu	Asn	Ala	Lys	Ser	Glu	Cys	Phe	Tyr	Ile	Pro	Asn	
225					230					235					240	

gac aac caa aac tat ccc tta caa gaa atg aga aaa gat tgt aaa gga	768
Asp Asn Gln Asn Tyr Pro Leu Gln Glu Met Arg Lys Asp Cys Lys Gly	
245 250 255	

tat gag cgc gtt gaa aag cag gtg gtt ttt aag aac aat aaa aac act	816
Tyr Glu Arg Val Glu Lys Gln Val Val Phe Lys Asn Asn Lys Asn Thr	
260 265 270	

gag ttg aac gaa ttg cct aag tat ttt aac aac gct aag aag tat taa	864
Glu Leu Asn Glu Leu Pro Lys Tyr Phe Asn Asn Ala Lys Lys Tyr	
275 280 285	

<210> 240  
 <211> 287  
 <212> PRT  
 <213> Helicobacter pylori

<220>  
 <221> misc\_feature  
 <222> (181)..(181)  
 <223> The 'Xaa' at location 181 stands for Gly, or Arg.

<220>  
 <221> misc\_feature  
 <222> (191)..(191)  
 <223> The 'Xaa' at location 191 stands for Leu.

<220>  
 <221> misc\_feature  
 <222> (209)..(209)  
 <223> The 'Xaa' at location 209 stands for Asn, or Ile.

<400> 240

Met Lys Thr Phe Lys Asn Leu Leu Cys Phe Ser Leu Ile Ala Met Ser
1 5 10 15

Trp Leu Gln Ala Asp Met Leu Asp Asn Phe Thr Arg Ala Ile Asn Ser
20 25 30

Tyr Thr Thr Lys Lys Leu Asn Glu Ile Lys Asp Gln Val Asn Ser Ala
35 40 45

Asn Pro Thr Lys Asn His Asn Thr Thr Tyr Asn Ala Asn Gly Met Leu
50 55 60

Ile Asn Ile Asp Cys Lys Val Leu Lys Asn Asn Phe Tyr Ser Val Cys
65 70 75 80



Tyr Ser Ser Glu Leu Lys Asn Pro Ile Tyr Gly Val Ser Val Leu Phe  
85 90 95

Gly Asp Leu Val Asp Lys Asn Asn Ile Glu Lys Arg Tyr Glu Phe Lys  
100 105 110

Thr Asp Thr Arg Leu Ala Lys Tyr Gln Gln Ala Thr Thr Gln Asp Tyr  
115 120 125

Thr Arg Ser Gly Phe Asp Arg Gly His Phe Val Ala Asn Asp Ala Ser  
130 135 140

Phe Asp Phe Ala Ser Asn Pro Leu Arg Glu Thr Tyr Arg Met Thr Asn  
145 150 155 160

Ile Thr Pro Glu Ala Lys Asn Thr Asn Arg His Ser Val Leu Leu Val  
165 170 175

Glu Lys Glu Gly Xaa Asn Leu Ala Arg Lys Tyr His Gln Val Xaa Val  
180 185 190

Glu Glu Leu Thr Ile Ile Lys Gln Gly Tyr Arg Thr Phe Ser Pro Lys  
195 200 205

Xaa Ile Ala Ile Pro Ser Gly Phe Trp Tyr His Tyr Asp Thr Arg Leu  
210 215 220

Thr Asp Ser Tyr Glu Asn Ala Lys Ser Glu Cys Phe Tyr Ile Pro Asn  
225 230 235 240

Asp Asn Gln Asn Tyr Pro Leu Gln Glu Met Arg Lys Asp Cys Lys Gly  
245 250 255

Tyr Glu Arg Val Glu Lys Gln Val Val Phe Lys Asn Asn Lys Asn Thr  
260 265 270

Glu Leu Asn Glu Leu Pro Lys Tyr Phe Asn Asn Ala Lys Lys Tyr  
275 280 285

<210> 241  
<211> 1072  
<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (2)..(1072)

<400> 241

t	tgt	att	ttt	tat	tgg	ctc	ttt	ttt	acg	act	cct	tac	att	gta	ggc	gat	49
	Cys	Ile	Phe	Tyr	Trp	Leu	Phe	Phe	Thr	Thr	Pro	Tyr	Ile	Val	Gly	Asp	
1					5					10					15		

att	ttg	caa	ttg	aaa	ttt	atc	cgt	caa	aag	ctc	tgc	gag	aag	ccc	gtt	97
Ile	Leu	Gln	Leu	Lys	Phe	Ile	Arg	Gln	Lys	Leu	Cys	Glu	Lys	Pro	Val	
		20						25					30			

tta	ctc	cca	caa	aag	gat	tat	gaa	gaa	gcg	gga	aat	tat	gcc	att	agg	145
Leu	Leu	Pro	Gln	Lys	Asp	Tyr	Glu	Glu	Ala	Gly	Asn	Tyr	Ala	Ile	Arg	
		35					40					45				

aaa	atg	caa	tta	tcc	att	att	tct	caa	att	tta	gac	ggg	ata	atc	ttt	193
Lys	Met	Gln	Leu	Ser	Ile	Ile	Ser	Gln	Ile	Leu	Asp	Gly	Ile	Ile	Phe	
	50					55					60					

gct	ggt	tgg	gtc	ttt	ttt	ggt	ttg	acg	cat	tta	gaa	gat	ttg	acg	cat	241
Ala	Gly	Trp	Val	Phe	Phe	Gly	Leu	Thr	His	Leu	Glu	Asp	Leu	Thr	His	
65					70					75					80	

tat	tta	aac	ctt	cct	gaa	acg	cta	ggt	tac	ttg	gtg	ttt	gcc	ttg	ttg	289
Tyr	Leu	Asn	Leu	Pro	Glu	Thr	Leu	Gly	Tyr	Leu	Val	Phe	Ala	Leu	Leu	
			85						90					95		

ttt	tta	gcg	att	caa	agc	ggt	tta	gct	tta	ccc	att	agc	tac	tac	acc	337
Phe	Leu	Ala	Ile	Gln	Ser	Val	Leu	Ala	Leu	Pro	Ile	Ser	Tyr	Tyr	Thr	
			100					105					110			

acc	atg	cat	ttg	gat	aag	gaa	ttt	ggc	ttt	tct	aag	gtg	agt	tta	tcg	385
Thr	Met	His	Leu	Asp	Lys	Glu	Phe	Gly	Phe	Ser	Lys	Val	Ser	Leu	Ser	
		115					120					125				

ttg	ttt	ttc	aag	gat	ttt	ttc	aaa	ggg	tta	tcg	ctc	act	tta	agc	gtg	433
Leu	Phe	Phe	Lys	Asp	Phe	Phe	Lys	Gly	Leu	Ser	Leu	Thr	Leu	Ser	Val	
	130					135					140					

ggg	ttg	ttg	ttg	att	tac	act	ctt	att	atg	atc	att	gaa	cat	gtg	gag	481
Gly	Leu	Leu	Leu	Ile	Tyr	Thr	Leu	Ile	Met	Ile	Ile	Glu	His	Val	Glu	
145					150					155					160	

cat	tgg	gag	att	agc	tca	ttt	ttt	gtc	gtg	ttt	ggt	ttt	atg	ata	tta	529
His	Trp	Glu	Ile	Ser	Ser	Phe	Phe	Val	Val	Phe	Val	Phe	Met	Ile	Leu	
				165					170					175		

gct	aat	ctt	ttt	tac	cct	aaa	atc	gct	cag	ctt	ttc	aac	caa	ttc	acc	577
Ala	Asn	Leu	Phe	Tyr	Pro	Lys	Ile	Ala	Gln	Leu	Phe	Asn	Gln	Phe	Thr	
			180					185					190			

ccc	ttg	aat	aat	agg	gat	ttg	gag	agt	caa	att	gag	agc	atg	atg	gat	625
Pro	Leu	Asn	Asn	Arg	Asp	Leu	Glu	Ser	Gln	Ile	Glu	Ser	Met	Met	Asp	
		195					200					205				
aag	gtg	ggt	ttt	aaa	tcc	gaa	ggc	att	ttt	gtg	atg	gac	gct	agc	aag	673
Lys	Val	Gly	Phe	Lys	Ser	Glu	Gly	Ile	Phe	Val	Met	Asp	Ala	Ser	Lys	
	210					215					220					
agg	gat	ggg	cgt	ttg	aat	gcg	tat	ttt	ggg	ggc	ttg	ggt	aaa	aac	aag	721
Arg	Asp	Gly	Arg	Leu	Asn	Ala	Tyr	Phe	Gly	Gly	Leu	Gly	Lys	Asn	Lys	
225					230					235					240	
cgg	gtg	gtg	ttg	ttt	gac	act	ttg	att	tct	aaa	gtt	ggg	aca	gaa	ggg	769
Arg	Val	Val	Leu	Phe	Asp	Thr	Leu	Ile	Ser	Lys	Val	Gly	Thr	Glu	Gly	
			245						250					255		
ctt	tta	gcc	att	tta	ggg	cat	gaa	tta	ggg	cat	ttt	aaa	aat	aag	gat	817
Leu	Leu	Ala	Ile	Leu	Gly	His	Glu	Leu	Gly	His	Phe	Lys	Asn	Lys	Asp	
		260						265					270			
ttg	ttg	aaa	agt	tta	ggg	att	atg	gga	ggc	ttg	ctc	gct	ctt	gtt	ttt	865
Leu	Leu	Lys	Ser	Leu	Gly	Ile	Met	Gly	Gly	Leu	Leu	Ala	Leu	Val	Phe	
		275					280					285				
gct	ctg	atc	gct	cat	ttg	cca	ccg	atc	gtt	ttt	gaa	ggc	ttt	aat	gtc	913
Ala	Leu	Ile	Ala	His	Leu	Pro	Pro	Ile	Val	Phe	Glu	Gly	Phe	Asn	Val	
	290					295					300					
tca	caa	acg	cca	gcg	agt	ttg	att	acg	att	tta	ctc	ttg	ttt	ttg	ccg	961
Ser	Gln	Thr	Pro	Ala	Ser	Leu	Ile	Thr	Ile	Leu	Leu	Leu	Phe	Leu	Pro	
305					310					315					320	
gtg	ttt	tcc	ttt	tac	gcc	atg	cct	ttg	atc	ggg	ttt	ttt	agc	cga	aag	1009
Val	Phe	Ser	Phe	Tyr	Ala	Met	Pro	Leu	Ile	Gly	Phe	Phe	Ser	Arg	Lys	
				325					330					335		
aat	gaa	tac	aat	gcg	gac	aag	ttt	ggg	gcg	agt	tta	agc	tct	aaa	gag	1057
Asn	Glu	Tyr	Asn	Ala	Asp	Lys	Phe	Gly	Ala	Ser	Leu	Ser	Ser	Lys	Glu	
			340					345					350			
gtt	tta	gcc	aaa	gcg												1072
Val	Leu	Ala	Lys	Ala												
			355													

<210> 242  
 <211> 357  
 <212> PRT  
 <213> Helicobacter pylori

<400> 242

Cys	Ile	Phe	Tyr	Trp	Leu	Phe	Phe	Thr	Thr	Pro	Tyr	Ile	Val	Gly	Asp
1				5					10					15	

Ile	Leu	Gln	Leu	Lys	Phe	Ile	Arg	Gln	Lys	Leu	Cys	Glu	Lys	Pro	Val			
			20					25					30					
Leu	Leu	Pro	Gln	Lys	Asp	Tyr	Glu	Glu	Ala	Gly	Asn	Tyr	Ala	Ile	Arg			
		35					40					45						
Lys	Met	Gln	Leu	Ser	Ile	Ile	Ser	Gln	Ile	Leu	Asp	Gly	Ile	Ile	Phe			
	50					55					60							
Ala	Gly	Trp	Val	Phe	Phe	Gly	Leu	Thr	His	Leu	Glu	Asp	Leu	Thr	His			
65					70					75					80			
Tyr	Leu	Asn	Leu	Pro	Glu	Thr	Leu	Gly	Tyr	Leu	Val	Phe	Ala	Leu	Leu			
				85					90					95				
Phe	Leu	Ala	Ile	Gln	Ser	Val	Leu	Ala	Leu	Pro	Ile	Ser	Tyr	Tyr	Thr			
			100					105					110					
Thr	Met	His	Leu	Asp	Lys	Glu	Phe	Gly	Phe	Ser	Lys	Val	Ser	Leu	Ser			
		115					120					125						
Leu	Phe	Phe	Lys	Asp	Phe	Phe	Lys	Gly	Leu	Ser	Leu	Thr	Leu	Ser	Val			
	130					135					140							
Gly	Leu	Leu	Leu	Ile	Tyr	Thr	Leu	Ile	Met	Ile	Ile	Glu	His	Val	Glu			
145					150					155					160			
His	Trp	Glu	Ile	Ser	Ser	Phe	Phe	Val	Val	Phe	Val	Phe	Met	Ile	Leu			
				165					170					175				
Ala	Asn	Leu	Phe	Tyr	Pro	Lys	Ile	Ala	Gln	Leu	Phe	Asn	Gln	Phe	Thr			
			180					185					190					
Pro	Leu	Asn	Asn	Arg	Asp	Leu	Glu	Ser	Gln	Ile	Glu	Ser	Met	Met	Asp			
		195					200					205						
Lys	Val	Gly	Phe	Lys	Ser	Glu	Gly	Ile	Phe	Val	Met	Asp	Ala	Ser	Lys			
	210					215					220							
Arg	Asp	Gly	Arg	Leu	Asn	Ala	Tyr	Phe	Gly	Gly	Leu	Gly	Lys	Asn	Lys			

225		230		235		240									
Arg	Val	Val	Leu	Phe	Asp	Thr	Leu	Ile	Ser	Lys	Val	Gly	Thr	Glu	Gly
				245					250					255	
Leu	Leu	Ala	Ile	Leu	Gly	His	Glu	Leu	Gly	His	Phe	Lys	Asn	Lys	Asp
			260						265					270	
Leu	Leu	Lys	Ser	Leu	Gly	Ile	Met	Gly	Gly	Leu	Leu	Ala	Leu	Val	Phe
		275					280						285		
Ala	Leu	Ile	Ala	His	Leu	Pro	Pro	Ile	Val	Phe	Glu	Gly	Phe	Asn	Val
	290					295						300			
Ser	Gln	Thr	Pro	Ala	Ser	Leu	Ile	Thr	Ile	Leu	Leu	Leu	Phe	Leu	Pro
305					310					315					320
Val	Phe	Ser	Phe	Tyr	Ala	Met	Pro	Leu	Ile	Gly	Phe	Phe	Ser	Arg	Lys
				325						330				335	
Asn	Glu	Tyr	Asn	Ala	Asp	Lys	Phe	Gly	Ala	Ser	Leu	Ser	Ser	Lys	Glu
			340					345					350		
Val	Leu	Ala	Lys	Ala											
		355													

<210> 243  
 <211> 357  
 <212> DNA  
 <213> Helicobacter pylori

<220>  
 <221> CDS  
 <222> (1)..(357)

<400>	243																	
ttg	gaa	tcc	tat	ggg	ttg	gct	tgc	tct	gac	cgc	agg	att	att	gca	gga			48
Leu	Glu	Ser	Tyr	Gly	Leu	Ala	Cys	Ser	Asp	Arg	Arg	Ile	Ile	Ala	Gly			
1				5					10					15				
tta	gtt	gga	ata	gtc	aga	tca	atc	tgg	agc	ttt	ttt	agt	tca	aga	tat			96
Leu	Val	Gly	Ile	Val	Arg	Ser	Ile	Trp	Ser	Phe	Phe	Ser	Ser	Arg	Tyr			
			20					25					30					
caa	aga	tcc	caa	caa	aaa	aaa	gaa	gtg	gat	aag	aat	tta	cat	caa	att			144

Gln	Arg	Ser	Gln	Gln	Lys	Lys	Glu	Val	Asp	Lys	Asn	Leu	His	Gln	Ile	
		35					40					45				
tgt	gaa	aaa	att	gtg	cag	gat	gtg	aaa	agc	cga	ctt	gaa	agt	cgc	aaa	192
Cys	Glu	Lys	Ile	Val	Gln	Asp	Val	Lys	Ser	Arg	Leu	Glu	Ser	Arg	Lys	
	50					55					60					
aaa	gac	ata	tgg	gaa	aag	att	gaa	aaa	ctc	aaa	gcc	aat	ctt	aga	cct	240
Lys	Asp	Ile	Trp	Glu	Lys	Ile	Glu	Lys	Leu	Lys	Ala	Asn	Leu	Arg	Pro	
65					70					75					80	
gtt	gat	aat	tac	gaa	cgc	atg	aaa	gga	caa	ttg	aaa	gaa	gcc	cat	gaa	288
Val	Asp	Asn	Tyr	Glu	Arg	Met	Lys	Gly	Gln	Leu	Lys	Glu	Ala	His	Glu	
				85					90					95		
aaa	tta	gga	tac	atc	tct	cat	agt	atc	cat	cta	aca	ata	tca	aaa	caa	336
Lys	Leu	Gly	Tyr	Ile	Ser	His	Ser	Ile	His	Leu	Thr	Ile	Ser	Lys	Gln	
			100					105					110			
gga	gca	tgc	aat	gaa	gaa	tga										357
Gly	Ala	Cys	Asn	Glu	Glu											
			115													

<210> 244  
 <211> 118  
 <212> PRT  
 <213> Helicobacter pylori

<400> 244

Leu	Glu	Ser	Tyr	Gly	Leu	Ala	Cys	Ser	Asp	Arg	Arg	Ile	Ile	Ala	Gly
1				5					10					15	
Leu	Val	Gly	Ile	Val	Arg	Ser	Ile	Trp	Ser	Phe	Phe	Ser	Ser	Arg	Tyr
			20					25					30		
Gln	Arg	Ser	Gln	Gln	Lys	Lys	Glu	Val	Asp	Lys	Asn	Leu	His	Gln	Ile
		35					40					45			
Cys	Glu	Lys	Ile	Val	Gln	Asp	Val	Lys	Ser	Arg	Leu	Glu	Ser	Arg	Lys
	50					55					60				
Lys	Asp	Ile	Trp	Glu	Lys	Ile	Glu	Lys	Leu	Lys	Ala	Asn	Leu	Arg	Pro
65					70					75					80
Val	Asp	Asn	Tyr	Glu	Arg	Met	Lys	Gly	Gln	Leu	Lys	Glu	Ala	His	Glu
				85					90					95	

Lys Leu Gly Tyr Ile Ser His Ser Ile His Leu Thr Ile Ser Lys Gln  
100 105 110

Gly Ala Cys Asn Glu Glu  
115

<210> 245  
<211> 1251  
<212> DNA  
<213> Helicobacter pylori

<220>  
<221> CDS  
<222> (1)..(1251)

<400> 245  
gat caa aaa acg gct caa aaa atg ctc gct gat ttg agc gtg gta ggg 48  
Asp Gln Lys Thr Ala Gln Lys Met Leu Ala Asp Leu Ser Val Val Gly  
1 5 10 15  
gcg tat ctt aaa aaa caa caa gag aat gaa aag gct caa agc cct tat 96  
Ala Tyr Leu Lys Lys Gln Gln Glu Asn Glu Lys Ala Gln Ser Pro Tyr  
20 25 30  
tac aga agc aac aac tat tac aac tct tac tat agc cct tac tat agc 144  
Tyr Arg Ser Asn Asn Tyr Tyr Asn Ser Tyr Tyr Ser Pro Tyr Tyr Ser  
35 40 45  
cct tat tat ggc atg tat ggc atg ggc atg tat gat ttt tat gac ttt 192  
Pro Tyr Tyr Gly Met Tyr Gly Met Gly Met Tyr Asp Phe Tyr Asp Phe  
50 55 60  
tat gat ggc atg tac ggg ttc tac cct aac atg ttg ttt atg atg caa 240  
Tyr Asp Gly Met Tyr Gly Phe Tyr Pro Asn Met Leu Phe Met Met Gln  
65 70 75 80  
gtt caa gat tac ttg atg tta gaa aat tac atg tat gca ctc gat caa 288  
Val Gln Asp Tyr Leu Met Leu Glu Asn Tyr Met Tyr Ala Leu Asp Gln  
85 90 95  
gaa gag att tta gac cat gac gct tct aat aat caa ctt gat acg cct 336  
Glu Glu Ile Leu Asp His Asp Ala Ser Asn Asn Gln Leu Asp Thr Pro  
100 105 110  
act gat gat gac aga gac gat aag gac gat aaa tcc ttg cag cag gca 384  
Thr Asp Asp Asp Arg Asp Asp Lys Asp Asp Lys Ser Leu Gln Gln Ala  
115 120 125  
aat ctt atg agc ttt tat cgt gat ccc aaa ttc agc aaa ggc att caa 432  
Asn Leu Met Ser Phe Tyr Arg Asp Pro Lys Phe Ser Lys Gly Ile Gln  
130 135 140

acc aac cgc ttg aat agc gct tta gtc aat tta gac aac agt cgc atg	480
Thr Asn Arg Leu Asn Ser Ala Leu Val Asn Leu Asp Asn Ser Arg Met	
145 150 155 160	
ctc aaa gac aat tcg ctt ttc cac act aaa gcc atg cct act aaa agc	528
Leu Lys Asp Asn Ser Leu Phe His Thr Lys Ala Met Pro Thr Lys Ser	
165 170 175	
gtg gat gcg ata act tct caa gcc aaa gag ctt aac cat tta gtg ggg	576
Val Asp Ala Ile Thr Ser Gln Ala Lys Glu Leu Asn His Leu Val Gly	
180 185 190	
caa atc aaa gaa atg aag caa gat ggg gcg agt cct agt aag att gat	624
Gln Ile Lys Glu Met Lys Gln Asp Gly Ala Ser Pro Ser Lys Ile Asp	
195 200 205	
tca gtg gtt cat aaa gct atg gaa gtg aga gac aaa tta gac aat aat	672
Ser Val Val His Lys Ala Met Glu Val Arg Asp Lys Leu Asp Asn Asn	
210 215 220	
ctc aac caa tta gac aat gac tta aaa gat caa aaa ggg ctt tca agc	720
Leu Asn Gln Leu Asp Asn Asp Leu Lys Asp Gln Lys Gly Leu Ser Ser	
225 230 235 240	
gag caa caa gcc caa gtg gat aaa gcc cta gac agc gtg caa caa tta	768
Glu Gln Gln Ala Gln Val Asp Lys Ala Leu Asp Ser Val Gln Gln Leu	
245 250 255	
agc cat agc agc gat gtg gtg ggg aat tat tta gac ggg agt ttg aaa	816
Ser His Ser Ser Asp Val Val Gly Asn Tyr Leu Asp Gly Ser Leu Lys	
260 265 270	
att gat ggc gat gat aga gac gat ttg aat gat gcg atg aat aac ccc	864
Ile Asp Gly Asp Asp Arg Asp Asp Leu Asn Asp Ala Met Asn Asn Pro	
275 280 285	
atg caa caa cct gca caa caa acg cct att aac aac atg gac aac acc	912
Met Gln Gln Pro Ala Gln Gln Thr Pro Ile Asn Asn Met Asp Asn Thr	
290 295 300	
cat gca aat gac agc aaa gat caa ggg agt aac gca ctc ata aac cct	960
His Ala Asn Asp Ser Lys Asp Gln Gly Ser Asn Ala Leu Ile Asn Pro	
305 310 315 320	
aac aac gcc act aac acc gat gac act cac acc gac gat act cac acc	1008
Asn Asn Ala Thr Asn Thr Asp Asp Thr His Thr Asp Asp Thr His Thr	
325 330 335	
gac act aac acc aca aac gat acc agc act act gac acc ccc act gat	1056
Asp Thr Asn Thr Thr Asn Asp Thr Ser Thr Thr Asp Thr Pro Thr Asp	
340 345 350	
gat aaa gat gct agc ggc aac aat acc ggc gat atg aat aac acg gac	1104
Asp Lys Asp Ala Ser Gly Asn Asn Thr Gly Asp Met Asn Asn Thr Asp	
355 360 365	



acc ggc aat act gat aac ggt aac act gat gat ata agc aac atg aac	1152
Thr Gly Asn Thr Asp Asn Gly Asn Thr Asp Asp Ile Ser Asn Met Asn	
370 375 380	
aac ggc aac gat gat gcg ggt aac gct aat gac gac atg ggt aat agc	1200
Asn Gly Asn Asp Asp Ala Gly Asn Ala Asn Asp Asp Met Gly Asn Ser	
385 390 395 400	
aac gac atg ggc gat gac atg aat aat gcg aac gac atg aac gat gac	1248
Asn Asp Met Gly Asp Asp Met Asn Asn Ala Asn Asp Met Asn Asp Asp	
405 410 415	
atg	1251
Met	

<210> 246  
 <211> 417  
 <212> PRT  
 <213> Helicobacter pylori

<400> 246

Asp Gln Lys Thr Ala Gln Lys Met Leu Ala Asp Leu Ser Val Val Gly	
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Ala Tyr Leu Lys Lys Gln Gln Glu Asn Glu Lys Ala Gln Ser Pro Tyr	
20 25 30	
Tyr Arg Ser Asn Asn Tyr Tyr Asn Ser Tyr Tyr Ser Pro Tyr Tyr Ser	
35 40 45	
Pro Tyr Tyr Gly Met Tyr Gly Met Gly Met Tyr Asp Phe Tyr Asp Phe	
50 55 60	
Tyr Asp Gly Met Tyr Gly Phe Tyr Pro Asn Met Leu Phe Met Met Gln	
65 70 75 80	
Val Gln Asp Tyr Leu Met Leu Glu Asn Tyr Met Tyr Ala Leu Asp Gln	
85 90 95	
Glu Glu Ile Leu Asp His Asp Ala Ser Asn Asn Gln Leu Asp Thr Pro	
100 105 110	
Thr Asp Asp Asp Arg Asp Asp Lys Asp Asp Lys Ser Leu Gln Gln Ala	
115 120 125	

Asn Leu Met Ser Phe Tyr Arg Asp Pro Lys Phe Ser Lys Gly Ile Gln  
 130 135 140

Thr Asn Arg Leu Asn Ser Ala Leu Val Asn Leu Asp Asn Ser Arg Met  
 145 150 155 160

Leu Lys Asp Asn Ser Leu Phe His Thr Lys Ala Met Pro Thr Lys Ser  
 165 170 175

Val Asp Ala Ile Thr Ser Gln Ala Lys Glu Leu Asn His Leu Val Gly  
 180 185 190

Gln Ile Lys Glu Met Lys Gln Asp Gly Ala Ser Pro Ser Lys Ile Asp  
 195 200 205

Ser Val Val His Lys Ala Met Glu Val Arg Asp Lys Leu Asp Asn Asn  
 210 215 220

Leu Asn Gln Leu Asp Asn Asp Leu Lys Asp Gln Lys Gly Leu Ser Ser  
 225 230 235 240

Glu Gln Gln Ala Gln Val Asp Lys Ala Leu Asp Ser Val Gln Gln Leu  
 245 250 255

Ser His Ser Ser Asp Val Val Gly Asn Tyr Leu Asp Gly Ser Leu Lys  
 260 265 270

Ile Asp Gly Asp Asp Arg Asp Asp Leu Asn Asp Ala Met Asn Asn Pro  
 275 280 285

Met Gln Gln Pro Ala Gln Gln Thr Pro Ile Asn Asn Met Asp Asn Thr  
 290 295 300

His Ala Asn Asp Ser Lys Asp Gln Gly Ser Asn Ala Leu Ile Asn Pro  
 305 310 315 320

Asn Asn Ala Thr Asn Thr Asp Asp Thr His Thr Asp Asp Thr His Thr  
 325 330 335

Asp Thr Asn Thr Thr Asn Asp Thr Ser Thr Thr Asp Thr Pro Thr Asp

340

345

350

Asp Lys Asp Ala Ser Gly Asn Asn Thr Gly Asp Met Asn Asn Thr Asp  
 355 360 365

Thr Gly Asn Thr Asp Asn Gly Asn Thr Asp Asp Ile Ser Asn Met Asn  
 370 375 380

Asn Gly Asn Asp Asp Ala Gly Asn Ala Asn Asp Asp Met Gly Asn Ser  
 385 390 395 400

Asn Asp Met Gly Asp Asp Met Asn Asn Ala Asn Asp Met Asn Asp Asp  
 405 410 415

Met

<210> 247  
 <211> 3880  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> chimeric vector

<400> 247  
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 cttgagcctc ctccaaccga aatagaaggg cgctgcgctt attatttcat tcagtcacgc 120  
 gctttcataa tctaacagac aacatcttcg ctgcaaagcc acgctacgcc aagggttttt 180  
 acgctacgat aacgcctggt ttaacgatta tgccgataac taaacgaaat aaacgctaaa 240  
 acgtctcaga aacgatthttg agacgtttta ataaaaaatc gctagtccga ggcctcgacc 300  
 cgattcaciaa aaaataggca cacgaaaaac aagttaaggg atgcagttta tgcatectcg 360  
 agccgcggct cgagggtgat tcattctgct aaccagtaag gcaaccccg cagcctagcc 420  
 gggtcctcaa cgacaggagc acgatcatgc gcacccgtgg ccaggacca acgctgcccg 480  
 agatgcgccg cgtgcggctg ctggagatgg cggacgcgat ggatatgttc tgccaagggt 540  
 tggtttgccg attcacagtt ctccgcaaga attgattggc tccaattctt ggagtgggtga 600  
 atccgttagc gaggtgccgc cggcttccat tcaggctcag gtggcccggc tccatgcacc 660  
 gcgacgcaac gcggggaggc agacaaggta tagggcggcg cctacaatcc atgccaaccc 720

gttccatgtg	ctcgccgagg	cggcataaat	cgccgtgacg	atcagcggtc	cagtgatcga	780
agttaggctg	gtaagagccg	cgagcgatcc	ttgaagctgt	ccctgatggg	cgtcatctac	840
ctgcctggac	agcatggcct	gcaacgcggg	catcccgatg	ccgccggaag	cgagaagaat	900
cataatgggg	aaggccatcc	agcctcgcg	cgcgaaacgcc	agcaagacgt	agcccagcgc	960
gtcggccgcc	atgccggcga	taatggcctg	cttctcgccg	aaacgtttgg	tggcgggacc	1020
agtgacgaag	gcttgagcga	gggcgtgcaa	gattccgaat	accgcaagcg	acaggccgat	1080
catcgtcg	ctccagcgaa	agcggtcctc	gccgaaaatg	accagagcgc	ctgccggcac	1140
ctgtcctacg	agttgcatga	taaagaagac	agtcataagt	gcggcgacga	tagtcatgcc	1200
ccgcgcccac	cggaaggagc	tgactggggt	gaaggctctc	aagggcacgc	gtcgacgctc	1260
tcccttatgc	gactcctgca	ttaggaagca	gccagtagtg	aggttgaggc	cgttgagcac	1320
cgccgcccga	aggaatggtg	catgcaagga	gatggcgccc	aacagtcccc	cggccacggg	1380
gcctgccacc	ataccacgc	cgaacaagc	gctcatgagc	ccgaagtggc	gagcccgatc	1440
ttcccatcg	gtgatgtcgg	cgatataggc	gccagcaacc	gcacctgtgg	cgccggtgat	1500
gccggccacg	atgcgtccgg	cgtagaggat	ccacaggacg	ggtgtgggtc	ccatgatcgc	1560
gtagtcgata	gtggctccaa	gtagcgaagc	gagcaggact	gggcggcggc	caaagcggtc	1620
ggacagtgc	ccgagaacgg	gtgcgcatag	aaattgcatc	aacgcatata	gcgctagcag	1680
cacgccatag	tgactggcga	tgctgtcgga	atggacgata	tcccgcaaga	ggcccggcag	1740
taccggcata	accaagccta	tgctacagc	atccagggtg	acggtgccga	ggatgacgat	1800
gagcgcattg	ttagatttca	tacacggtgc	ctgactgcgt	tagcaattta	actgtgataa	1860
actaccgcat	taaagcttat	cgatgataag	ctgtcaaaca	tgagccatgg	ctgcgcgtaa	1920
ccaccacacc	cgccgcgctt	aatgcgccgc	tacagggcgc	gtcccatcgc	ccattcaggc	1980
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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp	
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cta cat atg ttt atc att ccc tct cgc tct atg gta ggc acg ctc tat	144
Leu His Met Phe Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr	
35 40 45	
gag ggc gat atg ctc ttt gtc aaa aaa ttt tct tac ggc atc ccc att	192
Glu Gly Asp Met Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile	
50 55 60	
cct aaa atc cca tgg att gag ctt cct gtt atg cct gat ttt aaa aat	240
Pro Lys Ile Pro Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn	
65 70 75 80	
aac ggg cat ttg ata gag ggg gat cgc cct aaa cgc ggc gaa gtg gtg	288
Asn Gly His Leu Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val	
85 90 95	
gtg ttt atc cct ccc cat gaa aaa aaa tct tac tat gtc aaa agg aat	336

Val	Phe	Ile	Pro	Pro	His	Glu	Lys	Lys	Ser	Tyr	Tyr	Val	Lys	Arg	Asn	
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Phe	Ala	Ile	Gly	Gly	Asp	Glu	Val	Leu	Phe	Thr	Ser	Glu	Gly	Phe	Tyr	
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Leu	His	Pro	Phe	Glu	Ser	Gly	Thr	Asp	Lys	Thr	Tyr	Ile	Ala	Lys	His	
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Tyr	Pro	Asp	Ala	Met	Thr	Lys	Glu	Phe	Met	Gly	Lys	Ile	Phe	Val	Leu	
145					150					155					160	
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Asn	Pro	Tyr	Lys	Ser	Lys	His	Pro	Gly	Ile	His	Tyr	Gln	Lys	Asp	Asn	
			165						170					175		
gaa	acc	ttc	cat	tta	atg	gag	cag	tta	gcc	act	caa	ggc	gcg	gaa	gct	576
Glu	Thr	Phe	His	Leu	Met	Glu	Gln	Leu	Ala	Thr	Gln	Gly	Ala	Glu	Ala	
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Asn	Ile	Ser	Met	Gln	Leu	Ile	Gln	Met	Glu	Gly	Glu	Lys	Val	Phe	Tyr	
		195					200					205				
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Lys	Lys	Ile	Asn	Asp	Asp	Glu	Phe	Phe	Met	Ile	Gly	Asp	Asn	Arg	Asp	
		210				215					220					
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Asn	Ser	Ser	Asp	Ser	Arg	Phe	Trp	Gly	Ser	Val	Ala	Tyr	Lys	Asn	Ile	
225					230					235					240	
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Val	Gly	Ser	Pro	Trp	Phe	Val	Tyr	Phe	Ser	Leu	Ser	Leu	Lys	Asn	Ser	
			245						250					255		
ctg	gaa	atg	gat	gca	gaa	aat	aac	ccc	aaa	aaa	cgc	tat	ttg	gtg	cgt	816
Leu	Glu	Met	Asp	Ala	Glu	Asn	Asn	Pro	Lys	Lys	Arg	Tyr	Leu	Val	Arg	
			260					265					270			
tgg	gag	cgc	atg	ttt	aaa	agc	gtt	gaa	ggc	tta	gaa	aaa	atc	att	aaa	864
Trp	Glu	Arg	Met	Phe	Lys	Ser	Val	Glu	Gly	Leu	Glu	Lys	Ile	Ile	Lys	
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35 40 45

Glu Gly Asp Met Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile  
50 55 60

Pro Lys Ile Pro Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn  
65 70 75 80

Asn Gly His Leu Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val  
85 90 95

Val Phe Ile Pro Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn  
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Phe Ala Ile Gly Gly Asp Glu Val Leu Phe Thr Ser Glu Gly Phe Tyr  
115 120 125

Leu His Pro Phe Glu Ser Gly Thr Asp Lys Thr Tyr Ile Ala Lys His  
130 135 140

Tyr Pro Asp Ala Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu  
145 150 155 160

Asn Pro Tyr Lys Ser Lys His Pro Gly Ile His Tyr Gln Lys Asp Asn  
165 170 175

Glu Thr Phe His Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala  
180 185 190

Asn Ile Ser Met Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr  
195 200 205

Lys Lys Ile Asn Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp  
210 215 220

Asn Ser Ser Asp Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile  
225 230 235 240

Val Gly Ser Pro Trp Phe Val Tyr Phe Ser Leu Ser Leu Lys Asn Ser  
245 250 255

Leu Glu Met Asp Ala Glu Asn Asn Pro Lys Lys Arg Tyr Leu Val Arg  
260 265 270

Trp Glu Arg Met Phe Lys Ser Val Glu Gly Leu Glu Lys Ile Ile Lys  
275 280 285

Lys Glu Lys Ala Thr His  
290